



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 98953

TO: Phillip Gambel
Location: 8b03 / 9e12
Monday, July 21, 2003
Art Unit: 1644
Phone: 308-3997
Serial Number: 09 / 751797

From: Jan Delaval
Location: Biotech-Chem Library
CM1-1E07
Phone: 308-4498

jan.delaval@uspto.gov

Search Notes

09/751797

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

48953

Delaval, Jan

From: Gambel, Phillip
Sent: Wednesday, July 16, 2003 10:25 AM
To: Delaval, Jan
Subject: 09 / 751,797 decloux brief

jan

please perform a sequence and a sequence interference search for

09 / 751,797 dumotier brief

note that two of the squences are genomic sequences

thanx

phillip gambel
art unit 1644
308-3997

1644 maiblox 9e12

- 1) SEQ ID NO: 7
- 2) SEQ ID NO: 8
- 3) SEQ ID NO: 24
- 4) SEQ ID NO: 25

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

Access DB# 98953

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name _____ Examiner # _____ Date: _____
An Unit _____ Phone Number 30 _____ Serial Number _____
Mail Box and Bldg. Room Location _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

ADDITIONAL INFORMATION
800-000-0000 - 2000 FAX
ADDITIONAL INFORMATION
ADDITIONAL INFORMATION
ADDITIONAL INFORMATION

STAFF USE ONLY

Searcher _____
Searcher Phone # 4496
Searcher Location _____
Date Searcher Received 7/16/03
Date Completed 7/21/03
Searcher Prep & Review Time _____
Client Prep Time 20
Billing Time 15

Type of Search

NA Sequence (#) ✓ STN _____
AA Sequence (#) _____ Dialog _____
Structure (#) _____ Questral Orbit _____
Bibliographic _____ Dr. J. H. _____
Litigation _____ ADAMS Nexis _____
Fulltext _____ Sequence Systems ✓
Patent Family _____ WWW Internet _____
Other _____ Other Methods _____

Vendors and cost where applicable

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:06:30 ; Search time 979.633 Seconds

(without alignments)
18499.535 Million cell updates/sec

Title: US-09-751-797-7

Perfect score: 1119
Sequence: 1 taacagcgtctctctctcac.....tgcatacataaaaaaaaa 1119

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rpod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	618	55.2	700	11	AK005228 Mus muscu
2	173	15.5	256	9	AV030414 AV030414
3	76.8	6.9	562	17	AZ449260 1M0247321
4	76	6.8	1101	17	CNS0056VL AL069706 Drosophi1
5	73.8	6.6	637	17	CNS036CC AL229845 Tetraodon
6	71.2	6.4	1092	17	CNS020X7 AL175696 Tetraodon

Result No.	Score	Query Match	Length	ID	Description
7	71.2	6.4	1101	17	CNS0039G AL063921 Drosophi1
8	71	6.3	1092	17	CNS020K7 AL175696 Tetraodon
9	70.8	6.3	1043	17	CNS0145P AL107735 Drosophi1
10	70.8	6.3	1101	17	CNS016L1 AL106896 Drosophi1
11	70.2	6.3	1201	17	CNS016E1 AL106621 Drosophi1
12	70	6.3	1101	17	CNS00E07 AL069440 Drosophi1
13	69.4	6.2	1101	17	CNS00E0L AL069526 Drosophi1
14	69.2	6.2	1101	17	CNS000YWL AL066927 Drosophi1
15	69.2	6.2	1101	17	CNS017Z0 AL108704 Drosophi1
16	68.8	6.1	987	17	CNS014PQ AL104456 Drosophi1
17	68.8	6.1	1101	17	CNS00EVL AL069706 Drosophi1
18	67.8	6.1	928	17	CNS00DKY AL071865 Drosophi1
19	67.8	6.1	1083	12	BF271806 BF271806 GA_EB001
20	67.8	6.1	1225	17	CNS0161D AL106571 Drosophi1
21	67.6	6.0	340	9	AL513755 AL513755
22	67.6	6.0	1203	17	CNS015WU AL106008 Drosophi1
23	67.4	6.0	843	17	CNS00CS1 AL059666 Drosophi1
24	67	6.0	1101	17	CNS00FMC AL070972 Drosophi1
25	66.6	6.0	1101	17	CNS00BO1 AL057419 Drosophi1
26	66.2	5.9	945	17	CNS04D0K AL285149 Tetraodon
27	65.8	5.9	713	17	CNS06C1J AL392861 T7 end of
28	65.6	5.9	1101	17	CNS001F8 AL060732 Drosophi1
29	65.6	5.9	1190	17	CNS020N7 AL206908 Tetraodon
30	65.6	5.8	1190	17	CNS020N7 AL206908 Tetraodon
31	65.4	5.8	1101	17	CNS016L1 AL106896 Drosophi1
32	64.4	5.8	836	17	CNS02WQ2 AL1217379 Tetraodon
33	64	5.7	1101	17	CNS00E0L AL069526 Drosophi1
34	63.8	5.7	1029	17	CNS01ZGM AL174271 Tetraodon
35	63.8	5.7	1225	17	CNS0161D AL106601 Drosophi1
36	63.6	5.7	958	17	CNS0074D AL066801 Drosophi1
37	63.2	5.6	1101	17	CNS0039G AL063921 Drosophi1
38	63.2	5.6	1101	17	CNS003BD AL064091 Drosophi1
39	62.8	5.6	895	17	CNS06FSV AL396821 T7 end of
40	62.8	5.6	1043	17	CNS0145P AL103735 Drosophi1
41	62.6	5.6	804	17	A0895941 HS_5439 A
42	62.6	5.6	1029	17	CNS01ZGM AL174271 Tetraodon
43	62.2	5.6	732	17	AQ325717 AQ325717
44	62.2	5.6	981	17	CNS02BD8 AL189701 Tetraodon
45	62.2	5.6	1101	17	CNS00E07 AL069440 Drosophi1

ALIGNMENTS

RESULT 1
LOCUS AK005228 700 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500012D04:interleukin 10-related T cell-derived inducible factor, full insert sequence.
ACCESSION AK005228
VERSION AK005228.1 GI:12837639
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain: C57BL/6J) adult male cerebellum cDNA to mRNA, clone:1500012D04.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scleroglossa; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL MEDLINE
PUBMED

[illegible]

Db		697 CA 698	
RESULT 2			
LOCUS			
AV030414		256 bp	mRNA linear EST 31-AUG-1999
DEFINITION			
AV030414 Mus musculus adult C57BL/6J cerebellum Mus musculus cDNA clone 1500012D04, mRNA sequence.			
ACCESSION			
AV030414			
VERSION			
AV030414.1		GI:4829962	
KEYWORDS			
EST.			
SOURCE			
ORGANISM			
Mus musculus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE			
AUTHORS			
Carninci, P., Shibata, K., Ozawa, Y., Kono, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Horii, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Macaya, Y., Matsushima, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Suganara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y., Tomimaga, N., Muramatsu, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.			
TITLE			
JOURNAL			
Riken Mouse ESTs			
COMMENT			
Unpublished (1999)			
Contact: Chie Owa			
Genome Science Laboratory			
RIKEN			
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan			
Tel.: 81-298-36-9145			
Fax: 81-298-36-9098			
Email: genome-res@cc.riken.go.jp			
Thermotabilization and thermostabilization of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNAs (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))			
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))			
Please visit our web site (http://genome.riken.go.jp) for further details.			
FEATURES			
source			
location/Qualifiers			
1..256			
/organism="Mus musculus"			
/strain="C57BL/6J"			
/db_xref="taxon:10090"			
/clone_1ib="1500012D04"			
/clone_1lb="Mus musculus adult C57BL/6J cerebellum"			
/sex="male"			
/tissue_type="cerebellum"			
/dev_stage="adult"			
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCCCAATCTGAAGTGAGGAGCGGCCGGAATGTTTTTTTTTTTTTTTTTTTTTTTGTTCACCATCTGAAGTGAGGAGCGGCCGGAATGTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."			
Bondado."			
BASE COUNT			
ORIGIN			
88 a	29 c	41 g	98 t
Query Match	15.5%	Score 173;	DB 9; Length 256;
Best Local Similarity	90.3%;	Pred. No. 5.7e-25;	
Matches 196;	Conservative 0;	Mismatches 20;	Indels 1; Gaps 1;
992 TAGAAAAAAGCTTAGTAATTCCATTTCCAAATCCAAATATTTATATGTAAGTTAT			951
40 TGGAGAGATAGCCTATGTCATTTCTTCCATACACGATCTTATATATGAGATTAT			99

QY	1012	ATTATCTGCATATGATATTT-AGTATTAAGCAAAATATATTTATATGACAAATTAAGTATGAA	1070
Db	160	ATTATCTGCATGTTGATATTTGAGTATTAAGCAAAATATATTTATGATTAATTAAGTATGAA	219
QY	1071	ACAAGATATCTTAGGCTTTATATTAACAATGATATC	1107
Db	220	ACAAGATATCTTAGGCTTTATATTAACAATGATATC	256
RESULT 3			
LOCUS	AZ449260	562 bp	DNA linear
DEFINITION	1M0247J21F Mouse 10kb plasmid UGCGIM library Mus musculus genomic		
ACCESSION	AZ449260		
VERSION	AZ449260.1	GI:10602872	
KEYWORDS	GSS.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 562)		
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0247 row: 5 column: 21 Seq primer: CGTGTAAACGACGGCCACT Class: plasmid ends High quality sequence stop: 562. Location/Qualifiers 1. 562 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UGCGIM0247J21" /clone_1lb="Mouse 10kb plasmid UGCGIM library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnres/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473114[gb AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells		

BASE COUNT 119 a 155 c 116 g 172 t
 and selected for ampicillin resistance."

Query Match 6.9%; Score 76.8; DB 17; Length 562;
 Best Local Similarity 96.7%; Pred. No. 1.4e-05;
 Matches 89; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 304 GCTAAAGATCACTGCTTACCTGATGAGAGAGTGTCTCACTGACCTGGAGAGCTTCTG 363
 DB 472 GCTAAGATCACTGCTTACCTGATGAGAGAGTGTCTCACTGACCTGGAGAGCTTCTG 530
 QY 364 CTCCTCCAGTACGAGAGCTTCCAGCTTACAT 395
 DB 531 CTCCTCCAGTACGAGAGCTTCCAGCTTACAT 562

RESULT 4
 LOCUS CNS006VL 1101 bp DNA linear GSS 04-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC:
 BACR29B23 of RPCT-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.

ACCESSION AL069706.1 GI:4949849
 VERSION AL069706
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster.
 ORGANISM Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : sequefgenoscope.cns.fr
 - Web : www.genoscope.cns.fr)

COMMENT - Determination of this BAC end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazuo Osoegawa and
 Aaron Mamonos in Peter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCT-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1..1101
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="BACR29B23"
 /clone_id="RPCT-98"
 /note="end : T7"

BASE COUNT 419 a 91 c 60 g 299 t 232 others
 ORIGIN

Query Match 6.8%; Score 76; DB 17; Length 1101;
 Best Local Similarity 36.0%; Pred. No. 1.8e-05;
 Matches 180; Conservative 93; Mismatches 220; Indels 7; Gaps 2;

QY 620 GCTCTTCTGCTTCTTAAAAAACAATAGATCCCTGATGAGCTTTTACTTAAAG 679
 DB 4..0 SCCMMMMMMHAAATATCTCAHTTMMMMMAATWTWMAAAMAATATATWMAAA 499
 QY 680 AAGTGAAGAGCTACGTCATCATTTAGAGATTGACATGAAGTGGCTGCTAGTTG 739
 DB 500 AAAAAAAATTTTMMMMMAATWTWMAAATAAATAAATAAATAAATAAATAAATA 559

QY 740 AAAAAAATAGTGTCAAGTGTGCTGAGACCGAGGTAGCTTGATTAACCAAGA 799
 DB 560 ATAAATTAAMWATTTAAAMWATAT-ATTAAATWATTAATWATTAATTAATAAATA 617

QY 800 TTCAATGACATATTTTATTTGTCACGTATGATACAGAAATATATGCTTTAA 859
 DB 618 TTTTAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTAA 677

QY 860 ATTGTGAAGAGAGTGTACCTGCTTCTTGAAGAAAGCTTATGTAACCTCATTT 919
 DB 678 TAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 737

QY 920 CCATATCCATATTTTATATATGTAAGTTATTTATTAATTAAGTTATTTATAGT 979
 DB 738 AAAAAAATWATWATTAATTAATTAATTAATTAATTAATTAATTAATTAATW 792

QY 980 CAGTTTATTAATGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATG 1039
 DB 793 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 852

QY 1040 GCAATATATTTTATGACATTAATGAGAAACAAGATCTTATGCTTTAATAACA 1099
 DB 853 AATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 912

QY 1100 TGATATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1119
 DB 913 WAAWMAAATAAATAAATAAATA 932

RESULT 5
 LOCUS CNS036CC/ 637 bp DNA linear GSS 15-MAY-2000
 DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Orl end of clone
 215L21 of library G from Tetraodon nigroviridis, genomic survey
 sequence.

ACCESSION AL229845.1 GI:7888840
 VERSION AL229845
 GSS; genome survey sequence.
 KEYWORDS Tetraodon nigroviridis.
 SOURCE Tetraodon nigroviridis.
 ORGANISM Tetraodon nigroviridis.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 637)
 Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fitzmes,C., Wincker,P., Brottier,P., Quetier,F.,
 Saurin,W. and Weissenbach,J.
 Human gene number estimate provided by genome wide analysis using
 Tetraodon nigroviridis DNA sequence
 Unpublished

REFERENCE 2 (bases 1 to 637)
 Roest-Crollius,H., Jallion,O., Dasilva,C., Fitzmes,C., Fisher,C.,
 Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
 Weissenbach,J.
 Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis
 Unpublished

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

FEATURES
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 1..637
 /organism="Tetraodon nigroviridis"
 /db_xref="taxon:99883"
 /clone="215L21"
 /clone_id="G"

/nc="Genoscope sequence ID : C0AG215CF11SP1-end :
PUC-ori"
BASE COUNT 180 a 95 c 80 g 224 t 58 others
Origin
Query Match 6.6%; Score 73.8; DB 17; Length 637;
Best Local Similarity 43.2%; Pred. No. 5.6e-05;
Matches 144; Conservative 36; Mismatches 153; Indels 0; Gaps 0;
QY 787 ATAAACCAAGATTCATTGACAAATATTTATGTGCTAGTGTATACACAGAAAAATAA 846
Db AAAAAAAAAAAAAAAAAAAAAATTTTCTTTTCTTTTAAAAATAAAAAAWAW 570
QY 847 TGTACTTTAAAAATGTTGAAAGAGGTACCTCTATTCCTTTAGAAAAAAAGCTTA 906
Db WAAAAAAAAAAAAAAAAAWTTTWTWMAAAAAWTTTATATTTTTTTTTTAAAAA 510
QY 907 TGTAACTTCATTCATTCATTCATATATTTATATATATATATATATATATATATAC 966
Db WTTTTTTTTTAAAAAATAAATTTTTTTTMAWMTTWTTTTTTTTWTTTTTTAA 450
QY 967 ATTTATTTATATGTCAGTTATTTAAATATGATTTATTTATAGAAACATATCTGATATGA 1026
Db AAAATTTTTTTTTTTTTTTTATTTAAWMAAAWMTGCGGGAATTTTTTTTTTTT 390
QY 1027 TATTAGTATAGGCAATTAATTTATGACAAATPACTATGGAACAAGATATCTTACGC 1086
Db TTTTMMWMAAAWMAAAWMAAAWMTTTTTTMAAAAAAAWTTTMMGMMWTTWTT 330
QY 1087 TTTATATAACATGATATCATTAATAAAAAA 1119
Db TTTAAAAAAAAAAAAAAAAAAAAA 297
RESULT 6
CNS020K7/c
LOCUS
DEFINITION
Tetradon nigroviridis genome survey sequence T7 end of clone
222L1 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION
AL175696
VERSION
AL175696.1 GI:7813753
KEYWORDS
GSS; genome survey; sequence.
SOURCE
Tetradon nigroviridis.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Acartiophrya; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
REFERENCE
1 (bases 1 to 1092)
Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence
Unpublished
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 1092)
Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis
Unpublished
3 (bases 1 to 1092)
Genoscope.
JOURNAL
REFERENCE
AUTHORS
TITLE
Direct Submission
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large
scale clone and sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradon.
FEATURES
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RESULT 7
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 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

CNS00396 1101 bp DNA linear GSS 03-JUN-1999
 Drosophila melanogaster genome survey sequence Tenz end of BAC #
 BACR08K10 of Rpci-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL063921
 GSS.
 Drosophila melanogaster.
 Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : segr@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mamoser in Pictet de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named Rpci-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 Location/Qualifiers

project grant. The DNA was prepared from embryos by Alain Bucheton

melanogaster BAC library was prepared by Kazutoyo Oseegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of

TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage

<http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES
source

Location/Qualifiers
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ORIGIN

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Matches 106; Conservative 82; Mismatches 139; Indels 0; Gaps 0;

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Search completed: July 19, 2003, 19:39:03
Job time : 982.883 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:02:25 ; Search time 153.463 Seconds
(without alignments)
16420.772 Million cell updates/sec

Title: US-09-751-797-7

Perfect score: 1119

Sequence: 1 taacacagcctcctcctcctcac.....tggatcatcctcaaaaaaaaaa 1119

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1119	100.0	1119	21	Murine T cell indu
2	1119	100.0	1119	22	Mouse CDNA encodin
3	1119	100.0	1119	24	Mouse TIF alpha CD
4	1119	100.0	1119	24	Mouse T cell deriv
5	1107.8	99.0	1166	21	Murine GIL-19 prot
6	1047.8	93.6	1111	21	Murine T cell indu
7	1047.8	93.6	1111	22	Mouse CDNA for T c
8	1047.8	93.6	1111	24	Mouse TIF beta CDN
9	1047.8	93.6	1111	24	Mouse T cell deriv

10	768.4	68.7	778	22	AA099746	Mouse ZCYTO18 CDNA
11	601.4	53.7	7444	21	AA28815	Murine T cell indu
12	601.4	53.7	7445	22	AA514859	Mouse partial geno
13	601.4	53.7	7445	24	AA030628	Mouse TIF alpha ge
14	601.4	53.7	7445	24	AA027134	Mouse T cell deriv
15	555.2	49.6	5935	21	AA28818	Murine T cell indu
16	555.2	49.6	5935	22	AA514878	Mouse partial geno
17	555.2	49.6	5935	24	AA030660	Mouse TIF beta gen
18	555.2	49.6	5935	24	AA027153	Mouse T cell deriv
19	535.2	47.8	1177	21	AA081773	Human PRO10096 CDN
20	524.8	46.9	1152	22	AA092134	Nucleotide sequenc
21	524.8	46.9	1152	22	AA087053	Human anglogenesis
22	524.8	46.9	1152	24	AB195737	CDNA encoding huma
23	524.8	46.9	1152	24	ABK1847	Human PRO10096 CDN
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25	524.8	46.9	1152	24	ABK3657	Human cytokine, ZC
26	524.4	46.9	1116	22	AA097719	Human IL-TIF polyp
27	524.4	46.9	1116	22	AA083741	Human CDNA encodin
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29	521.8	46.6	1132	22	AA084310	Human interleukin-
30	520	46.6	1132	22	AA028841	Mouse secreted exp
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33	409.2	36.6	690	22	AA514875	Human TIF CDNA
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45	60.6	5.4	12025	24	AB133298	Human immune syste

ALIGNMENTS

RESULT 1	AAA28815	standard; CDNA; 1119 BP.
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DT	04-SEP-2000	(first entry)
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DE	Murine T cell inducible factor alpha CDNA.	
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KW	TIF-alpha; T cell derived inducible factor; interleukin 9; STAT; IL-9;	
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XX		

DR WPI; 2000-422495/36.
 DR P-PSDB; AAY32877.
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 PT New nucleic acid molecule encoding a T cell derived inducible factor
 PT for treating asthma, an allergy or lymphoma
 XX
 XX Claim 1; Page 33; 46pp; English.
 CC This cDNA encodes T cell derived inducible factor (TIF) alpha identified
 CC by subtraction cloning from a murine lymphoma cell line BW5147 in the
 CC presence or absence of interleukin 9 (IL-9). BW5147, can be grown in
 CC vitro, without the need to add any cytokines to its culture medium. Many
 CC IL-9 activities are mediated by activation of STAT transcription
 CC factors. The novel TIFs were expressed in the presence of IL-9, but not
 CC in its absence. TIFs induce STAT activation in cells. They can be used,
 CC e.g. in the stimulation of regeneration of targeted tissues. Their
 CC inhibitors or antagonists can be used to retard, prevent or inhibit
 CC differentiation of other tissues. The TIFs and their coding sequences are
 CC useful in the treatment of asthma, allergies and lymphoma (claimed). They
 CC are also useful for identifying compounds that inhibit or activate T cell
 CC induced factor activity in a cell (claimed).
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 Query Match 100.0%; Score 1119; DB 21; Length 1119;
 Best Local Similarity 100.0%; Pred. No. 2,1e-230;
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 AC AAS14858;
 AC AAS14858;
 DT 19-DEC-2001 (first entry)
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 XX Mouse; T cell derived inducible factor; TIFalpha; ss; anti-allergic;
 KM antileukemic; cytokine; interleukin-9; IL-9; STAT transcription factor;
 KM cancer; lymphoma; immune system disorder; allergy; asthma;
 KM acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
 KM thyroiditis; melanoma; hepatoma.
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 PA (LOUA/) LOUAHED J.

Query Match 100.0%; Score 1119; DB 24; Length 1119;
 Best Local Similarity 100.0%; Pred. No. 2,1e-230;
 Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TAAACAGGCTCTCTCTCACTTATCAAGTGTGACACTTGTGCGATCTGTAGAGGCTGTC 60
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QY 781 GACTGATTAACCAAGATTCATGCAATATTTATGTCATGATGATGATGATGATGATGATG 840
DB 781 GACTGATTAACCAAGATTCATGCAATATTTATGTCATGATGATGATGATGATGATGATG 840
QY 841 AATAAATGTAATTAATAAATGTTGAAAGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
DB 841 AATAAATGTAATTAATAAATGTTGAAAGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
QY 901 AGCTTATGTAATTCATTTCCATATCCAAATTTTATATATGTAAGTTTATATATATAT 960
DB 901 AGCTTATGTAATTCATTTCCATATCCAAATTTTATATATGTAAGTTTATATATATAT 960
QY 961 GTATACATTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
DB 961 GTATACATTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020

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QY 1021 TATGATATTTAGTATTAAGGCAATATATTTATGACATATATGAAACAGATATTC 1080
DB 1021 TATGATATTTAGTATTAAGGCAATATATTTATGACATATATGAAACAGATATTC 1080
QY 1081 TTAGCTTTATTAATAACATGATATCAATTAATAAATAAATAA 1119
DB 1081 TTAGCTTTATTAATAACATGATATCAATTAATAAATAAATAA 1119

```

RESULT 5

AAC81774
 ID AAC81774 standard; cDNA; 1166 BP.

XX AAC81774;

XX 23-FEB-2001 (first entry)

XX Murine GIL-19 protein coding sequence.

XX Mouse; GIL-19/AE289; IL-10; interleukin-10; nutrition; cell proliferation; immune stimulation; immune suppression;

XX haematopoiesis regulation; tissue growth; inflammation; cancer; ss.

XX Mus sp.

XX WO200065027-A2.

XX 02-NOV-2000.

XX 28-APR-2000; 2000MO-US11479.

XX 28-APR-1999; 99US-0131473.

XX (GENY) GENETICS INST INC.

XX Jacobs K, Fouser L, Spaulding V, Xuan D;

XX WPI; 2000-687325/67.

XX Human GIL-19 protein that shows a high degree of homology to IL (interleukin)-10, useful in upregulation of humoral immune responses,

XX as an antiinflammatory agent and as a modulator of immune responses associated with injury.

XX Disclosure; Fig 1; 60bp; English.

XX The present invention provides the protein and coding sequences for the novel human GIL-19/AE289 protein. The protein shows homology to

XX interleukin-10 (IL-10) and is assumed to be a cytokine. It can be used in the regulation of cell proliferation and differentiation,

XX haematopoiesis, immune stimulation or suppression, tissue growth and tumour inhibition. In addition, it also has uses in the treatment of

XX inflammation and in nutrition.

XX Sequence 1166 BP; 375 A; 241 C; 244 G; 306 T; 0 other;

XX Query Match 99.0%; Score 1107.8; DB 21; Length 1166;

XX Best Local Similarity 99.4%; Pred. No. 5.3e-228;

XX Matches 1112; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

QY 1 TAAACAGGCTCTCTCTCACTTATCAAGTGTGACACTTGTGCGATCTGTAGGCTGTC 60
DB 24 TAAACAGGCTCTCTCTCTCACTTATCAAGTGTGACACTTGTGCGATCTGTAGGCTGTC 83
QY 61 CTGCAAAATCTATGAGTTTTCCTTATGAGGAGCTTGTGCGCCGACGCTGCTCTC 120
DB 84 CTGCAAAATCTATGAGTTTTCCTTATGAGGAGCTTGTGCGCCGACGCTGCTCTC 143
QY 121 ATTGCTGTGGGCGCCAGAGAGCAAAATGCGCTCCGCTCAACACCGGTGCAAGCTTGTAG 180
DB 144 ATTGCTGTGGGCGCCAGAGAGCAAAATGCGCTCCGCTCAACACCGGTGCAAGCTTGTAG 203
QY 181 GTGTCCAACTTCCAGAGCGGTACATGTCACCGGACCTTATGCTGGCCAGAGAGGCC 240

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Db 204 GTGTCACACTTCACGACGACATACATGTCACACGACCTTTATGCTGGCCAGAGAGGCC 263
Qy 241 AGCCTTCAGATTAACAACAAGACGTCGGGCTCATCGGGAGAGAACTGTTCCGAGAGTC 300
Db 264 AGCCTTCAGATTAACAACAAGATGTCCGGCTCATCGGGAGAGAACTGTTCCGAGAGTC 323
Qy 301 AGTCTTAAGATCATGCTCTACCTGATAGACAGGTGCTCAACCTTCGAGAGAGCTT 360
Db 324 AGTCTTAAGATCATGCTCTACCTGATAGACAGGTGCTCAACCTTCGAGAGAGCTT 383
Qy 361 CTGCTCCCCCAGTCAGACAGGTTCACCTCAGCTACATGAGAGAGGTGTAACCTTCTCTACC 420
Db 384 CTGCTCCCCCAGTCAGACAGGTTCACCTCAGCTACATGAGAGAGGTGTAACCTTCTCTACC 443
Qy 421 AAATCAGCAATCAGCTCAGCTCCTGTCACTACATGAGAGAGGTGTAACCTCAGAG 480
Db 444 AAATCAGCAATCAGCTCAGCTCCTGTCACTACATGAGAGAGGTGTAACCTCAGAG 503
Qy 481 AATGTCAAGAGGCTGAAGAGACAGTGAAGAAAGCTTGAAGAGAGTGAAGATCAGAGCG 540
Db 504 AATGTCAAGAGGCTGAAGAGACAGTGAAGAAAGCTTGAAGAGAGTGAAGATCAGAGCG 563
Qy 541 ATTGGGGAACCTGACCTGCTGTTTATGTCTCTGAAGAAATGCTTGCCTGAGAGAGAGA 600
Db 564 ATTGGGGAACCTGACCTGCTGTTTATGTCTCTGAAGAAATGCTTGCCTGAGAGAGAGA 623
Qy 601 AGCTAGAAACGAAAGAACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
Db 624 AGCTAGAAACGAAAGAACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 683
Qy 661 TGGACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 684 TGGACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 743
Qy 721 ATGAAACCTGCTCAGTGAAGAAAGAAATATGTCTCAAGTTGCTCATGAGACAGAGGTA 780
Db 744 ATGAAACCTGCTCAGTGAAGAAAGAAATATGTCTCAAGTTGCTCATGAGACAGAGGTA 803
Qy 781 GACTGTATACCAAAAGATTCATGACATATTTTATGTCATGATGATGATGATGATGATGATG 840
Db 804 GACTGTATACCAAAAGATTCATGACATATTTTATGTCATGATGATGATGATGATGATGATG 863
Qy 841 AAATATATGATCTTAAAGAAATGTTGTAAGAGAGTAACTCTCATCTCTTGAAGAAAGAA 900
Db 864 AAATATATGATCTTAAAGAAATGTTGTAAGAGAGTAACTCTCATCTCTTGAAGAAAGAA 923
Qy 901 AGCTTATGTAACCTTCATTTCCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 960
Db 924 AGCTTATGTAACCTTCATTTCCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 983
Qy 961 GTATACATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1020
Db 984 GTATACATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1043
Qy 1021 TATGATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1080
Db 1044 TATGATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1103
Qy 1081 TTAGGCTTTAATAACACATGATATCATTAATAATAATAATAATAATAATAATAATAATA 1119
Db 1104 TTAGGCTTTAATAACACATGATATCATTAATAATAATAATAATAATAATAATAATAATA 1142

```

RESULT 6

AAA28817 standard; cDNA; 1111 BP.

AAA28817;

04-SEP-2000 (first entry)

Murine T cell inducible factor beta cDNA.

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XX TIF-beta; T cell derived inducible factor; interleukin 9; STAT; IL-9;
KW Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist; ss.
KM
XX
OS Mus sp.
PH
FT Key Location/Qualifiers
FT CDS 50..589
FT /tag= a
PN MO200024758-A1.
XX
PD 04-MAY-2000.
XX
PF 18-OCT-1999; 99MO-US24424.
XX
PR 26-OCT-1998; 98US-0178973.
PR 16-JUL-1999; 99US-0054243.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX Dumoutier L, Louhed J, Renaud J;
XX WPI; 2000-422495/36.
XX DR P-PSDB; AAY92878.
XX
PT New nucleic acid molecule encoding a T cell derived inducible factor
PT for treating asthma, an allergy or lymphoma
XX
XX Claim 1; Page 33-34; 46pp; English.
XX
CC This cDNA encodes T cell derived inducible factor (TIF) beta identified
CC by subtraction cloning from a murine lymphoma cell line BW5147 in the
CC presence or absence of interleukin 9 (IL-9). There was a great deal of
CC homology with TIF-alpha cDNA (AAA28815). The main difference was that
CC the promoters where not homologous suggesting independent regulation.
CC BW5147, can be grown in vitro, without the need to add any cytokines to
CC its culture medium. Many IL-9 activities are mediated by activation of
CC STAT transcription factors. The novel TIFs were expressed in the presence
CC of IL-9, but not in its absence. TIFs induce STAT activation in cells.
CC They can be used, e.g. in the stimulation of regeneration of targeted
CC tissues. Their inhibitors or antagonists can be used to retard, prevent
CC or inhibit differentiation of other tissues. The TIFs and their coding
CC sequences are useful in the treatment of asthma, allergies and lymphoma
CC (claimed). They are also useful for identifying compounds that inhibit or
CC activate T cell induced factor activity in a cell (claimed).
XX
XX Sequence 1111 BP; 346 A; 232 C; 236 G; 297 T; 0 other;
XX
XX Query Match 93.6%; Score 1047.8; DB 21; Length 1111;
XX Best Local Similarity 97.0%; Pred. No. 3,8e-215;
XX Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;
Qy 3 AACAGGCTCTCTCTCACTTATCACTTTGACACTTTGCGATCTCTGATGCTGCTCT 62
Db 1 AACAGGCTCTCTCTCACTTATCACTTTGACACTTTGCGATCTCTGATGCTGCTCTCT 60
Qy 63 GCAGAAATCTATAGTATTTTCCCTTATGAGGACCTTTGAGCCGAGCTGCTGCTCTCAT 122
Db 61 GCAGAAATCTATAGTATTTTCCCTTATGAGGACCTTTGAGCCGAGCTGCTGCTCTCAT 120
Qy 123 TGGCCTGTGGGCCAGAGGCAATAGCGTCCCGTCAACACCCGGGTGCAAGCTTGAAGT 182
Db 121 TGGCCTGTGGGCCAGAGGCAATAGCGTCCCGTCAACACCCGGGTGCAAGCTTGAAGT 180
Qy 183 GTCCAACTTCACAGACCGGTGACATGCTCAACCGCACCTTTATGCTGGCCAAAGAGCCAG 242
Db 181 GTCCAACTTCACAGACCGGTGACATGCTCAACCGCACCTTTATGCTGGCCAAAGAGCCAG 240
Qy 243 CTTTGCAGATTAACAACAAGACGTCGGGCTCATCGGGAGAGAACTGTTCCGAGAGAGTCAG 302
Db 241 CTTTGCAGATTAACAACAAGACGTCGGGCTCATCGGGAGAGAACTGTTCCGAGAGAGTCAG 300

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QY 303 TGCTAAAGATCACTGCTACCTGATGAAGAGGCTCACTTCAACCTCGGAAGACGTTCT 362
DB 301 TGCTAAGATCACTGCTACCTGATGAAGAGGCTCACTTCAACCTCGGAAGACATTTCT 360
QY 363 GCTCCCCCAGTCAAGAGGTTCCAGCCCTACATGACAGAGTGTACTTTCTTGACCAA 422
DB 361 GCTCCCCCAGTCAAGAGGTTCCAGCCCTACATGACAGAGTGTACTTTCTTGACCAA 420
QY 423 ACTCAGCAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
DB 421 ACTCAGCAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 483 TGCTCAAGGCTGAAGAGGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
DB 481 TGCTCAAGGCTGAAGAGGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 543 TGGGGAAGTCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
DB 541 CGGGGAAGTCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 603 CTAGAAAAGCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662
DB 601 CTAGAAAAGCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 663 GACTTTTACTTAAAGGAAAGTGAAGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
DB 661 GACTTTTACTTAAAGGAAAGTGAAGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 723 GAAACCTGGCTGAGTGAAGAAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 782
DB 721 GAAACCTGGCTGAGTGAAGAAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 783 CTGTGTAACCAAGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 842
DB 781 CTGTGTAACCAAGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 843 ATAAAGTACTTTAAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
DB 841 ATAAAGTACTTTAAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 903 CTATGTAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 962
DB 901 CTATGTAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 963 ATACATTTTATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1022
DB 961 ATACATTTTATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1023 TTGATATTT-AGTATTAAGCAAAATATTTATGACATPACTATGAAAACAAAGATATCT 1081
DB 1021 TTGATATTTAGATATTAAGCAAAATATTTATGATATTAATGAAAACAAAGATATCT 1080
QY 1082 TAGGCTTTAATAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1112
DB 1081 TAGGCTTTAATAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1111

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RESULT 7
AAS14860

ID AAS14860 standard; cDNA; 1111 BP.

XX AAS14860;

XX 19-DEC-2001 (first entry)

XX Mouse cDNA for T cell derived inducible factor, TIFbeta.

XX Mouse; T cell derived inducible factor; TIFbeta; ss; anti-IL-9; IL-9; STAT transcription factor;

XX anti-leukemic; cytokine; interleukin-9; IL-9; STAT transcription factor;

XX cancer; lymphoma; immune system disorder; allergy; asthma;

XX acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;

XX thyroiditis; melanoma; hepatoma.

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OS Mus musculus.
XX
XX US2001024652-A1.
XX
XX 27-SEP-2001.
XX
XX 29-DEC-2000; 2000US-0751797.
XX
XX 18-OCT-1999; 99US-0419568.
XX
XX 26-OCT-1998; 98US-0178973.
XX
XX 16-JUL-1999; 99US-0354243.
XX
XX (DUMC/) DUMOUTIER L.
XX (LOUH/) LOUHED J.
XX (RENA/) RENAULD J.
XX
XX Dumoutier L, Louhed J, Renauld J;
XX WPI; 2001-638496/73.
XX
XX New isolated nucleic acid molecules encoding T cell inducible factors,
XX useful as markers for expression or effect of interleukin (IL)-9 in a
XX subject and diagnosing susceptibility to asthma or allergy -
XX Claim 1, Page 14; 26pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule, which encodes
XX a T cell derived inducible factor (TIF) which are upregulated by the
XX cytokine interleukin-9 (IL-9) and induce STAT transcription factor
XX activation. The TIF proteins (or their nucleins) may be used to test IL-9
XX and/or agonists for their potency against lymphomas, immune system
XX disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
XX autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
XX or inhibit differentiation of tissue types in which they are active and
XX therefore be used to develop treatments for melanomas and hepatomas.
XX The present sequence is a cDNA for mouse TIFbeta.
XX
XX Sequence 1111 BP; 346 A; 232 C; 236 G; 297 T; 0 other;
XX
XX Query Match 93.6%; Score 1047.8; DB 22; Length 1111;
XX Best Local Similarity 97.0%; Pred. No. 3.8e-215;
XX Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

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Db	421	ACTGACGATAGCTCAGCTCCTCTGTCACATCAGTGTGATCGACGACGAAACATCCAGAGAA	480
Oy	483	TGTCGAAGGCTGGAAGAGACAGTGAATAAGCTTGGAGAGAGTGAGAGATCAGGCCAT	542
Db	481	TGTCGAAGGCTGGAAGAGACAGTGAATAAGCTTGGAGAGAGCGGAGAGATCAGGCCAT	540
Oy	543	TGGGAACTGGAACCTGCTGTTATATGCTCTGAGAAATGCTTCCGCTGAGCGAGAAAG	602
Db	541	CGGGAACTGGAACCTGCTGTTATATGCTCTGAGAAATGCTTCCGCTGAGCGAGAAAG	600
Oy	603	CTAGAAAAGAGAACTGCTCCTCTCTGCTCTTCTAATAAAGAACATAAGATCCTGAATG	662
Db	601	CTAGAAAAGAGAACTGCTCCTCTCTGCTCTTCTAATAAAGAACATAAGATCCTGAATG	660
Oy	663	GACCTTTTTCATAAGGAAAGGAGAACTAACGCTCAATCATCATTAAGATTTCAAT	722
Db	661	GACCTTTTTCATAAGGAAAGGAGAACTAACGCTCAATCATCATTAAGATTTCAAT	720
Oy	723	GAAACCTGCTCAGTTGAAAAAGAAATAGTGTCAAGTTGTCCATGAGACGAGAGTGA	782
Db	721	GAAACCTGCTCAGTTGAAAGAGAAATAGTGTCAAGTTGTCCATGAGACGAGAGTGA	780
Oy	783	CTTGATAACCAAGAGATTCAATGCAATATTTTATGTCACTGATGATACACAGAAA	842
Db	781	CTTGATAACCAAGAGATTCAATGCAATATTTTATGTCACTGATGATGCAACAGAAA	840
Oy	843	ATAATGCTCTTAAAAAAATGTTTGAAGAGAGTAACTCTCATTCCTTAGAAAAAAG	902
Db	841	AGTAGTACTTTAAAAAATGTTTGAAGAGAGTAACTCTCATTCCTCTAGAAAAAAG	900
Oy	903	CTTATGTAACCTTCATTCATATCCAAATATTTTATATATATGTAAGTTTATTTATTAAGT	962
Db	901	CCTATGTAACCTTCATTCATATCCAAATATTTTATATATGTAAGTTTATTTATTAAGT	960
Oy	963	ATACATTTATTTAATGAGCTTATTAATATGATTAATTTTATTAAGATTAATATGCTGA	1022
Db	961	ATACATTTATTTAATGAGCTTATTAATATGATTAATTTTATTAAGATTAATATGCTGATG	1020
Oy	1023	TTGATATATT-AGTATAGGCAATATATATTTATGCAATAACTATAGAAACAAAGATATCT	1082
Db	1021	TTGATATATTGAGTATTAAGCAAAATATATTTATGATTAATTAAGTATAGAAACAAAGATATCT	1080
Oy	1082	TAGGCTTATTAACACATGGAATATCATPAA	1112
Db	1081	TAGGCTTATTAACACATGGAATATCATPAA	1111

RESULT 8	
AAD30629	
ID	AAD30629 standard; cDNA; 1111 bp.
XX	
AC	AAD30629;
XX	
DT	21-MAY-2002 (first entry)
XX	
DE	Mouse TIF beta cDNA.
XX	
KW	T cell derived inducible factor; TIF; interleukin-21; IL-21; mouse
KW	STAT transcription factor; acute phase protein; inflammation; ss.
XX	
OS	Mus musculus.
XX	
PH	Key
FT	Location/Qualifiers
FT	50..589
FT	/*Cag= a
FT	/product= "Mouse TIF beta protein"
XX	
PN	W0200210393-A2.
XX	
PD	07-FEB-2002.
XX	
PF	27-JUN-2001; 2001WO-US20485.
XX	

Query Match	Best Local Similarity	97.0%	Pred. No. 3.8e-215	Mismatches 1078	Conservative 0	Mismatches 32	Indels 1	Gaps 1
XX	27-JUL-2000; 2000US-0626617.							
XX	(LUDW-) LUDWIG INST CANCER RES.							
XX	Dumoutier L, Renaud J;							
XX	WPI: 2002-195964/25.							
XX	P-PSDB; AAE19236.							
XX	Stimulating expression of STAT transcription factor and inducing							
XX	production of acute phase protein in a cell, involves contacting a cell							
XX	capable of expressing STAT with T cell derived inducible factors -							
XX	Example 9; Page 53; 64pp; English.							
XX	The invention relates to nucleic acid molecules encoding T cell							
XX	derived inducible factors (TIFs) also known as interleukin-21 (IL-21).							
XX	TIF polynucleotides are upregulated by the cytokine, IL-9, IL-TIF or							
XX	IL-21 molecules are implicated in activation of STAT transcription							
XX	factors, acute phase proteins and inflammation. The present sequence							
XX	is mouse TIF beta cDNA.							
XX	Sequence 1111 BP; 346 A; 232 C; 236 G; 297 T; 0 other;							
QY	Query Match	93.6%	Score 1047.8	DB 24	Length 1111			
Db	1 AACAGGCTCTCTCTCACTTATCAACTGTGCGATCTGTGATGGCTGCT							
QY	63 GCAGAAATCTATGAGTTTTCCTTATGGGCACTTTGGCCGACCTGCTCTTCTCAT							
Db	61 GCAGAAATCTATGAGTTTTCCTTATGGGCACTTTGGCCGACCTGCTCTTCTCAT							
QY	123 TGCCCTGTGGGCCCGAGGCGAAATGCGCTGCGCTCAACCCGGTGCACGTTGAGGT							
Db	121 TGCCCTGTGGGCCCGAGGCGAAATGCGCTGCGCTCAACCCGGTGCACGTTGAGGT							
QY	183 GTCCAACTTTCAGACGCGCTACATGCTCAACCGCACTTTATGCTGGCCAGAGGCCAG							
Db	181 GTCCAACTTTCAGACGCGCTACATGCTCAACCGCACTTTATGCTGGCCAGAGGCCAG							
QY	243 CCTTGACATTAACAACAGACAGTCCGCTCATCGGGAGAAACTGTTCCGAGAGTCA							
Db	241 CCTTGACATTAACAACAGACAGTCCGCTCATCGGGAGAAACTGTTCCGAGAGTCA							
QY	303 TGCTAAAGATCAGTCTCACTCTGATGAACAGGTCCTCACTTACCTCGAAACGTTCT							
Db	301 TGCTAAAGATCAGTCTCACTCTGATGAACAGGTCCTCACTTACCTCGAAACGTTCT							
QY	363 GCTGCCCAATCAAGACAGGTTCCAGCCTCAATGACAGAGTGTGTAACCTTCTGACCA							
Db	361 GCTGCCCAATCAAGACAGGTTCCAGCCTCAATGACAGAGTGTGTAACCTTCTGACCA							
QY	423 ACTCAGCAATCAGCTCAGCTCCTCTGATCAATCAAGCGGTGACGACAGAAATCAGAGAA							
Db	421 ACTCAGCAATCAGCTCAGCTCCTCTGATCAATCAAGCGGTGACGACAGAAATCAGAGAA							
QY	483 TGTCAAGAGGTGAAGAGAGACAGTGAAGAAAGCTTGAAGAGTGAAGATCAAGCGAT							
Db	481 TGTCAAGAGGTGAAGAGAGACAGTGAAGAAAGCTTGAAGAGTGAAGATCAAGCGAT							
QY	541 TGGGGAATCGAATCTGCTGTTATGTCTCTGAGAAATGCTTGCCTGTCGACGAGAAAG							
Db	543 TGGGGAATCGAATCTGCTGTTATGTCTCTGAGAAATGCTTGCCTGTCGACGAGAAAG							
QY	603 CTAGAAACGAAAGATGCTGCTCTGCTCTGCTCTTCTTAAAGAAATTAAGATCCGTAAT							
Db	601 CTAGAAACGAAAGATGCTGCTCTGCTCTGCTCTTCTTAAAGAAATTAAGATCCGTAAT							
QY	663 GACTTTTACTTAAAGAAAGTGAAGATCAAGCTCAATCATATTGAAGATTTCAT							
Db	663 GACTTTTACTTAAAGAAAGTGAAGATCAAGCTCAATCATATTGAAGATTTCAT							


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Db      661 GACCTTTTAAAGAAAGTGAAGCTTAACCTCCACCTCATTAGAAAGTTTCACAT 720
Qy      723 GAAACCTGGCTCACTGTAAGAAAGAAATAGTGTCAAGTTGCCATGAGACCAAGAGTGA 782
Db      721 GAAACCTGGCTCACTGTAAGAAAGAAATAGTGTCAAGTTGCCATGAGACCAAGAGTGA 780
Qy      783 CTGTATTAACCAAGATTCATTGACATATTTTATTTGCTACTGATGTACACAGAAA 842
Db      781 CTGTATTAACCAAGATTCATTGACATATTTTATTTGCTACTGATGTACACAGAAA 840
Qy      843 ATAATGACTTTAAATAATGTTTGAAGAGAGTACCTCATCTCTTTAGAAAAAAG 902
Db      841 AGTATGTACTTTAAATAATGTTTGAAGAGAGTACCTCATCTCTTTAGAAAAAAG 900
Qy      903 CTATGTAACTTCATTTCCATATCCAAATATTTATATATGTAAGTTTATTTATTAAGT 962
Db      901 CCTATGTAACTTCATTTCCATATCCAAATATTTATATGTAAGTTTATTTATTAAGT 960
Qy      963 ATACATTTTATTTATGTCAGTTTATTAATATGATTTATTTATAGAAAATTATCTGCTA 1022
Db      961 ATACATTTTATTTATGTCAGTTTATTAATATGATTTATTTATAGAAAATTATCTGATG 1020
Qy      1023 TTGATATTT-AGTATAGGCAAAATATATTTATATGACATTAATACTAGAAAGATATCT 1081
Db      1021 TTGATATTTAGTATTAAGCAAAATATATTTATATGATTAATACTAGAAAGATATCT 1080
Qy      1082 TAGGCTTTAATTAACACATGATATCAATAA 1112
Db      1081 TAGGCTTTAATTAACACATGATATCAATAA 1111

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RESULT 9

AAD27135
ID AAD27135 standard; DNA; 1111 BP.

XX AAD27135;

XX 09-APR-2002 (first entry)

XX Mouse T cell derived inducible factor (TIF) beta cDNA.

XX T cell derived inducible factor; TIF; cytokine; interleukin-9; IL-9;

XX protein therapy; STAT activation; differentiation; mouse; ss.

XX Mus musculus.

XX US6331613-B1.

XX 18-DEC-2001.

XX 18-OCT-1999; 99US-0419568.

XX 26-OCT-1998; 98US-0178973.

XX 16-JUL-1999; 99US-0354243.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Dumoulier L, Louhed J, Renaud J;

XX WPI; 2002-105277/14.

XX Nucleic acids encoding T cell derived inducible factors useful for

XX inducing STAT activation in cells -

XX Claim 1; Column 25-26; 24pp; English.

XX The present invention relates to an isolated nucleic acid molecule, which

XX encodes a T cell derived inducible factor comprising an amino acid

XX sequence encoded by 6 defined nucleotide sequences. The nucleic acid

XX molecules are shown to be up regulated by the cytokine interleukin-9

XX (IL-9) and are described as T Cell derived inducible Factors (TIFs). The

XX invention is used in protein therapy. The nucleic acid molecules encode

CC proteins which induce STAT activation in cells. They can be used, for
CC example, in the stimulation of regeneration of targeted tissues.
CC Further, their inhibitors or antagonists can be used to retard, prevent
CC or inhibit differentiation of other tissues. The present sequence is
CC mouse TIF beta cDNA.

SO Sequence 1111 BP; 346 A; 232 C; 236 G; 297 T; 0 other;
Query Match 93.6%; Score 1047.8; DB 24; Length 1111;
Best Local Similarity 97.0%; Pred. No. 3.8e-215;
Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

```

Qy      3 AACAGCTTCCTCCTCACTTATCAACCTTTGACACTTGTGATCGGTAAGGCTGCTCT 62
Db      1 AACAGCTTCCTCCTCACTTATCAACCTTTGACACTTGTGATCGGTAAGGCTGCTCT 60
Qy      63 GCAGAAATCTATGATTTTCCCTTAAGGGGACTTTGGCGGCGAGCTGCTGCTTCTCAT 122
Db      61 GCAGAAATCTATGATTTTCCCTTAAGGGGACTTTGGCGGCGAGCTGCTGCTTCTCAT 120
Qy      123 TGCCCTGTGGGCCGAGAGGCAATGGCGCTGCGCGTCAACACCCGGTGCAAGCTTGAAGT 182
Db      121 TGCCCTGTGGGCCGAGAGGCAATGGCGCTGCGCGTCAACACCCGGTGCAAGCTTGAAGT 180
Qy      183 GTCCAACTTCGACGACCGCTTATCTGCAACCGCACTTTATGCTGGCCAAAGAGGCCAG 242
Db      181 GTCCAACTTCGACGACCGCTTATCTGCAACCGCACTTTATGCTGGCCAAAGAGGCCAG 240
Qy      243 CCTTGCAATATCAACAACAGACGTCGCGGCTCATGCGGGAGAACTGTTCCGAGAGTGTAG 302
Db      241 CCTTGCAATATCAACAACAGACGTCGCGGCTCATGCGGGAGAACTGTTCCGAGAGTGTAG 300
Qy      303 TGCTAAGATCATGCTACCTGATGATGAAGACAGTGTCTCACTTCACTCGAAGACGTTCT 362
Db      301 TGCTAAGATCATGCTACCTGATGATGAAGACAGTGTCTCACTTCACTCGAAGACGTTCT 360
Qy      363 GCTCCCGCAGTCAGACAGGTTCCAGCCCTTACATGACAGAGGTGTACTTCTTGACCA 422
Db      361 GCTCCCGCAGTCAGACAGGTTCCAGCCCTTACATGACAGAGGTGTACTTCTTGACCA 420
Qy      423 ACTGAGAACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
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Qy      483 TGTCAAGAGCTGAAGAGACAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAGGCGAT 542
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Qy      543 TGGGGAACCTGACCTGCTGTTATGCTCTGAGAAATGCTTGCTGAGCGAAGAG 602
Db      541 CGGGGAACCTGACCTGCTGTTATGCTCTGAGAAATGCTTGCTGAGCGAAGAG 600
Qy      603 CTGAAGAAACGAAAGACGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662
Db      601 CTGAAGAAACGAAAGACGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Qy      663 GACTTTTCTTAAAGAAAGTGAAGACTTAACGTCATCATCTTGAAGATTTTCACAT 722
Db      661 GACTTTTCTTAAAGAAAGTGAAGACTTAACGTCATCATCTTGAAGATTTTCACAT 720
Qy      723 GAAACCTGGCTCACTGTAAGAAAGAAATAGTGTCAAGTTGCCATGAGACCAAGAGTGA 782
Db      721 GAAACCTGGCTCACTGTAAGAAAGAAATAGTGTCAAGTTGCCATGAGACCAAGAGTGA 780
Qy      783 CTGTATTAACCAAGATTCATTGACATATTTTATTTGCTACTGATGTACACAGAAA 842
Db      781 CTGTATTAACCAAGATTCATTGACATATTTTATTTGCTACTGATGTACACAGAAA 840
Qy      843 ATAATGACTTTAAATAATGTTTGAAGAGAGTACCTCATCTCTTTAGAAAAAAG 902
Db      841 AGTATGTACTTTAAATAATGTTTGAAGAGAGTACCTCATCTCTTTAGAAAAAAG 900
Qy      903 CTATGTAACTTCATTTCCATATCCAAATATTTATATATGTAAGTTTATTTATTAAGT 962

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Db      |||||
901 CCTATGTAAGTTCATTCATCCATACCAATACCTTATATATGTAAGTTATTTATATATAGT 960
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Db      961 ATACATTTTATTTATGTCAGTTTATTTATATGATTTTATATAGAAAAATATCTGTATG 1020
Qy      1023 TTGATATTT-AGTATAGAGCAAAATATTTATATGACATTAACATATAGAAACAGATATCT 1081
Db      1021 TTGATATTTGAGTATTAAGCAAAATATTTATGATTAATTAAGTATAGAAACAGATATCT 1080
Qy      1082 TAGGCTTATATTAACACATGATATATCATPAA 1112
Db      1081 TAGGCTTATATTAACACATGATATATCATPAA 1111

RESULT 10
AAD09746 ID AAD09746 standard; cDNA; 778 BP;
XX
AC AAD09746;
XX
DT 10-SEP-2001 (first entry)
XX
DE Mouse ZCYTO18 cDNA.
XX
KW Mouse; cytoskeletal; cytokine; ZCYTO18 protein; genetic abnormality;
XX cancer; inflammation; gene therapy; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 47..586
FT /*tag= a
FT /product= "Mouse ZCYTO18 protein"
FT sig_peptide 47..145
FT /*tag= b
FT mat_peptide 146..583
FT /*tag= c
FT /product= "Mouse mature ZCYTO18 protein"
XX
PN WO200146422-A1.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-US35308.
XX
PR 23-DEC-1999; 99US-0471767.
XX PR 01-DEC-2000; 2000US-0250841.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Kindsvogel W;
XX WPI: 2001-408648/43.
XX DR P-PSDB; AAE05052.
XX
PT Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer -
XX
PS Example 5; Page 160-162; 167pp; English.
XX
XX The patent discloses novel human cytokine, ZCYTO18 protein and its
XX corresponding DNA. ZCYTO18 protein induces proliferation of cells
XX expressing ZCYTOR11, a receptor for ZCYTO18 or induces cytotoxicity
XX in K562 cells. ZCYTO18 DNA is useful for detecting a genetic
XX abnormality in a patient. ZCYTO18 DNA and its antibodies are useful
XX for detecting cancer and inflammation. ZCYTO18 protein is useful for
XX killing cancer cells. It is useful for increasing platelets in a
XX patient or injured tissue. It is also used in gene therapy.
XX The present sequence is a cDNA encoding mouse cytokine, ZCYTO18.
XX
SQ Sequence 778 BP; 213 A; 193 C; 197 G; 175 T; 0 other;

```

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Query Match 68.7%; Score 768.4; DB 22; Length 778;
Best Local Similarity 99.2%; Pred. No. 2.8e-155;
Matches 772; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      6 AGGCTTCCTCTCACTTATATCACTGTGTGACACTGTGTGAGTCTGTATGCTGTCCGCA 65
Db      1 AGGCTTCCTCTCTCACTTATATCACTGTGTGACACTGTGTGAGTCTGTATGCTGTGTGCA 60
Qy      66 GAATCTATGAGTTTTCCTTATGAGGACCTTTGGCCGACGCTGCTTCTCATTTGC 125
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Qy      126 CTTGTGGGCCCCAGAGAGCAATGCGCTGCCGTCACACCCGGTGCACCTTGAGGTGC 185
Db      121 CTTGTGGGCCCCAGAGAGCAATGCGCTGCCGTCACACCCGGTGCACCTTGAGGTGC 180
Qy      186 CAATCTCCAGCAGCCGTCATCTGTCACCCGACCTTTATGCTGGCCAAAGGCGCAGCT 245
Db      181 CAATCTCCAGCAGCCGTCATCTGTCACCCGACCTTTATGCTGGCCAAAGGCGCAGCT 240
Qy      246 TGCAGATTAACAACACAGACGTCGGGCTCATGCGGGAGAACTGTTCCGAGAGTCAGTGC 305
Db      241 TGCAGATTAACAACACAGACGTCGGGCTCATGCGGGAGAACTGTTCCGAGAGTCATATGC 300
Qy      306 TAAAGATCAGTGTCTACCTGATGAAGCAGGTGCTCACTTCACTCCCTGAAAGCGTTCTGCT 365
Db      301 TAAAGATCAGTGTCTACCTGATGAAGCAGGTGCTCACTTCACTCCCTGAAAGCGTTCTGCT 360
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Db      421 CAGCAATAGCTCAGCTCCTCTGCATCATGAGGGGTGAGAGCCAGAAACATCCAGAAATGT 480
Qy      486 CAGAAAGCTGAAGAGNACAGTGAAGAAAGCTTTGAGAGAGTGAAGATCAAGCGGATTGG 545
Db      481 CAGAAAGCTGAAGAGNACAGTGAAGAAAGCTTTGAGAGAGTGAAGATCAAGCGGATTGG 540
Qy      546 GGAATGGAAGCTGCTGTTTATGCTCTGAGAAATGCTTGGCTGTGAGGAGAAAGCTGA 605
Db      541 GGAATGGAAGCTGCTGTTTATGCTCTGAGAAATGCTTGGCTGTGAGGAGAAAGCTGA 600
Qy      606 GAAACGAAAGAACTGCTCCTTCTCTTAAAGAAACATATAGATCCCTGAATGAC 665
Db      601 GAAACGAAAGAACTGCTCCTTCTCTTAAAGAAACATATAGATCCCTGAATGAC 660
Qy      666 TTTTCTTAAAGAAAGTGAAGACTAAGCTCATCATCTTAAAGATTTCACATGA 725
Db      661 TTTTCTTAAAGAAAGTGAAGACTAAGCTCATCATCTTAAAGATTTCACATGA 720
Qy      726 ACTGCTCAGTGAAGAAAGAAATAGTGTCAAGTTGTCCATGAGAACGAGAGTGAAC 783
Db      721 ACTGCTCAGTGAAGAAAGAAATAGTGTCAAGTTGTCCATGAGAACGAGAGTGAAC 778

RESULT 11
AAA28816 ID AAA28816 standard; DNA; 7444 BP.
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AC AAA28816;
XX
DT 04-SEP-2000 (first entry)
XX
DE Murine T cell inducible factor alpha genomic DNA.
XX
DE TIF-alpha; T cell derived inducible factor; interleukin 9; STAT; IL-9;
XX Anti-asthmatic; anti-allergic; cytoskeletal; inhibitor; antagonist; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers

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Db      6835 ATATTTATGTCACGTGATGATACACAGAAAAATAATGACTTTAAATAATGTTGAA 6894
QY      870 AGAGGTTACCTCTCATCTTCCTTTAGAAAAAGCTTATGTAATCTTCAATTCCTCA 929
Db      6895 AGAGGTTACCTCTCATCTTCCTTTAGAAAAAGCTTATGTAATCTTCAATTCCTCA 6954
QY      930 TATTTATATATGTAATGTTATTTATATATAGTATACATTTTATTTATGTCAGTTTATTA 989
Db      6955 TATTTATATATGTAATGTTATTTATATATAGTATACATTTTATTTATGTCAGTTTATTA 7014
QY      990 ATATGATTTTATTTATATGAAACATTAATCTGCTATGTAATTTAGTATAGGCAAAATATA 1049
Db      7015 ATATGATTTTATTTATATGAAACATTAATCTGCTATGTAATTTAGTATAGGCAAAATATA 7074
QY      1050 TTTATGACATTAATCTATGAAACAGATATCTTAGGCTTTATATACATGATATCAT 1109
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QY      1110 AAA 1112
Db      7135 AAA 7137

RESULT 14
AAD27134
ID      AAD27134 standard; DNA; 7445 BP.
XX
AC      AAD27134;
XX
DT      09-APR-2002 (first entry)
XX
DE      Mouse T cell derived inducible factor (TIF) alpha genomic DNA.
XX
KM      T cell derived inducible factor; TIF; cytokine; interleukin-9; IL-9;
XX      protein therapy; STAT activation; differentiation; mouse; ds.
XX
OS      Mus musculus.
XX
PN      US6331613-B1.
XX
PD      18-DEC-2001.
XX
PF      18-OCT-1999; 99US-0419568.
XX
PR      26-OCT-1998; 98US-0178973.
XX      16-JUL-1999; 99US-0354243.
XX
PA      (LUDW-) LUDWIG INST CANCER RES.
XX
PI      Dumoutier L, Loubet J, Renaud J;
XX
DR      WPI; 2002-105277/14.
XX
PT      Nucleic acids encoding T cell derived inducible factors useful for
XX      inducing STAT activation in cells -
XX
PS      Claim 1; Column 19-26; 24pp; English.
XX
CC      The present invention relates to an isolated nucleic acid molecule, which
XX      encodes a T cell derived inducible factor comprising an amino acid
XX      sequence encoded by 6 defined nucleotide sequences. The nucleic acid
XX      molecules are shown to be up regulated by the cytokine interleukin-9
XX      (IL-9) and are described as T Cell Derived Inducible Factors (TIFs). The
XX      invention is used in protein therapy. The nucleic acid molecules encode
XX      proteins which induce STAT activation in cells. They can be used, for
XX      example, in the stimulation of regeneration of targeted tissues.
XX      Further, their inhibitors or antagonists can be used to retard, prevent
XX      or inhibit differentiation of other tissues. The present sequence is
XX      mouse TIF alpha cDNA.
XX
SQ      Sequence 7445 BP; 2058 A; 1570 C; 1597 G; 2220 T; 0 other;
Query Match      53.7%; Score 601.4; DB 24; Length 7445;

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Best Local Similarity 99.8%; Pred. No. 3 7e-119;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      510 AAAGCTTGAGAGAGTGAAGATCAAGGCGATTGGGAACTGAGCTGTTATGTC 569
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QY      570 TCTGAGAAATGCTTGGCTCTGAGCGGAGAAAGACTGAAAGCAAGAACTGCTTCTT 629
Db      6595 TCTGAGAAATGCTTGGCTCTGAGCGGAGAAAGACTGAAAGCAAGAACTGCTTCTT 6654
QY      630 GCCCTGAAAAAGAACATATAGATCCCTGATGAGCTTTTCTAAGGAAAGTGAGAA 689
Db      6655 GCCCTGAAAAAGAACATATAGATCCCTGATGAGCTTTTCTAAGGAAAGTGAGAA 6714
QY      690 GCTAAGCTCCATCATGATTTGAAAGATTTGCATGAAACCTGCTCAGTTGAAAAAGAAA 749
Db      6715 GCTAAGCTCCATCATGATTTGAAAGATTTGCATGAAACCTGCTCAGTTGAAAAAGAAA 6774
QY      750 TAGTGCAAGTTGTCATGAGAGACCAGAGGTAGACTTGATACCAAAAGATTCATTGACA 809
Db      6775 TAGTGCAAGTTGTCATGAGAGACCAGAGGTAGACTTGATACCAAAAGATTCATTGACA 6834
QY      810 ATATTTTATTTGTCACGTGATGATACACAGAAAAATAATGACTTTAAAAAATGTTGAA 869
Db      6835 ATATTTTATTTGTCACGTGATGATACACAGAAAAATAATGACTTTAAAAAATGTTGAA 6894
QY      870 AGAGGTTACCTCTCATCTTCCTTTAGAAAAAAGCTTATGTAATCTTCAATTCCTATGCA 929
Db      6895 AGAGGTTACCTCTCATCTTCCTTTAGAAAAAAGCTTATGTAATCTTCAATTCCTATGCA 6954
QY      930 TATTTATATATGTAATGTTATTTATATATAGTATACATTTTATTTATGTCAGTTTATTA 989
Db      6955 TATTTATATATGTAATGTTATTTATATATAGTATACATTTTATTTATGTCAGTTTATTA 7014
QY      990 ATATGATTTTATTTATATGAAACATTAATCTGCTATGTAATTTAGTATAGGCAAAATATA 1049
Db      7015 ATATGATTTTATTTATATGAAACATTAATCTGCTATGTAATTTAGTATAGGCAAAATATA 7074
QY      1050 TTTATGACATTAATCTATGAAACAGATATCTTAGGCTTTATATACATGATATCAT 1109
Db      7075 TTTATGACATTAATCTATGAAACAGATATCTTAGGCTTTATATACATGATATCAT 7134
QY      1110 AAA 1112
Db      7135 AAA 7137

RESULT 15
AAA28818
ID      AAA28818 standard; DNA; 5935 BP.
XX
AC      AAA28818;
XX
DT      04-SEP-2000 (first entry)
XX
DE      Murine T cell inducible factor beta genomic DNA.
XX
KM      TIF-beta; T cell derived inducible factor; interleukin 9; STAT; IL-9;
XX      Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist; ss.
XX
OS      Mus sp.
XX
FH      Key      Location/Qualifiers
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XX      exon      355..584
XX      FT      /number= 1
XX      FT      /tag= b
XX      Intron      585..975
XX      FT      /*tag= c
XX      exon      976..1041
XX      FT      /*tag= d

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 FT 1141..1284
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 FT /*tag= i
 FT exon 5225..5824
 FT /*tag= j
 FT /number= 5
 PN WO20024758-A1.
 XX 04-MAY-2000.
 XX 18-OCT-1999; 99WO-US24424.
 XX 26-OCT-1998; 98US-0178973.
 PR 16-JUL-1999; 99US-0354243.
 XX (LUDWIG-) LUDWIG INST CANCER RES.
 XX Dumoutier L, Louhed J, Renauld J;
 XX WPI; 2000-422495/36.
 DR P-PSDB; AAY92878.
 XX New nucleic acid molecule encoding a T cell derived inducible factor
 PT for treating asthma, an allergy or lymphoma
 PT Claim 1; Page 41-42; 46pp; English.
 XX This DNA encodes T cell derived inducible factor (TIF) beta identified
 CC by subtraction cloning from a murine lymphoma cell line BM5147 in the
 CC presence or absence of interleukin 9 (IL-9). As compared to the coding
 CC region for TIF-alpha (see AA428816), that of TIF-beta has six silent
 CC changes. There are two changes which result in an inconsequential amino
 CC acid change (at both of positions 36 and 103, Val in TIF-alpha becomes
 CC Ile in TIF-beta). There is also a more significant change at position
 CC 112, where Gln becomes Arg. Many IL-9 activities are mediated by
 CC activation of STAT transcription factors. The novel TIFs were expressed
 CC in the presence of IL-9, but not in its absence. TIFs induce STAT
 CC activation in cells. They can be used, e.g. in the stimulation of
 CC regeneration of targeted tissues. Their inhibitors or antagonists can be
 CC used to retard, prevent or inhibit differentiation of other tissues. The
 CC TIFs and their coding sequences are useful in the treatment of asthma,
 CC allergies and lymphoma (claimed). They are also useful for identifying
 CC compounds that inhibit or activate T cell induced factor activity in a
 CC cell (claimed).
 SQ Sequence 5935 BP; 1732 A; 1174 C; 1346 G; 1683 T; 0 other;
 Query Match 49.6%; Score 555.2; DB 21; Length 5935;
 Best Local Similarity 96.0%; Pred. No. 2.8e-109;
 Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;
 QY 510 AAAGCTTGAGAGAGATGAGATCAAGGCGATGGGGAAGTGAAGCTGTTATATGTC 569
 DB 5221 ATAGCTTGAGAGAGAGATGAGATCAAGGCGATGGGGAAGTGAAGCTGTTATATGTC 5280
 QY 570 TCTGAGAAATGCTTCGCTGAGAGAGAGAAAGTGAAGAAAGAAAGTCTCTCTCT 629
 DB 5281 TCTGAGAAATGCTTCGCTGAGAGAGAGAAAGTGAAGAAAGAAAGTCTCTCTCT 5340
 QY 630 GCCTTCTAAGAAAGAAAGTGAAGTCCCTGAATGGAATTTTACTAAGAGAAAGTGAAGA 689
 DB 5341 GCCTTCTAAGAAAGAAAGTGAAGTCCCTGAATGGAATTTTACTAAGAGAAAGTGAAGA 5400

QY 690 GCTAAGCTCCATCATCATTTAGAAAGATTTCACATGAAAAGTGGCTCACTGAAAAAGAAAA 749
 DB 5401 GCTAAGCTCCATCATCATTTAGAAAGATTTCACATGAAAAGTGGCTCACTGAAAAAGAAAA 5460
 QY 750 TAGTGTAAGTGTGCTCCATGAGACCAAGGTGAGTGAAGTGAATACCAAGAAAGTCACTGACA 809
 DB 5461 TAGTGTAAGTGTGCTCCATGAGACCAAGGTGAGTGAAGTGAATACCAAGAAAGTCACTGACA 5520
 QY 810 ATATTATATGTCAGTGAATGATACCAAGAAAGTGAAGTGAATACCAAGAAAGTCACTGACA 869
 DB 5521 ATATTATATGTCAGTGAATGATACCAAGAAAGTGAAGTGAATACCAAGAAAGTCACTGACA 5580
 QY 870 AGAGAGTACCTCATCTCTTTGAAAAAGTGAAGTGAAGTGAATACCAAGAAAGTCACTGACA 929
 DB 5581 AGAGAGTACCTCATCTCTTTGAAAAAGTGAAGTGAAGTGAATACCAAGAAAGTCACTGACA 5640
 QY 930 TATTATATATGTAAGTGAATGATATATATATATATATATATATATATATATATATATAT 989
 DB 5641 TATTATATATGTAAGTGAATGATATATATATATATATATATATATATATATATATATAT 5700
 QY 990 ATATGATTTATTTATAGAAACATTTATCTGCTATTGATATTT-AGTAAAGCAAAATAT 1048
 DB 5701 ATATGATTTATTTATAGAAACATTTATCTGCTATTGATATTT-AGTAAAGCAAAATAT 5760
 QY 1049 ATTATGACATTAATCTATGGAACAGATATCTTAGCTTTATATAAACATGATATCA 1108
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 QY 1109 TAAA 1112
 DB 5821 TAAA 5824

Search completed: July 19, 2003, 09:41:06
 Job time : 156.463 secs

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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:03:00 ; Search time 1874.61 Seconds

(without alignment)

17372.171 Million cell updates/sec

Title: US-09-751-797-7

Perfect score: 1119

Sequence: 1 taacaagcgtctctctcac.....tggatatacataaaaaaaa 1119

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1119	100.0	1119	6	AR201397 Sequence
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4	1119	100.0	1121	10	MMU249491 Sequence
5	1056.4	94.4	1118	10	MMU249492 Sequence
6	1047.8	93.6	1111	6	AR165228 Sequence
7	1047.8	93.6	1111	6	AR201399 Sequence
8	1047.8	93.6	1111	6	AX459955 Sequence
9	768.4	68.7	778	6	AX179614 Sequence
10	601.4	53.7	7445	6	AR165227 Sequence
11	601.4	53.7	7445	6	AR201398 Sequence
12	601.4	53.7	7445	6	AX459954 Sequence
13	601.4	53.7	8270	10	MMU294727 Sequence
14	555.2	49.6	5935	6	AR165234 Sequence
15	555.2	49.6	5935	6	AR201417 Sequence
16	555.2	49.6	5935	6	AX459988 Sequence
17	555.2	49.6	5935	10	MMU294728 Sequence
18	553.6	47.7	1167	9	AF279437 Sequence
19	524.8	46.9	1152	6	AX092422 Sequence
20	524.8	46.9	1152	6	AX358990 Sequence
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22	524.8	46.9	1152	6	AX392477 Sequence
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25	524.8	46.9	1152	6	AX491246 Sequence
26	524.4	46.9	1116	6	AX151713 Sequence
27	524.4	46.9	1116	6	AX179578 Sequence
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29	521.8	46.9	1132	6	AX048204 Sequence
30	520	46.5	1139	6	AX054620 Sequence
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33	409.2	36.6	690	6	HSAR27247 Sequence
34	306	27.3	537	6	AX054622 Sequence
35	288.4	25.8	501	6	AX179581 Sequence
36	223.6	20.0	418	6	AX459964 Sequence
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ALIGNMENTS

RESULT 1
LOCUS AR165226 1119 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 7 from patent US 6274710.
ACCESSION AR165226
VERSION AR165226.1 GI:16238719
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1119)
AUTHORS Dumoutier, L., Loubred, J. and Renaud, J.-C.
TITLE Antibodies which specifically bind T cell inducible factors (Tifs)
JOURNAL Patent: US 6274710-A 7 14-AUG-2001;
FEATURES Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a


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DB 241 AGCCTTGCAATTAACAACAACAAGTCGCGCTCATCGGGAGAAACTGTTCCGAGAGATC 300
QY 301 AGTGCTAAAGATCAGTGTCTACTGTATGAGCAAGTGTCTCAACTTCGAGAAAGCTT 360
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RESULT 2
AR201397      1119 bp      DNA      linear      PAT 20-APR-2002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1119)
AUTHORS
Dumontier, B., Louhed, J. and Renaud, J.-C.
TITLE
Isolated nucleic acid molecules which encode T cell inducible
factors (TIFs), the proteins encoded, and uses therefor
JOURNAL
Patent: US 6359117-A 7 19-MAR-2002;
FEATURES
Location/Qualifiers
source
1. .1119
/organism="unknown"
BASE COUNT   352 a      233 c      232 g      302 t
ORIGIN
Query Match 100.0%; Score 1119; DB 6; Length 1119;
Best Local Similarity 100.0%; Pred. No. 1.6e-215;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAACAGGCTCTCTCTCACTATCACTGTGACACTGTGGAGATCTGATGGCTGC 60
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RESULT 3
AX459953 1119 bp DNA linear PAT 08-JUL-2002
LOCUS Sequence 7 from Patent W00210393.
DEFINITION AX459953
ACCESSION AX459953
VERSION AX459953.1 GI:21725689
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Dimoutier, L. and Renaud, J. C.
Isolated nucleic acid molecules which encode c cell inducible
factors, or interleukin-21, the proteins encoded, and uses thereof
Patent: WO 0210393-A 7-07-FEB-2002;
JOURNAL LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
FEATURES
Source 1. 1119
Location/Qualifiers
BASE COUNT 352 a 233 c 232 g 302 t
ORIGIN

Query Match 100.0%; Score 1119; DB 6; Length 1119;
Best Local Similarity 100.0%; Pred. No. 1.6e-215;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1081 TTAGCTTTTATTAATAACACATGATATCATAAAAA 1119

RESULT 4
NMU249491 1121 bp mRNA linear ROD 30-MAY-2001
LOCUS Mus musculus mRNA for TIF alpha protein (IL-22 gene).
DEFINITION AJ249491
ACCESSION AJ249491.1 GI:6996553
VERSION IL-2 gene; IL-Tifa gene; TIF alpha protein.
KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1121)
AUTHORS Dumoutier, L., Louahed, J. and Renaud, J. C.
TITLE Cloning and characterization of IL-10-related T cell-derived inducible factor (IL-TIF): a novel cytokine structurally related to IL-10 and inducible by IL-9
JOURNAL Immunology 164, 1814-1819 (2000)
REFERENCES 2 (bases 1 to 1121)
AUTHORS Renaud, J. C.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-1999) Renaud, J. C., Cytokine group, Ludwig Institute for Cancer Research, 74, Avenue Hippocrate, Brussels, B-1200, BELGIUM

FEATURES
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BASE COUNT 352 a 235 c 232 g 302 f
ORIGIN

Query Match 100.0%; Score 1119; DB 10; Length 1121;
Best Local Similarity 100.0%; Pred. No. 1.6e-215;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1081 TTAGGCTTAAATAACATGATATCTATAAAAAA 1119
DB 1083 TTAGGCTTAAATAACATGATATCTATAAAAAA 1121

RESULT 5
NMU249492 1118 bp mRNA linear ROD 16-FEB-2000
LOCUS Mus musculus mRNA for TIF beta protein (IL-Tif gene).
DEFINITION AJ249492
ACCESSION AJ249492.1 GI:6996555
VERSION IL-Tif gene; TIF beta protein.
KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1118)
AUTHORS Dumoutier, L., Louahed, J. and Renaud, J. C.
TITLE Cloning and characterization of TIF, a new IL-10-related cytokine induced by IL-9
JOURNAL Immunology 164, 1814-1819 (2000)
REFERENCES 2 (bases 1 to 1118)
AUTHORS Renaud, J. C.
TITLE Direct Submission

JOURNAL, Submitted (14-SEP-1999) Renauld J.C., Cytochrome group, Ludwig
Institute for Cancer Research, 74, Avenue Hippocrate, Brussels,
B-1200, BELGIUM

FEATURES

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Location/Qualifiers
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CDS

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BASE COUNT 353 a 233 c 235 g 297 t
ORIGIN

Query Match 94.4%; Score 1056.4; DB 10; Length 1118;
Best Local Similarity 97.1%; Pred. No. 6.9e-203;
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RESULT 6
LOCUS AR165228 1111 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 9 from patent US 6274710.
ACCESSION AR165228
VERSION AR165228.1 GI:16238721
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1111)
AUTHORS Dumoutier, L., Louned, J. and Renauld, J.-C.
TITLE Antibodies which specifically bind T cell inducible factors (TIFs)
JOURNAL Patent: US 6274710-A 9 14-AUG-2001;
FEATURES
source 1. 1111
BASE COUNT 346 a 232 c 236 g 297 t
ORIGIN
Query Match 93.6%; Score 1047.8; DB 6; Length 1111;
Best Local Similarity 97.0%; Pred. No. 3.8e-201;
Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

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QY 423 ACTCAGCAATCAGTCACTGATGAGAGAGGTCTCACTTCACTCGGAGAGCTCT 480
Db 421 ACTCAGCAATCAGTCACTGATGAGAGAGGTCTCACTTCACTCGGAGAGCTCT 480
QY 483 TGTCAGAGAGTCAAG 542
Db 481 TGTCAGAGAGTCAAG 540
QY 543 TGGGGAAGTCAAG 602
Db 541 CGGGGAAGTCAAG 600
QY 603 CTAG 662
Db 601 CTAG 660
QY 663 GACTTTTCTAAG 722
Db 661 GACTTTTCTAAG 720
QY 723 GAAACCTGCTCAAG 782
Db 721 GAAACCTGCTCAAG 780
QY 783 CTGATACCAAG 842
Db 781 CTGATACCAAG 840
QY 843 ATATGTAAGTCAAG 902
Db 841 ATATGTAAGTCAAG 900
QY 903 CTTATGTAAGTCAAG 962
Db 901 CTTATGTAAGTCAAG 960
QY 963 ATACATTTTATTAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1022
Db 961 ATACATTTTATTAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1023 TTGATATTTTATTAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1081
Db 1021 TTGATATTTTATTAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1082 TAGGCTTATTAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1112
Db 1081 TAGGCTTATTAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1111

RESULT 7
AR201399 1111 bp DNA linear PAT 20-APR-2002
LOCUS AR201399 Sequence 9 from patent US 6359117.
ACCESSION AR201399
VERSION AR201399.1 GI:20252287
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1111)
AUTHORS Dumoutier, L., Louned, J. and Renault, J.-C.
TITLE Isolated nucleic acid molecules which encode T cell inducible

Factors (Tifs), the proteins encoded, and uses therefor
JOURNAL Patent: US 6359117-A 9 19-MAR-2002;
FEATURES Location/Qualifiers
source 1..1111
BASE COUNT 346 a 232 c 236 g 297 t
ORIGIN
Query Match 93.6%; Score 1047.8; DB 6; Length 1111;
Best Local Similarity 97.0%; Pred. No. 3.8e-201;
Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;
QY 3 AACAGGCT 62
Db 1 AACAGGCT 60
QY 63 GCAGAAATCTATGAGTTTCCCTTATGAGGAGCTTGGGCGAGGCTGCTCTCTCAT 122
Db 61 GCAGAAATCTATGAGTTTCCCTTATGAGGAGCTTGGGCGAGGCTGCTCTCTCAT 120
QY 123 TGCCCTGTGGGCGCAGAGGCAAAATGCGCTGCCCTCAACACCCGGTGCAAGTTGAGT 182
Db 121 TGCCCTGTGGGCGCAGAGGCAAAATGCGCTGCCCTCAACACCCGGTGCAAGTTGAGT 180
QY 183 GTCCAACTTCAG 242
Db 181 GTCCAACTTCAG 240
QY 243 CTTTGAAGTAAACAG 302
Db 241 CTTTGAAGTAAACAG 300
QY 303 TGCTTAAGATCAGTCACTGATGAGAGAGGTCTCACTTCACTCGGAGAGCTTCT 362
Db 301 TGCTTAAGATCAGTCACTGATGAGAGAGGTCTCACTTCACTCGGAGAGCTTCT 360
QY 363 GCTCCCCAGTCAACAGAGTTCAGCCCTCATGACAGAGGTGTACTTTCTGACCA 422
Db 361 GCTCCCCAGTCAACAGAGTTCAGCCCTCATGACAGAGGTGTACTTTCTGACCA 420
QY 423 ACTCAGCAATCAGTCACTGATGAGAGAGGTCTCACTTCACTCGGAGAGCTCT 480
Db 421 ACTCAGCAATCAGTCACTGATGAGAGAGGTCTCACTTCACTCGGAGAGCTCT 480
QY 483 TGTCAGAGAGTCAAG 542
Db 481 TGTCAGAGAGTCAAG 540
QY 543 TGGGGAAGTCAAG 602
Db 541 TGGGGAAGTCAAG 600
QY 603 CTAG 662
Db 601 CTAG 660
QY 663 GACTTTTCTAAG 722
Db 661 GACTTTTCTAAG 720
QY 723 GAAACCTGCTCAAG 782
Db 721 GAAACCTGCTCAAG 780
QY 783 CTGATACCAAG 842
Db 781 CTGATACCAAG 840
QY 843 ATATGTAAGTCAAG 902
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QY 903 CTTATGTAAGTCAAG 962

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Qy	963	ATACATTTTATTTATGTCAGATTTTAAATATGATTTATTTATATGAAACATTAATCTGCTA	10222
Db	961	ATGATTTTATTTATGTCAGATTTTAAATATGATTTATTTATATGAAAAATTAATCTGATG	102020
Qy	1023	TTGATATTTT-AGTATATAGGCAATATATTTATGCAATTAATCTATGAAACAGATATCT	108111
Db	1021	TTGATATTTTGGATATTAAGCAAAATATTTTATGATATTAATCTATGAAACAGATATCT	108010
Qy	1082	TAGGCTTAAATTAACACATGATATCAATAA	11112
Db	1081	TAGGCTTAAATTAACACATGATATCAATAA	11111
RESULT 8			
AX459955			
LOCUS	AX459955	1111 bp	DNA linear PAT 08-JUL-2002
DEFINITION	Sequence 9 from Patent WO0210393.		
ACCESSION	AX459955		
VERSION	AX459955.1	GI:21726691	
KEYWORDS			
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Emmaliya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Dumoutier, L. and Renaud, J. C.		
TITLE	1 Isolated nucleic acid molecules which encode a cell inducible factor, or interleukin-21, the proteins encoded, and uses thereof		
JOURNAL	Patent: WO 0210393-A 9 07-FEB-2002;		
FEATURES	LUDWIG INSTITUTE FOR CANCER RESEARCH (US)		
source	1. 1111 location/Qualifiers		
BASE COUNT	346 a 232 c 236 g 297 t		
ORIGIN	1. 1111 /organism="Mus musculus" /db_xref="taxon:10090"		
Query Match	93.6% Score 1047.8; DB 6; Length 1111;		
Best Local Similarity	97.0%; Pred. No. 3.8e-201;		
Matches 1078; Conservative	0; Mismatches 32; Indels 1; Gaps 1;		
Qy	3	AACAGGCTCTCCTCTCACTTATCAACTGTGTGACCTTGTGAGTCTGTAGTGGCTGCT	62
Db	1	AACAGGCTCTCCTCTCACTTATCAACTTTTGACATTTGTGGATGGGATGGCTGCT	60
Qy	63	GCAGAAATCTATGAGTTTTTCCCTTATGGGAATTGGCCGCGACGCTGCTTTCAT	122
Db	61	GCAGAAATCTATGAGTTTTTCCCTTATGGGACCTTGGCCGCGACGCTGCTTTCAT	120
Qy	123	TGCCCTGTGGGCGCCAGAGGCAAAATGGGCTGCCGTCAACACCGGTGCAAGCTTGAGST	182
Db	121	TGCCCTGTGGGCGCCAGAGGCAAAATGGGCTGCCGTCAACACCGGTGCAAGCTTGAGST	180
Qy	183	GTCCAATCTTCAGACGCGCTGACATGTCACACGCACTTTATGTGTGCGCAAGAGCCAG	242
Db	181	GTCCAATCTTCAGACGCGCTGACATGTCACACGCACTTTATGTGTGCGCAAGAGCCAG	240
Qy	243	CCTTGCAATTAACAAACACAGAGCTGCGGCTCATGGGGAAGAACTGTTCCAGAGAGTCAG	302
Db	241	CCTTGCAATTAACAAACACAGAGCTGCGGCTCATGGGGAAGAACTGTTCCAGAGAGTCAG	300
Qy	303	TGCTAAATATAGTCTACCTGATGTAAGAGGTGCTCAACTCAACCTGGAAGAGCTTCT	362
Db	301	TGCTAAATATAGTCTACCTGATGTAAGAGGTGCTCAACTCAACCTGGAAGAGATTTCT	360
Qy	363	GCTCCCCAGTCAGACAGATTCAGACCCCTTACATGACAGAGGTGTATCTTTCTTGACAA	422
Db	361	GCTCCCCAGTCAGACAGATTCAGACCCCTTCAATGACAGAGGTGTATCTTTCTTGACAA	420
Qy	423	ACTAGCAATACGCTCAGCTCCTGTCAATCAGCGGTGACGACCAAGAAATTCAGAGAA	482

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IKAIQELDLLEFMSLNACV"

BASE COUNT
ORIGIN

213 a 193 c 197 g 175 t

Query Match 68.7%; Score 768.4; DB 6; Length 778;
Best Local Similarity 99.2%; Pred. No. 7.9e-145;
Matches 772; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 AGGCTCTCTCTCACTTATCAACTGTGACACTTGTGGATCTTGATGGCTGTCTGCA 65
DB 1 AGGCTCTCTCTCACTTATCAACTGTGACACTTGTGGATCTTGATGGCTGTCTGCA 60
QY 66 GAAATCTATGAGTTTTCCTTATGAGGAGCTTGGCCGACAGTCGCTCTCATGGC 125
DB 61 GAAATCTATGAGTTTTCCTTATGAGGAGCTTGGCCGACAGTCGCTCTCATGGC 120
QY 126 CCGTGGGCGCCAGAGGCAATGCGCTGCGCTCAACACCCGATGCAAGCTTGAGGTGC 185
DB 121 CCGTGGGCGCCAGAGGCAATGCGCTGCGCTCAACACCCGATGCAAGCTTGAGGTGC 180
QY 186 CAAGTTCCAGAGCGCTGATGTCGACCCGACCTTTATGCTGGCCAGAGGCGCAAGCT 245
DB 181 CAAGTTCCAGAGCGCTGATGTCGACCCGACCTTTATGCTGGCCAGAGGCGCAAGCT 240
QY 246 TGCAGATTAACACACAGAGCGCGGCTCATGCGGAGGAACTGTTCCAGAGGAGTGC 305
DB 241 TGCAGATTAACACACAGAGCGCGGCTCATGCGGAGGAACTGTTCCAGAGGAGTGC 300
QY 306 TAAAGATCAGTCTGATGATGAGAGGAGTGTCTCACTTCACTTCACTGAAAGCTTCTGCT 365
DB 301 TAAAGATCAGTCTGATGATGAGAGGAGTGTCTCACTTCACTTCACTGAAAGCTTCTGCT 360
QY 366 CCCCCAGTACAGAGGTTCCAGCCCTCACTGACAGAGGAGTGTGTAACCTTCTGACCAACT 425
DB 361 CCCCCAGTACAGAGGTTCCAGCCCTCACTGACAGAGGAGTGTGTAACCTTCTGACCAACT 420
QY 426 CAGCAATCAGCTCAGCTCTGTCATACAGCGGTCACGACGAAACATCCAGAAAGT 485
DB 421 CAGCAATCAGCTCAGCTCTGTCATACAGCGGTCACGACGAAACATCCAGAAAGT 480
QY 486 CAGAGGCTGAAAGAGACAGTAAAAAGCTTGAAGAGTGAAGAGATCAAGCGCATTTGG 545
DB 481 CAGAGGCTGAAAGAGACAGTAAAAAGCTTGAAGAGTGAAGAGATCAAGCGCATTTGG 540
QY 546 GGAATCTGACCTGCTGTTTATGTCTCTGAGAAATGCTTGGCTGTGAGCGAGAAAGCTA 605
DB 541 GGAATCTGACCTGCTGTTTATGTCTCTGAGAAATGCTTGGCTGTGAGCGAGAAAGCTA 600
QY 606 GAAACGAAAGAGTCTGCTCTGCTCTTAAAGAACATTAAGATCCCTGATGGAC 665
DB 601 GAAACGAAAGAGTCTGCTCTGCTCTTAAAGAACATTAAGATCCCTGATGGAC 660
QY 666 TTTTCTTAAAGAGAGTGAAGAGTAACTGTCATCATCATTTAGAGATTTTCAATGAA 725
DB 661 TTTTCTTAAAGAGAGTGAAGAGTAACTGTCATCATCATTTAGAGATTTTCAATGAA 720
QY 726 ACCTGCTTAAAGAGAGTGAAGAGTAACTGTCATCATCATTTAGAGATTTTCAATGAA 783
DB 721 ACCTGCTTAAAGAGAGTGAAGAGTAACTGTCATCATCATTTAGAGATTTTCAATGAA 778

RESULT 10

LOCUS AR165227 7445 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 8 from patent US 6274710.
ACCESSION AR165227
VERSION AR165227.1 GI:16238720
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 7445)
AUTHORS Dumoutier, L., Louhed, J., and Renaud, J.-C.
TITLE Antibodies which specifically bind T cell inducible factors (TIFs)
JOURNAL Patent: US 6274710-A 8 14-Aug-2001;
FEATURES Location/Qualifiers
SOURCE 1..7445
/organism="unknown"

BASE COUNT 2058 a 1570 c 1597 g 2220 t
ORIGIN

Query Match 53.7%; Score 601.4; DB 6; Length 7445;
Best Local Similarity 99.8%; Pred. No. 5.3e-111;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 510 AAAGCTGGAAGAGTGAAGATCAAGGCAATGAGGAACTGACCTGCTGTTATGTC 569
DB 6535 ATAGCTTGAAGAGTGAAGATCAAGGCAATGAGGAACTGACCTGCTGTTATGTC 6594
QY 570 TCTGAGAAATGCTTGGCTGAGGAGAGAGGAGTGAAGAAAGAACTGCTCTTCT 629
DB 6595 TCTGAGAAATGCTTGGCTGAGGAGAGAGGAGTGAAGAAAGAACTGCTCTTCT 6654
QY 630 GCCTTTAAAAAGAAATTAAGATCCTGATGAGATTTTCTTAAAGAGAGAGAA 689
DB 6655 GCCTTTAAAAAGAAATTAAGATCCTGATGAGATTTTCTTAAAGAGAGAGAA 6714
QY 690 GCTAACGTCATCATCATTAAGATTTTCAATGAACTGAGTCACTGAGTGAAGAA 749
DB 6715 GCTAACGTCATCATCATTAAGATTTTCAATGAACTGAGTCACTGAGTGAAGAA 6774
QY 750 TAGTGTCAAGTGTGATGATGAGACAGAGAGTGAAGTGAAGTGAAGTGAAGTGA 809
DB 6775 TAGTGTCAAGTGTGATGATGAGACAGAGAGTGAAGTGAAGTGAAGTGAAGTGA 6834
QY 810 ATATTATTTTGTCTACTGATGATACACAGAAATTAAGTACTTTAAAAATTTGTTGA 869
DB 6835 ATATTATTTTGTCTACTGATGATGATACACAGAAATTAAGTACTTTAAAAATTTGTTGA 6894
QY 870 AGGAGGTACCTCATCTCTTGAAGAAAGGATGATGATGATGATGATGATGATGAT 929
DB 6895 AGGAGGTACCTCATCTCTTGAAGAAAGGATGATGATGATGATGATGATGATGAT 6954
QY 930 TATTTATATATGTAAGTATTTATTAAGTATACATTTTATTTATGTCAGTTATTA 989
DB 6995 TATTTATATATGTAAGTATTTATTAAGTATACATTTTATTTATGTCAGTTATTA 7014
QY 990 ATATGATTTATTTATTAAGAACTTATGCTATGATGATTTAGTATAGGCAATATA 1049
DB 7015 ATATGATTTATTTATTAAGAACTTATGCTATGATGATTTAGTATAGGCAATATA 7074
QY 1050 TTTATGACAAATTAATGAGAAACAGATATCTTATGAGCTTTATTAACACATGATATCAT 1109
DB 7075 TTTATGACAAATTAATGAGAAACAGATATCTTATGAGCTTTATTAACACATGATATCAT 7134
QY 1110 AAA 1112
DB 7135 AAA 7137

RESULT 11

LOCUS AR201398 7445 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 8 from patent US 6359117.
ACCESSION AR201398
VERSION AR201398.1 GI:20252286
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7445)
AUTHORS Dumoutier, L., Louhed, J., and Renaud, J.-C.
TITLE Isolated nucleic acid molecules which encode T cell inducible

Factors (Tifs), the proteins encoded, and uses therefor
JOURNAL Patent: US 6359117-A 8-19-MAR-2002;
FEATURES Location/Qualifiers
Source 1..7445
/organism="unknown"

BASE COUNT 2058 a 1570 c 1597 g 2220 t
ORIGIN

Query Match 53.7%; Score 601.4; DB 6; Length 7445;
Best Local Similarity 99.8%; Pred. No. 5.3e-111;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 510 AAAGCTTGAGAGAGTGGAGATCAAGGCGATTGGGGAACCTGGACCTGCTGTTATGTC 569
DB 6535 ATAGCTTGAGAGAGTGGAGATCAAGGCGATTGGGGAACCTGGACCTGCTGTTATGTC 6594
QY 570 TCTGAGAAATGCTTGCTGAGCGAGAGAGATAGAAAAAGAGAACTGCTCTTCT 629
DB 6595 TCTGAGAAATGCTTGCTGAGCGAGAGAGATAGAAAAAGAGAACTGCTCTTCT 6654
QY 630 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGACTTTTCTAAAGAGAGAGAA 689
DB 6655 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGACTTTTCTAAAGAGAGAGAA 6714
QY 690 GCTAACGTCATCATCTATTAGAAAGATTTCACATGAAACCTGGCTCACTGAAAAAGAAA 749
DB 6715 GCTAACGTCATCATCTATTAGAAAGATTTCACATGAAACCTGGCTCACTGAAAAAGAAA 6774
QY 750 TAGGTCAAGTTGTCATGAGACGAGAGGATGAGACTTGATTAACCAAGAGATTCATTGACA 809
DB 6775 TAGGTCAAGTTGTCATGAGACGAGAGGATGAGACTTGATTAACCAAGAGATTCATTGACA 6834
QY 810 ATATTTTATGTCATGATGATATACACAGAAAAATTAATGACTTTAAATAATGTTTGA 869
DB 6835 ATATTTTATGTCATGATGATATACACAGAAAAATTAATGACTTTAAATAATGTTTGA 6894
QY 870 AGAGAGTTACCTCTCATCTCTTTAGAAAAAAGCTTATGTAATTCATTCCATATCCAA 929
DB 6895 AGAGAGTTACCTCTCATCTCTTTAGAAAAAAGCTTATGTAATTCATTCCATATCCAA 6954
QY 930 TATTTTATATATGATGATTTATTTATATATAGTATACATTTTATTTATGTCAGTTTATTA 989
DB 6955 TATTTTATATATGATGATTTATTTATATATAGTATACATTTTATTTATGTCAGTTTATTA 7014
QY 990 ATATGATTTATTTATATGAAACATTAATCTGCTATTTAGTATTTAGTATAGCAATATATA 1049
DB 7015 ATATGATTTATTTATATGAAACATTAATCTGCTATTTAGTATTTAGTATAGCAATATATA 7074
QY 1050 TTTATGCAATTAATATGAAACAGATATCTTAGGCTTTATATTAACACATGATATCAT 1109
DB 7075 TTTATGCAATTAATATGAAACAGATATCTTAGGCTTTATATTAACACATGATATCAT 7134
QY 1110 AAA 1112
DB 7135 AAA 7137

RESULT 12
AX459954 7445 bp DNA linear PAT 08-JUL-2002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX459954 Sequence 8 from Patent WO0210393.
AX459954.1 GI:21725690
house mouse.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
TITLE
JOURNAL
1 Dumoutier, L. and Renaud, J.C.
Isolated nucleic acid molecules which encode t cell inducible
factors, or interleukin-21, the proteins encoded, and uses thereof
Patent: WO 0210393-A 8-07-FEB-2002;

LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
FEATURES Location/Qualifiers
Source 1..7445
/organism="Mus musculus"
/db_xref="taxon:10090"

BASE COUNT 2059 a 1568 c 1597 g 2221 t
ORIGIN

Query Match 53.7%; Score 601.4; DB 6; Length 7445;
Best Local Similarity 99.8%; Pred. No. 5.3e-111;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 510 AAAGCTTGAGAGAGTGGAGATCAAGGCGATTGGGGAACCTGGACCTGCTGTTATGTC 569
DB 6535 ATAGCTTGAGAGAGTGGAGATCAAGGCGATTGGGGAACCTGGACCTGCTGTTATGTC 6594
QY 570 TCTGAGAAATGCTTGCTGAGCGAGAGAGATAGAAAAAGAGAACTGCTCTTCT 629
DB 6595 TCTGAGAAATGCTTGCTGAGCGAGAGAGATAGAAAAAGAGAACTGCTCTTCT 6654
QY 630 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGACTTTTCTAAAGAGAGAGAA 689
DB 6655 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGACTTTTCTAAAGAGAGAGAA 6714
QY 690 GCTAACGTCATCATCTATTAGAAAGATTTCACATGAAACCTGGCTCACTGAAAAAGAAA 749
DB 6715 GCTAACGTCATCATCTATTAGAAAGATTTCACATGAAACCTGGCTCACTGAAAAAGAAA 6774
QY 750 TAGGTCAAGTTGTCATGAGACGAGAGGATGAGACTTGATTAACCAAGAGATTCATTGACA 809
DB 6775 TAGGTCAAGTTGTCATGAGACGAGAGGATGAGACTTGATTAACCAAGAGATTCATTGACA 6834
QY 810 ATATTTTATGTCATGATGATATACACAGAAAAATTAATGACTTTAAATAATGTTTGA 869
DB 6835 ATATTTTATGTCATGATGATATACACAGAAAAATTAATGACTTTAAATAATGTTTGA 6894
QY 870 AGAGAGTTACCTCTCATCTCTTTAGAAAAAAGCTTATGTAATTCATTCCATATCCAA 929
DB 6895 AGAGAGTTACCTCTCATCTCTTTAGAAAAAAGCTTATGTAATTCATTCCATATCCAA 6954
QY 930 TATTTTATATATGATGATTTATTTATATATAGTATACATTTTATTTATGTCAGTTTATTA 989
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QY 990 ATATGATTTATTTATATGAAACATTAATCTGCTATTTAGTATTTAGTATAGCAATATATA 1049
DB 7015 ATATGATTTATTTATATGAAACATTAATCTGCTATTTAGTATTTAGTATAGCAATATATA 7074
QY 1050 TTTATGCAATTAATATGAAACAGATATCTTAGGCTTTATATTAACACATGATATCAT 1109
DB 7075 TTTATGCAATTAATATGAAACAGATATCTTAGGCTTTATATTAACACATGATATCAT 7134
QY 1110 AAA 1112
DB 7135 AAA 7137

RESULT 13
NMU294727 8270 bp DNA linear ROD 30-MAY-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

NMU294727 IL-22 protein; IL-TIF alpha protein; ILTIFA gene; interleukin.
AJ294727.1 GI:11967892
house mouse.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
TITLE
JOURNAL
1 Dumoutier, L., Van Roost, E., Amey, G., Michaux, L. and Renaud, J.C.
IL-TIF/IL-22: genomic organization and mapping of the human and
mouse genes

JOURNAL Genes Immun. 1 (8), 488-494 (2000)
MEDLINE 21069354
PUBMED 11197690
REFERENCE 2 (bases 1 to 8270)
AUTHORS Renaud J.C.
JOURNAL Direct Submission
TITLE Submitted (18-SEP-2000) Renaud J.C., UCL 74.59, Ludwig Institute
for Cancer Research, Avenue Hippocrate, 74, B-1200 Brussels,
BELGIUM

FEATURES
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/strain="129"
/db_xref="taxon:10090"
/chromosome="10"
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/gene="ILT1Fa"
CAAT_signal 2673..2676
/gene="ILT1Fa"
TATA_signal 2705..2709
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/product="IL-TIF alpha protein, (IL-22)"
exon 2736..2757
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BASE COUNT 2324 a 1743 c 1722 g 2481 t
ORIGIN
Query Match 53.7% Score 601.4; DB 10; Length 8270;
Best Local Similarity 99.8%; Pred. No. 5,4e-11;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 510 AAACCTTGAGAGAGTGGAGAGATCAAGGCGATTGGGAACTGGACCTGCTTTATATGTC 569
DB 7360 ATACTTGAGAGAGTGGAGAGATCAAGGCGATTGGGAACTGGACCTGCTTTATATGTC 7419
QY 570 TCTGAAGAAATGCTTGCCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 629
DB 7420 TCTGAAGAAATGCTTGCCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7479
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DB 7480 GCCTTTAAAAAGAAACATAGATCCCTGATGAGACTTTTAAAGAAAGTGAAGAA 7539
QY 690 GCTAACGTCATCATCATTTAGAGATTTCACATGAACTGGCTCAGTTGAAAAAGAAA 749
DB 7540 GCTAACGTCATCATCATTTAGAGATTTCACATGAACTGGCTCAGTTGAAAAAGAAA 7539
QY 750 TAGTGTCAAGTTGCTCCATGAGACCGAGTGAAGTGTGATTAACCAAGATTCATTGACA 809
DB 7600 TAGTGTCAAGTTGCTCCATGAGACCGAGTGAAGTGTGATTAACCAAGATTCATTGACA 7659
QY 810 ATATTTATTTGTCAGTCACTGATGATACAGAAAAATATGACTTTAAAAAATGTTGCA 869
DB 7660 ATATTTATTTGTCAGTCACTGATGATACAGAAAAATATGACTTTAAAAAATGTTGCA 7719
QY 870 AGAGGTTACCTCATCTCTTTAGAAAAAAGCTTATGTAATTCATTGCAATATCCAA 929
DB 7720 AGAGGTTACCTCATCTCTTTAGAAAAAAGCTTATGTAATTCATTGCAATATCCAA 7779
QY 930 TATTTTATATATGTAAGTTTATTTATATGTAATTCATTGTAATGTAATGTAATGTAAT 989
DB 7780 TATTTTATATATGTAAGTTTATTTATATGTAATTCATTGTAATGTAATGTAATGTAAT 7839
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DB 7960 AAA 7962
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ARI65234
LOCUS ARI65234 5935 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 17 from patent US 6274710.
ACCESSION ARI65234
VERSION ARI65234.1 GI:16238731
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5935)
AUTHORS Dumoutier L., Louhed J., and Renaud J.C.
TITLE Antibodies which specifically bind T Cell inducible factors (TIFs)
JOURNAL Patent: US 6274710-A 17-14-AUG-2001;
FEATURES Location/Qualifiers
source 1..5935
/organism="unknown"
BASE COUNT 1732 a 1174 c 1346 g 1603 t
ORIGIN
Query Match 49.6%; Score 555.2; DB 6; Length 5935;

Best Local Similarity 96.0%; Pred. No. 1.1e-101;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

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Db	5401	GCTAACGTCATCATCTAGATGAGATTTCAATGAACTGGCTCAGTTGAAAAAGAA	5460
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Db	5581	AGAGGTTACCTCTCATCTCTTTAGAAAAAAGCTATGTAATTCATTCCATATCCAA	5640
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QY	990	ATATGATTTATTTATGAAACATTTATGCTATGATATTT-AGTATAAGCAATATAT	1048
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Db	5821	TAAA 5824	

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QY	750	TAGTCAAGTTGTCATGAGACCAAGAGTACTGATTAACCAAGAAATTCATTGACA	809
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QY	1109	TAAA 1112	
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Job time : 1877.61 secs

RESULT 15
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LOCUS AR201417 5935 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 29 from patent US 6359117.
ACCESSION AR201417
VERSION AR201417.1 GI:20252305
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5935)
AUTHORS Dumoulier, L., Louhed, J. and Renaud, J.-C.
TITLE Isolated nucleic acid molecules which encode T cell inducible factors (Tifs), the proteins encoded, and uses therefor
JOURNAL Patent: US 6359117-A 29-19-MAR-2002;
FEATURES
Location/Qualifiers
1..5935
BASE COUNT 1732 a 1174 c 1346 g 1683 t
ORIGIN /organism="unknown"

Query Match 49.6%; Score 555.2; DB 6; Length 5935;
Best Local Similarity 96.0%; Pred. No. 1.1e-101;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 16:17:16 ; Search time 158.321 Seconds
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Title: US-09-751-797-7

Perfect score: 1119
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1047.8	93.6	1111	10	US-09-751-797-9
4	993.2	88.8	1050	15	US-10-090-365-40
5	993.2	88.8	1050	15	US-10-104-919-42
6	601.4	53.7	7445	10	US-09-751-797-8
7	555.2	49.6	5935	10	US-09-751-797-29
8	535.2	47.8	1191	15	US-10-084-298-1
9	524.8	46.9	1152	11	US-09-870-574-1
10	524.8	46.9	1152	14	US-10-063-588-153
11	524.8	46.9	1152	15	US-10-066-867-153
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13	524.8	46.9	1152	15	US-10-063-547-153
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15	524.8	46.9	1152	15	US-10-063-502-153
16	524.8	46.9	1152	15	US-10-227-884-243

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18	524.8	46.9	1152	15	US-10-066-273-125	Sequence 125, App
19	524.8	46.9	1152	15	US-10-066-494-125	Sequence 125, App
20	524.8	46.9	1152	15	US-10-230-163-243	Sequence 243, App
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36	524.8	46.9	1152	15	US-10-230-434-243	Sequence 243, App
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ALIGNMENTS

RESULT 1
US-09-751-797-7
Sequence 7, Application US/09751797
Patent No. US20010024652A1
GENERAL INFORMATION:
APPLICANT: Dumontier, Laure
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible 1
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/751, 797
CURRENT FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 09/419, 568
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/178, 973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 7
LENGTH: 1119
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-751-797-7
Query Match 100.0%; Score 1119; DB 10; Length 1119;
Match Local Similarity 100.0%; Pred. No. 1.5e-222;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAAACAGGCTCTCTCTCACTTATCAACTGTGACACTTGTGAGTCTTGAGTGGCTGC 60
Db 1 TAAACAGGCTCTCTCTCACTTATCAACTGTGACACTTGTGAGTCTTGAGTGGCTGC 60
QY 61 CTGCAAGATCTTATGAGTTTTCCTTATGAGGACATTGGCCCGCCAGCTGCCTTC 120
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Db 181 GTGTCCAACTTCCAGCAGCCGTACATGTCACACCGCACTTTATGCTGGCCAGAGGCC 240
QY 241 AGCTTGCAGATTAACAACAGAGCTCCGCTCATTCGGGGAGAACTGTTCCGAGAGTC 300
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RESULT 2
US-10-084-298-3
; Sequence 3, Application US/10084298
; Publication No. US20030099649A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth

APPLICANT: Pitman, Debra
APPLICANT: Fouser, Lynette
APPLICANT: Spaulding, Vikki
APPLICANT: Xuan, Dejun
TITLE OF INVENTION: Composition and Method for Treating Inflammatory
FILE REFERENCE: G1538 CIP
CURRENT APPLICATION NUMBER: US/10/084,298
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/270,823
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/281,353
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/131,473
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/561,811
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1166
TYPE: DNA
ORGANISM: Murine
US-10-084-298-3

Query Match 99.0%; Score 1107.8; DB 15; Length 1166;
Best Local Similarity 99.4%; Pred. No. 3.2e-220;
Matches 1112; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY	661	TGACCTTTTACTAAAGAAAGTAAAGCTAACGTCACATCATATATTAGAAAGTTTCAC	720
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RESULT 3
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Sequence 9, Application US/09751797
Patent No. US20010024652A1
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factors
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/751,797
CURRENT FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 09/419,568
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-751-797-9

Query Match          93.6%; Score 1047.8; DB 10; Length 1111;
Best Local Similarity 97.0%; Pred. No. 9e-208;
Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

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Cy 123 TGCCTGTGGGCCCCAGAGGCGAAATGCGCTGCCCTCAACACCCGGTGCAGACTTGAGGT 182
Db 121 TGCCTGTGGGCCCCAGAGGCGAAATGCGCTGCCCTCAACACCCGGTGCAGACTTGAGGT 180

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QY	303	TGCTTAAGATTAAGTGTCACTCTGAATGAAGCAGGTGCTCAACTTCAACCTCGAAGACGTTCT	362
Db	301	TGCTTAAGATTAAGTGTCACTCTGAATGAAGCAGGTGCTCAACTTCAACCTCGAAGACATTTCT	360
QY	363	GCTCCCCAGCTCAACAACAAGTCCAGACCTTACATGCAGAGAGGTGGTAACTTTCTCGACCA	422
Db	361	GCTCCCCAGCTCAACAACAAGTCCAGACCTTACATGCAGAGAGGTGGTAACTTTCTCGACCA	420
QY	423	ACTGAGCAATCAGCTCAGCTCTGTCACTAGCGGTGACGACCAAGAACATCCAGAAAGAA	482
Db	421	ACTGAGCAATCAGCTCAGCTCTGTCACTAGGTGTGACGACCAAGAACATCCAGAAAGAA	480
QY	483	TGTCAGAAAGCTGAAGAGACAGTGAAGAAAGCTTGGAGAGGTGAGAGATCCAGGCCAT	542
Db	481	TGTGAGAAAGCTGAAGAGACAGTGAAGAAAGCTTGGAGAGGTGAGAGATCCAGGCCAT	540
QY	543	TGGGGAACCTGACCTGCTGTTATGTCTGTAGAAAAGCTTGCGCTGTGAGGAGAGAAAG	602
Db	541	CGGGGAACCTGACCTGCTGTTATGTCTGTAGAAAAGCTTGCGCTGTGAGGAGAGAAAG	600
QY	603	CTAGAAAACGAAGAAGTCTGCTCTTCTTCTTAAAGAAAGAACATAAGATCCCTGAATG	662
Db	601	CTAGAAAACGAAGAAGTCTGCTCTTCTTCTTAAAGAAAGAACATAAGATCCCTGAATG	660
QY	663	GACTTTTTTACTAAAGAAAGTGAAGCTAACGTCATCATTTAGAAAGTTTCACAT	722
Db	661	GACTTTTTTACTAAAGAAAGTGAAGCTAACGTCATCATTTAGAAAGTTTCACAT	720
QY	723	GAAGACCTGGCTCAGTTGAAAAAGAAATAGTGTCAAGTGTCCATGAGACGAGAGGTGAG	782
Db	721	GAAGACCTGGCTCAGTTGAAAAAGAAATAGTGTCAAGTGTCCATGAGACGAGAGGTGAG	780
QY	783	CTTGATTAACAACAAGAAGTTCATGTACATAATTTATTTGTCACTGATGATACACAGAAA	842
Db	781	CTTGATTAACAACAAGAAGTTCATGTACATAATTTATTTATTTGTCACTGATGATACACAGAAA	840
QY	843	ATAATGTACTTTAAAAAATTTGTTGAAAGAGGTTAACTCTCATTTCTTTAGAAAAAAG	902
Db	841	AGTATGTACTTTAAAAAATTTGTTGAAAGAGGTTAACTCTCATTTCTCTAGAAAAAAG	900
QY	903	CTTATGTACTTCACTTCCATATCCAAATATTTTATATATGAAGTATTTATTTATATAGT	962
Db	901	CTTATGTACTTCACTTCCATATCCAAATATTTTATATATGAAGTATTTATTTATATAGT	960
QY	963	ATACATTTTATTTATGTCAGTTTATTTAATAATGATTTATTTATAGAAACATTTATCTGTA	1022
Db	961	ATACATTTTATTTATGTCAGTTTATTTAATAATGATTTATTTATAGAAAAATTTATCTGATG	1020
QY	1023	TTGATATTTT-AGATTAAGCAAAATATATTTATGACATAATACTATGGAACACAGATATCT	1081
Db	1021	TTGATATTTTGTGATTAAGCAAAATATATTTATGATATATACTATGGAACACAGATATCT	1080
QY	1082	TAGGCTTTAATAACACATGATCTCATAAA	1112
Db	1081	TAGGCTTTAATAACACATGATCTCATAAA	1111

RESULT 4
US-10-090-365-40
; Sequence 40, Application US/10090365
; Publication No. US20030077706A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng

APPLICANT: Kindsvogel, Wayne
 APPLICANT: Chen, Zhi
 TITLE OF INVENTION: Mouse Cytokine Receptor
 FILE REFERENCE: 01-08
 CURRENT APPLICATION NUMBER: US/10/090,365
 PRIOR FILING DATE: 2002-03-04
 PRIOR APPLICATION NUMBER: US 60/273,035
 PRIOR FILING DATE: 2001-03-02
 PRIOR APPLICATION NUMBER: US 60/279,232
 PRIOR FILING DATE: 2001-03-27
 NUMBER OF SEQ ID NOS: 49
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 40
 LENGTH: 1050
 TYPE: DNA
 ORGANISM: Mus musculus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (50)...(589)
 US-10-090-365-40

Query Match 88.8%; Score 993.2; DB 15; Length 1050;
 Best Local Similarity 97.2%; Pred. No. 1.9e-196;
 Matches 1021; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

3 AACAGGCTCTCTCTCACTTATCACTGTGACACTTGTGCGATCTCTGATGAGTCTCT 62
 1 AACAGGCTCTCTCTCTCACTTATCACTTGTGACACTTGTGCGATCTCTGATGAGTCTCT 60
 63 GCAGAAATCTATGATTTTTCCTTATGAGGAACTTTGCGCGACAGTCTCTCTCTCT 122
 61 GCAGAAATCTATGATTTTTCCTTATGAGGAACTTTGCGCGACAGTCTCTCTCTCT 120
 123 TGGCTGTGGGCGCCAGAGGCAAAATGCGTCCCGGCAACCCGGTGAAGCTTGAAGT 182
 121 TGGCTGTGGGCGCCAGAGGCAAAATGCGTCCCGGCAACCCGGTGAAGCTTGAAGT 180
 183 GTCCAACTTCCAGCAGCCGTACATCGTCAACCGCACTTATGCTGGCCAGAGGCGCAG 242
 181 GTCCAACTTCCAGCAGCCGTACATCGTCAACCGCACTTATGCTGGCCAGAGGCGCAG 240
 243 CCTTGAGATTAACAACACAGACGTCGGGCTCATCGGGGAGAACTGTTCGAGAGTCA 302
 241 CCTTGAGATTAACAACACAGACGTCGGGCTCATCGGGGAGAACTGTTCGAGAGTCA 300
 303 TGTCTAAGATCACTGCTACCTGATGAGAGAGTCTCACTTCAACCCGGAAGAGCTTCT 362
 301 TGTCTAAGATCACTGCTACCTGATGAGAGAGTCTCACTTCAACCCGGAAGAGCTTCT 360
 363 GCTCCCCCAGTCAAGAGTCCAGCCCTACATGACAGAGTGTGTACTCTTCTCTGACCA 422
 361 GCTCCCCCAGTCAAGAGTCCAGCCCTACATGACAGAGTGTGTACTCTTCTCTGACCA 420
 423 ACTGACCAATCACTGCTCTCTGTCATCATGCGGTGACGACAGACAGATCCAGAGAA 482
 421 ACTGACCAATCACTGCTCTCTGTCATCATGCGGTGACGACAGACAGATCCAGAGAA 480
 483 TGTCAAGAGTCAAGAGAGAGAGTGAAGAAAGCTTGAAGAGAGTGAAGAGTCAAGCGAT 542
 481 TGTCAAGAGTCAAGAGAGAGAGTGAAGAAAGCTTGAAGAGAGTGAAGAGTCAAGCGAT 540
 543 TGGGGAAGTGAAGTCTGTTTATGCTCTGAGAAATGCTTGGCTGAGCGAGAGAG 602
 541 CGGGGAAGTGAAGTCTGTTTATGCTCTGAGAAATGCTTGGCTGAGCGAGAGAG 600
 603 CTGAGAAAGAGAGAGTCT 662
 601 CTGAGAAAGAGAGAGTCT 660
 663 GACTTTTATCTAAGAGAGAGTGAAGAGTGAAGTCAAGTCAATCATTTAAGAGATTTTCA 722
 661 GACTTTTATCTAAGAGAGAGTGAAGAGTGAAGTCAAGTCAATCATTTAAGAGATTTTCA 720

723 GAAACCTGGCTCACTTGAAGAAAGAAATAGTGTCAAGTGTCCATGAGACCGAGAGTGA 782
 721 GAAACCTGGCTCACTTGAAGAAAGAAATAGTGTCAAGTGTCCATGAGACCGAGAGTGA 780
 783 CTGATACCAACCAAGAGTCTTGAAGAAATATTTATGTCATGATGATACAGAGAA 842
 781 CTGATACCAACCAAGAGTCTTGAAGAAATATTTATGTCATGATGATACAGAGAA 840
 843 ATATGATCTTAAAGAAATGTTTGAAGAGAGTCACTCTCATCTCTTGAAGAAAG 902
 841 AGATGATCTTAAAGAAATGTTTGAAGAGAGTCACTCTCATCTCTGAAGAAAG 900
 903 CTATGATCTTCACTTCCATATCCATATTTTATATATGATGATTTATTTATGAT 962
 901 CTATGATCTTCACTTCCATATCCATATTTTATATATGATGATTTATTTATGAT 960
 963 ATACATTTATATATGATGATTTATATATGATGATTTATATATGATGATGATGAT 1022
 961 ATACATTTATATATGATGATTTATATATGATGATTTATATATGATGATGATGAT 1020
 1023 TTGATATTT-AGTATAGCAAAATATATTT 1051
 1021 TTGATATTTAGTATATAGCAAAATATATTT 1050

RESULT 5
 US-10-104-919-42
 Sequence 42, Application US/10104919
 Publication NO. US20030099608A1

GENERAL INFORMATION:
 APPLICANT: Presnell, Scott R.
 APPLICANT: Xu, Wenfeng
 APPLICANT: Kindsvogel, Wayne
 APPLICANT: Chen, Zhi
 APPLICANT: Hughes, Steven D.
 TITLE OF INVENTION: Human Cytokine Receptor
 FILE REFERENCE: 01-12
 CURRENT APPLICATION NUMBER: US/10/104,919
 PRIOR FILING DATE: 2002-03-23
 PRIOR APPLICATION NUMBER: US 60/279,222
 PRIOR FILING DATE: 2001-03-27
 NUMBER OF SEQ ID NOS: 62
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 42
 LENGTH: 1050
 TYPE: DNA
 ORGANISM: Mus musculus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (5)...(589)
 US-10-104-919-42

Query Match 88.8%; Score 993.2; DB 15; Length 1050;
 Best Local Similarity 97.2%; Pred. No. 1.9e-196;
 Matches 1021; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

3 AACAGGCTCTCTCTCACTTATCACTGTGACACTTGTGCGATCTCTGATGAGTCTCT 62
 1 AACAGGCTCTCTCTCTCACTTATCACTTGTGACACTTGTGCGATCTCTGATGAGTCTCT 60
 63 GCAGAAATCTATGATTTTTCCTTATGAGGAACTTTGCGCGACAGTCTCTCTCTCT 122
 61 GCAGAAATCTATGATTTTTCCTTATGAGGAACTTTGCGCGACAGTCTCTCTCTCTCT 120
 123 TGGCTGTGGGCGCCAGAGGCAAAATGCGTCCCGGCAACCCGGTGAAGCTTGAAGT 182
 121 TGGCTGTGGGCGCCAGAGGCAAAATGCGTCCCGGCAACCCGGTGAAGCTTGAAGT 180
 183 GTCCAACTTCCAGCAGCCGTACATCGTCAACCGCACTTATGCTGGCCAGAGGCGCAG 242
 181 GTCCAACTTCCAGCAGCCGTACATCGTCAACCGCACTTATGCTGGCCAGAGGCGCAG 240
 243 CCTTGAGATTAACAACACAGACGTCGGGCTCATCGGGGAGAACTGTTCGAGAGTCA 302

page 6

us-09-751-797-7.rnpb

Query Match	49.6%	Score 555.2;	DB 10;	Length 5935;
Best Local Similarity	96.0%	Pred. No. 3.6e-105;		
Matches 580;	Conservative 0;	Mismatches 23;	Indels 1;	Gaps 1;

Qy	5110	AAAGCTTGAGAGAGACTGAGAGATCAAGGCCGATTTGGGAACTGGACCTGCTGTTATATC	569
Db	5221	ATAGCTTGAGAGAGCGGAGAGATCAAAAGCGATCGGGGAACTGGACCTGCTGTTATATC	528
Qy	5170	TCTGAGAAATGCTTGCCTGTGAGCCAGAAAGAACTGAGAAACGAGAACTGCTCTTCT	629
Db	5281	TCTGAGAAATGCTTGCCTGTGAGCCAGAAAGAACTGAGAAACGAGAACTGCTCTTCT	5340
Qy	630	GCCTCTTAAAGAAACAATTAAGATCCCGAATGSACTTTTACTAAAGAAAGAGACA	689
Db	5361	GCCTCTTAAAGAAACAATTAAGATCCCGAATGSACTTTTACTAAAGAAAGAGACA	5400
Qy	690	GCTAACGTCCATCATCATTTAGAGATTTACATGAACTGGCTCAGTTGAAAAAGAAA	749
Db	5401	GCTAACGTCCACCATCATTTAGAGATTTACATGAACTGGCTCAGTTGAAAAAGAAA	5460
Qy	750	TAGTGTCAAGTTGTCCATGAGACAGAGGTAGACTTGATTAACCAAAAGATTCATTGA	809
Db	5461	TAGTGTCAAGTTGTCCATGAGACAGAGGTAGACTTGATTAACCAAAAGATTCATTGA	5520
Qy	810	ATATTTTATGTCACATGATGATACACAGAAAAAAGTCTTAAAGAAATGTTTGA	869
Db	5521	ATATTTTATGTCACATGATGATACACAGAAAAAAGTCTTAAAGAAATGTTTGA	5580
Qy	870	AGAGAGTTACCTTCATTCCTTTAGAAAAAAAAGCTTATGTACTCATTTCCATATCCA	929
Db	5581	AGAGAGTTACCTTCATTCCTTCAGAAAAAGCTTATGTACTCATTTCCATATCCA	5640
Qy	930	TATTTTATATATGTAAGTTTATTTATTAATAGATATACATTTATTTATGTCAGTTATTA	989
Db	5641	TATTTTATATATGTAAGTTTATTTATTAATAGATATACATTTATTTATGTCAGTTATTA	5700
Qy	990	ATATGATTTTATTTATAGAAACATATATGCTATGATATTT-AGTATTAAGCAATAT	1040
Db	5701	ATATGATTTTATTTATAGAAATATATGCTATGATATTTAGATATTAAGCAATATAT	5760
Qy	1049	ATTATGACAATTAATATGAGAAACAAGATATCTTAGGCTTATTAACATGATATATCA	1108
Db	5761	ATTATGATATTAATATTAAGAAACAAGATATCTTAGGCTTATTAACATGATATATCA	5820
Qy	1109	TAAA 1112	
Db	5821	TAAA 5824	

Query Match	47.8%;	Score 535.2;	DB 15;	Length 1191;
Best Local Similarity	73.4%;	Pred. No. 2,3e-101;		
Matches 843;	Conservative 0;	Mismatches 268;	Indels 37;	Gaps 11;

QY	9	CTCTCCCTCACTATCAACGTTGACACCTGTGCGAATCTGTGAAAGCTGTCTGCAADA	68
Db	28	CTCTCTCCCAAGTCAACAGTTGCTCTGAATTGAATTTGCTGCATGTGCGCCCTGCAADA	87
QY	69	ATCTAATAGTTTTTCCCTTAATGGGACCTTTGGCCGACAGTGCCTGCTTCATATGCCCT	128
Db	88	ATCTGTAGCTCTTTCCTTAATGGGGAACCTGTGGACACAGCTGCCTCTTCTTGGCCCT	147
QY	129	GTGGGCCCAAGAGCAAAATGCGCTGCGCTGTCAACACCGGGTGCAAGCTTGAAGTCCAA	188
Db	148	CTTGGTACAGGGAAGAGACGCTGGCGCCATCAGTCTCCACATGCAAGCTTGCAAACTCCAA	207
QY	189	CTTCACAGAGCCGTACATCCGTCAACCCGACCTTTATGTGTGACCAAGAGGACAGCCTTGC	248
Db	208	CTTCACAGAGCCCTATATACCAACCCGACCTTTCATGTGCTAAGAGGCTAGCTTGGC	267
QY	249	AGATTAACAACAAGACGTCGGGCTCATTCGGGAGAACTGTTCCGAGAGTCAAGTCTAA	308
Db	268	TGATTAACAACAAGACGTTGCTTCATTTGGGAGAAACTGTTCCAGGAGTCAAGTATAG	327
QY	309	AGATCAGTGTCACTGTATGAAGCAGGTCTCACTTCAACCTGGAAACGTTCTGCTCC	368
Db	328	TGACCGCTGTATGTATGAAGCAGGTGTAACTTCAACCTTGAAGAGTGTGTTCC	387
QY	369	CCAGTCAAGACGTTTCCAGCCCTACATGACAGAGGTGTACTTTCCTGACCAAACTCAG	428
Db	388	TCAATCTGTATGTTTCCAGCTTTATATGCAAGAGGTGTGCTTCTCTGGCCAGCTCAG	447
QY	429	CAATCAGTCAAGCTCTGTCAATCAGCGGTGACGACCCAGAACATCCAGAAATGTGAG	488
Db	448	CAACAGGTAAGCAATGTCAATTGAAGTGAATGACCTGCATATCCAGAGGAATGTCA	507
QY	489	AAGCTGAAGAGACAGTGA AAAAGCTTGAAGAGATGGAAGATCAAGCGATTGGGA	548
Db	508	AAACCTGAAGACACAGTGA AAAAGCTTGAAGAGATGGAAGATCAAAAGCATTTGGGA	567
QY	549	ACTGACCTGTGTTTATGTCTCGAGAAATGCTTGCCTGAGCGAGAAAGCTTAAG	608
Db	568	ACTGAAATTTGCTGTTTATGTCTCTGAGAAATGCTCTCAATTTGACCAAGCAAAAGCTGAA	627
QY	609	AACGAGAAGTGTCTTCCTCTGCTCTTAA AAAGAACATTAAGATCCCTGAATGACATT	668
Db	628	AATGAATATACTAACCCCTTTCCTCTGTAGAAATTAACAATTAGATGCCCAAGAGGATTT	687
QY	669	TTTA-----CTTAAGAAAGTGAAGAGCTAACGTGCATCATATTATGAAGATTTCAATGA	724
Db	688	TTTTTAACCAAAAGAAAGATGGGAAGCCAACTCATCATATGATGGTGGATTTCCAAAGA	747
QY	725	AACCTGGCTAGTTGA AAAAAGAAATATGTGCA--GTTGTCCATGAGACAG--AGTATG	781
Db	748	ACCCTGCTTATGTTACAAAGAAACCAATGCCACTTTTGTATTAAACCAAGAAAGTATG	807
QY	782	ACTTGATTAACCAAGATTCATTGACATAATTTTATTTGCACTGATG---ATAACA	837

Db 808 ACTTCAGACATGATTTATGATACATTTTCATGCTGCTGCTATACACAG 867
 Qy 838 GAAAAATATGATCTTTAAAAATTTT-----GAAGAGGTTACTTCACTTCT 890
 Db 868 AAAACAATTTATTTTAAATTAATGCTTTTCCATAAAAAGATTAATCTTCCATCT 927
 Qy 891 TTA---GAAAAAGCTATGTAATCTCA--TTTCCATATCCATATTTTATATATGAA 945
 Db 928 TTAGGGGAAAAAACCCCTAAATAGCTTCATGTTCCATATACAGTACTTATATTTATAA 987
 Qy 946 GTTATTTATATATAGTAATA-----CATTTATTTATGTCAGTTTATATATAGATTT 999
 Db 988 ATGATTTATATATATATATATAGTACGCTTTTATTTATATCATTTTATATATAGATTT 1047
 Qy 1000 ATTATATAGAAACATTATCTGCTATGATA--TTAGATATAGGCAATA--ATATTTATG 1055
 Db 1048 ATTATATAGAAACATTCATTCATGATTTGCTACTTGAAGTAAAGCTAAATATGATATTTATG 1107
 Qy 1056 ACAATTAATATGCTATATACATATGCTTAAATTAACATGATATCATAA 1111
 Db 1108 ACAATTAATATGAGCTATATACATGTTATTTGACCTCAATAAACATTTGATATCTCTAA 1167
 Qy 1112 AAAAAAA 1119
 Db 1168 AAAAAAA 1175

RESULT 9

US-09-870-574-1

; Sequence 1, Application US/09870574
 ; Patent No. US2002010273A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Austen L.
 ; APPLICANT: Aggarwal, Sudeepa
 ; APPLICANT: Xie, Ming-Hong
 ; APPLICANT: Maruoka, Ellen M.
 ; APPLICANT: Foster, Jessica S.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: INTERLEUKIN-22 POLYPEPTIDES, NUCLEIC ACIDS ENCODING
 ; TITLE OF INVENTION: THE SAME AND METHODS FOR THE TREATMENT OF PANCREATIC DISORDERS
 ; FILE REFERENCE: P2806-1(US)
 ; CURRENT APPLICATION NUMBER: US/09/870, 574
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: US 60/169,495
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: PCT/US00/14042
 ; PRIOR FILING DATE: 2000-05-22
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-24
 ; NUMBER OF SEQ ID NOS: 7
 ; SEQ ID NO 1
 ; LENGTH: 1152
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-09-870-574-1

Query March 46.9%; Score 524.8; DB 11; Length 1152;
 Best Local Similarity 73.2%; Pred. No. 3.3e-99;
 Matches 832; Conservative 0; Mismatches 267; Indels 37; Gaps 11;

Qy 9 CTCTCTCTCACTATCACTGTTGACACTTGTGAGATCTGATGGCTGTCTGACAGAA 68
 Db 15 CTCCTCCCAAGTACCAAGTGTGCTGAGTTGAAATGTCGCAATGGCCGCCCTGCAAA 74
 Qy 69 ATCTATGATTTTTCCTTATAGGGGACTTTGGCCGCAAGCTGCTGCTTCTCATTTGCCCT 128
 Db 75 ATCTGTGAGCTCTTCTTATAGGGGAGCCCTGGCCACACAGCTGCTCTTCTTGGGCCCT 134
 Qy 129 GTGGGCCAGGAGGCAATGCGCTGCCCTGCAACACCCGGGGAAGCTTGAAGGTGCA 188
 Db 135 CTGTGTACAGGAGGAGGAGGAGCTGCGCCCATCATGCTCCCACTGACAGGCTTGAACAGTCCAA 194

Qy 189 CTTCAGACGCCGATACATGCTCAACGCGACCTTTATGCTGCGCAAGGAGCGACCTTGC 248
 Db 195 CTTCAGACGCCCTATATATCAACGCGACCTTCAATGCTGCTAAGAGGCTGATGGC 254
 Qy 249 AGATAACAACAAGACGCTCGGCTCATCGGGGAGAACTGCTCCGAGAGTCAAGTGTAA 308
 Db 255 TGATTAACAACAAGACGCTTGGTCTCATTTGGGGAGAACTGCTCCAGGAGTCAAGTATGAG 314
 Qy 309 AGATCACTGCTACCTGATGAGAGAGGTCCTCAACCTTCAACCTGGAAGACCTTGTCTCC 368
 Db 315 TGAGCGCTGCTATGATGAGAGGTCCTCAACCTTCAACCTGGAAGACCTTGTCTCC 374
 Qy 369 CCACTCAACAAGGTCCTCAACGCTTCAACGCTTCAACGCTTCAACGCTTCAACGCTTCA 428
 Db 375 TCATCTGATAGGTTCCAGGCTTATATAGCAGAGAGTGTGCTTCCGCTGAGCTGAG 434
 Qy 429 CAATCACTGAGCTCCTGTCACATCAAGGAGGAGCAGACATCCAGAGAGATGTCTAG 488
 Db 435 CAACAGCTAAGCAGATGCTATTTGAAGGTGATGACCTGCTATTCAGAGAGATGTGCA 494
 Qy 489 AAGCTGAAGAGAGACAGTGAAGAAAGCTTGAAGAGAGTGAAGATCAAGGCTATGGGA 548
 Db 495 AAGCTGAAGAGAGACAGTGAAGAAAGCTTGAAGAGAGTGAAGATCAAGGCTATGGGA 554
 Qy 549 ACTGACCTGCTGTTATGCTCTGAGAAATGCTTGGCTGAGCGAAGAGCTAGAA 608
 Db 555 ACTGATTTGCTGTTATGCTCTGAGAAATGCTTGGCTGAGCGAAGAGCTAGAA 614
 Qy 609 AAGCAAGACTGCTCTTCTGCTTAAAGAAACAAATTAAGTCCCTGAATGACCTT 668
 Db 615 AATGAATTAATCAACCCCTTCTGCTGTAAGAAATTAAGTCCCTGAATGACCTT 674
 Qy 669 TTTA---CTAAGAGAAAGTGAAGTAAAGTCAATCATCATATAGAAATTTGACATGA 724
 Db 675 TTTTAAACCAAGAGAGAGTGAAGGCAATCTCAATCATGATGGTGAATCCAAATGA 734
 Qy 725 AACCTGCTGAGTGAAGAAAGAAATATGTCAA--GTTGCTCATGAGACAG--AGGTAG 781
 Db 735 ACCCTGCTGAGTGAAGAAAGAAATATGTCAA--GTTGCTCATGAGACAG--AGGTAG 794
 Qy 782 ACTGATTAACCAAGAGAGTGAAGTAAATTTATTTATGTCAGTGAAG---ATACACA 837
 Db 795 ACTTCTAAGCAATGAATATTTATGTAACATTTCACTGAGTGTCTATACACAG 854
 Qy 838 GAAAAATATGATCTTAAATAAATGTTT-----GAAGGAGGTTACCTGATCTCT 890
 Db 855 AAAACAATTTATTTTAAATTAATGCTTTTCCATAAATAAAGATTAATCTTCCATTTCT 914
 Qy 891 TTA---GAAAAAGCTATGTAATCTCA--TTTCCATATCCATATTTATATATATGAA 945
 Db 915 TTAGGGGAAAAAACCCCTAAATAGCTTCATGTTCCATATACAGTACTTATATATTTAA 974
 Qy 946 GTTATTTATATATAGTAATA-----CATTTATTTATGTCAGTTTATATATAGATTT 999
 Db 975 ATGATTTATATATATATATATAGACTGCAATTTTATATATATATATATATATGATTT 1034
 Qy 1000 ATTATAGAAACATTATCTGCTATGATA--TTAGATATAGGCAATA--ATATTTATG 1055
 Db 1035 ATTATAGAAACATTATCTGATATGCTACTTGAAGTAAAGCTTAAATTTGATATTTATG 1094
 Qy 1056 ACAATTAATATG---AAACAAGATATCTTAAATTAACACATGATATG 1107
 Db 1095 ACAATTAATATGAGCTATTAACATGTTATTTGACCTCAATTAACATTTGATATG 1150

RESULT 10

US-10-063-588-153

; Sequence 153, Application US/10063588
 ; Publication No. US20030130483A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Filvaroff, Ellen

PRIOR APPLICATION NUMBER: 60/088825
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088863
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089952
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/090246
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090444
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090688
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090696
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090862
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091628
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/096012
 PRIOR FILING DATE: 1998-08-10
 PRIOR APPLICATION NUMBER: 60/096757
 PRIOR FILING DATE: 1998-08-17
 PRIOR APPLICATION NUMBER: 60/096949
 PRIOR FILING DATE: 1998-08-18
 PRIOR APPLICATION NUMBER: 60/096959
 PRIOR FILING DATE: 1998-08-18
 PRIOR APPLICATION NUMBER: 60/097954
 PRIOR FILING DATE: 1998-08-26
 PRIOR APPLICATION NUMBER: 60/097971
 PRIOR FILING DATE: 1998-08-26
 PRIOR APPLICATION NUMBER: 60/097979
 PRIOR FILING DATE: 1998-08-26
 PRIOR APPLICATION NUMBER: 60/098749
 PRIOR FILING DATE: 1998-09-01
 PRIOR APPLICATION NUMBER: 60/099741
 PRIOR FILING DATE: 1998-09-10
 PRIOR APPLICATION NUMBER: 60/099763
 PRIOR FILING DATE: 1998-09-10
 PRIOR APPLICATION NUMBER: 60/099792
 PRIOR FILING DATE: 1998-09-10
 PRIOR APPLICATION NUMBER: 60/099812
 PRIOR FILING DATE: 1998-09-10
 PRIOR APPLICATION NUMBER: 60/099815
 PRIOR FILING DATE: 1998-09-10
 PRIOR APPLICATION NUMBER: 60/100627
 PRIOR FILING DATE: 1998-09-16
 PRIOR APPLICATION NUMBER: 60/100662
 PRIOR FILING DATE: 1998-09-16
 PRIOR APPLICATION NUMBER: 60/100683
 PRIOR FILING DATE: 1998-09-17
 PRIOR APPLICATION NUMBER: 60/100684
 PRIOR FILING DATE: 1998-09-17
 PRIOR APPLICATION NUMBER: 60/100930
 PRIOR FILING DATE: 1998-09-17
 PRIOR APPLICATION NUMBER: 60/101279
 PRIOR FILING DATE: 1998-09-22
 PRIOR APPLICATION NUMBER: 60/101475
 PRIOR FILING DATE: 1998-09-23
 PRIOR APPLICATION NUMBER: 60/101738
 PRIOR FILING DATE: 1998-09-24
 PRIOR APPLICATION NUMBER: 60/101743
 PRIOR FILING DATE: 1998-09-24
 PRIOR APPLICATION NUMBER: 60/101916
 PRIOR FILING DATE: 1998-09-24
 PRIOR APPLICATION NUMBER: 60/102570
 PRIOR FILING DATE: 1998-09-30
 PRIOR APPLICATION NUMBER: 60/103449

PRIOR FILING DATE: 1998-10-06
 PRIOR APPLICATION NUMBER: 60/103678
 PRIOR FILING DATE: 1998-10-08
 PRIOR APPLICATION NUMBER: 60/103679
 PRIOR FILING DATE: 1998-10-08
 PRIOR APPLICATION NUMBER: 60/103711
 PRIOR FILING DATE: 1998-10-08
 PRIOR APPLICATION NUMBER: 60/105000
 PRIOR FILING DATE: 1998-10-20
 PRIOR APPLICATION NUMBER: 60/105002
 PRIOR FILING DATE: 1998-10-20
 PRIOR APPLICATION NUMBER: 60/105881
 PRIOR FILING DATE: 1998-10-27
 PRIOR APPLICATION NUMBER: 60/106030
 PRIOR FILING DATE: 1998-10-28
 PRIOR APPLICATION NUMBER: 60/106464
 PRIOR FILING DATE: 1998-10-30
 PRIOR APPLICATION NUMBER: 60/106856
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Query Match	46.9%	Score 524.8;	DB 15;	Length 1152;
Best Local Similarity	73.2%	Pred. No. 3.3e-99;		
Matches 832;	Conservative 0;	Mismatches 267;	Indels 37;	Gaps 11;

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Db	75	ATCTGTGAGCTCTTCTTATGGGGACCTGGCCACGAGTCGCTCTTCTTGGCCCT	134
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QY	249	AGATTAACAACAAGACGTCGGCTCATGGGGAGAACTGTTCCGAGAGTCAGTCTAA	308
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QY	309	AGATCAGGTCACCTGATGAAGAGGAGTCTCAACTCAACCTGGAAGAAGTTCTGTCTCC	368
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QY	429	CAATCAGTCAAGCTCTCTGTACATAGCGGTGACACCAAGAACTCCAGAGAAATGTCAg	488
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QY	489	AAGGTGAAGAGACAGTGAAGAAACCTTGAGAGAGTGGAGATCAAGGCCGATTGGGGG	548
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QY	549	ACTGACCCGTGTTTATGTCTGTAGAAATGCTTGCGTCTGAGCGAGAGAAAGCTAGAA	608
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QY	609	AACGAGAAGCTGCTCTTCTGCTGCTCTTCTTAAAGAAACAATAAGTCTCTGAATGACCTT	668
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RESULT 12
/ Sequence 125, Application US/10066500
/ Publication No. US20020177165A1
/ GENERAL INFORMATION:
/ APPLICANT: Avi J. Ashkenazi
/ APPLICANT: Kevin P. Baker
/ APPLICANT: David A. Botstein
/ APPLICANT: Luc Desnoyers
/ APPLICANT: Dan L. Eaton
/ APPLICANT: Napoleone Ferrara
/ APPLICANT: Sherman Fong
/ APPLICANT: Wei-Qiang Gao
/ APPLICANT: Hanspeter Geber
/ APPLICANT: Mary E. Gerltsen
/ APPLICANT: Audrey Goddard
/ APPLICANT: Paul J. Godowski
/ APPLICANT: Austin L. Gurney
/ APPLICANT: Ivar J. Kjavlin
/ APPLICANT: Jennie P. Macher
/ APPLICANT: Mary A. Napier
/ APPLICANT: James Pan
/ APPLICANT: Nicholas F. Paoni
/ APPLICANT: Margaret Ann Roy
/ APPLICANT: Timothy A. Stewart
/ APPLICANT: Daniel Tumas
/ APPLICANT: Colin K. Watanabe
/ APPLICANT: P. Mickey Williams
/ APPLICANT: William I. Wood
/ APPLICANT: Zemin Zang
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P313OR1C7
/ CURRENT APPLICATION NUMBER: US/10/066,500
/ CURRENT FILING DATE: 2002-02-01
/ PRIOR APPLICATION NUMBER: 10/002,796
/ PRIOR FILING DATE: 2001-11-15
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 PRIOR APPLICATION NUMBER: PCT/US99/20594
 PRIOR FILING DATE: 1999-09-08

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 Db 615 AATGATTAACCTAAGCCCT 674
 QY 669 TTTA---CTAAGAGAAAGTGAAGAGCTAAGCTCATCATCATTAAGAAATTTCAATGA 724
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 QY 725 AACTGCTGCTGTTGAGAAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 781
 Db 735 ACCCTGCTGTTGAGAAAG 794
 QY 782 ACTGATTAACCAAG 837
 Db 795 ACTTCTTAAGAGATGATATTTATTTGATTAACATTTGATTTGATTTGATTTGATTTGAT 854
 QY 838 GAAAAATTAATGACTTTTAAAAATTTGTT-----GAAAGAGGTTAAGCTCTCATTCCT 890
 Db 855 AAAACAATTTATTTTAAATTAATTTGCTTTTTCATTAAGAAAGATTTCTTCCATTCCT 914
 QY 891 TTA---GAAAAAGCTTAATGTAATCA--TTTCCATATCCATATTTTATATATGTA 945
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 QY 946 GTTATTTATATATAGTATA-----CATTTATTTATGAGTATTTATATATGATTT 999
 Db 975 ATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1034
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 Db 1035 ATTTATGAAACATTTATCTGCTATTTGATA--TTTATATATAGGCAATA---ATATTTATG 1094
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 ; Sequence 153, Application US/10063616
 ; Publication No. US20030013855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gettisen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Matanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,616
 ; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 153
 ; LENGTH: 1152
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-063-616-153

Query Match 46.94; Score 524.8; DB 15; Length 1152;
 Best Local Similarity 73.24; Pred. No. 3.3e-99;
 Matches 832; Conservative 0; Mismatches 267; Indels 37; Gaps 11;
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 15 CTCCTCTCTCACTATCACTGTTGACACTGTGCGATCTCTGATGGCTGCTCGACAA 74
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 Db 75 ATCTGATGCTCTTCTCTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 134
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 QY 309 AGATTAAGTCTACTGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 368
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 QY 369 CCACTGACAG 428
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 QY 609 AACGAGACAGTCTCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 668
 Db 615 AATGATTAACCTAAGCCCT 674
 QY 669 TTTA---CTAAGAGAAAGTGAAGAGCTAAGCTCATCATCATTAAGAAATTTCAATGA 724
 Db 675 TTTTAAACCAAG 734
 QY 725 AACTGCTGCTGTTGAGAAAG 781
 Db 735 ACCCTGCTGTTGAGAAAG 794
 QY 782 ACTGATTAACCAAG 837
 Db 795 ACTTCTTAAGAGATGATATTTATTTGATTAACATTTGATTTGATTTGATTTGATTTGAT 854
 QY 838 GAAAAATTAATGACTTTTAAAAATTTGTT-----GAAAGAGGTTAAGCTCTCATTCCT 890
 Db 855 AAAACAATTTATTTTAAATTAATTTGCTTTTTCATTAAGAAAGATTTCTTCCATTCCT 914
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QY 1000 ATTATAGAAACATATCTGCTATGATA-TTATAGTAAAGCAATA---AATTTATG 1055
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 QY 1056 ACAATAGCTATG----AACAAGATATCTAGCTTATTAACATGATATC 1107
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RESULT 15
 US-10-063-502-153

/ Sequence 153, Application US/10063502
 / Publication No. US2003023042A1
 / GENERAL INFORMATION:
 / APPLICANT: Ealon, Dan L.
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Gerlitsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Goddard, Paul J.
 / APPLICANT: Grimaldi, Christopher J.
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Matanabe, Colin K.
 / APPLICANT: Wood, William I.
 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 / FILE OF INVENTION: ACIDS ENCODING THE SAME
 / FILE REFERENCE: P3230R1C1
 / CURRENT APPLICATION NUMBER: US/10/063,502
 / CURRENT FILING DATE: 2002-05-01
 / Prior Application removed - See File Wrapper or Palm
 / NUMBER OF SEQ ID NOS: 170
 / SEQ ID NO 153
 / LENGTH: 1152
 / TYPE: DNA
 / ORGANISM: Homo Sapien
 US-10-063-502-153

Query Match 46.9%; Score 524.8; DB 15; Length 1152;
 Best Local Similarity 73.2%; Pred. No. 3.3e-99;
 Matches 832; Conservative 0; Mismatches 267; Indels 37; Gaps 11;

QY 9 CTCTCCCTCACTATTAACCTGTTGACACTTGGCCACTCTCTATGCTGCTCCGCGA 68
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 QY 838 GAAATTAATGACTTTAAATTTGTT-----GAAAGAGGTAACTCTCATTTCT 890
 Db 855 AAACAAATTTATTTTAAATTTGTT-----GAAAGAGGTAACTCTCATTTCT 914
 QY 891 TTA---GAAAGAAAGCTTATGTAAGTCA--TTTCATATCCATATTTTATATATGTA 945
 Db 915 TTGGGGAAGAAAGCTTATGTAAGTCA--TTTCATATCCATATTTTATATATGTA 974
 QY 946 GTTATTTATTTATTAAGTATA-----CATTTATTTATGTCAGTTTATTAATGATTT 999
 Db 975 ATGATTTATTTATTTATTAAGTATA-----CATTTATTTATGTCAGTTTATTAATGATTT 1034
 QY 1000 ATTATAGAAACATATCTGCTATGATA-TTATAGTAAAGCAATA---AATTTATG 1055
 Db 1035 ATTATAGAAACATATCTGCTATGATA-TTATAGTAAAGCAATA---AATTTATG 1094
 QY 1056 ACAATAGCTATG----AACAAGATATCTAGCTTATTAACATGATATC 1107
 Db 1095 ACAATATATATAGCTATATACATGTTTATTAACCTCAATAAACCTTGGATATC 1150

Search completed: July 20, 2003, 03:45:26
 Job time: 163.321 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:07:55 ; Search time 35.2798 Seconds
(without alignments)
9727.122 Million cell updates/sec

Title: US-09-751-797-7
Sequence: 1119
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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6: /cgn2_6/ptodata/1/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1119	100.0	1119	US-09-178-973B-7	Sequence 7, Appl
2	1119	100.0	1119	US-09-419-568F-7	Sequence 7, Appl
3	1119	100.0	1119	US-09-354-243B-7	Sequence 9, Appl
4	1047.8	93.6	1111	US-09-178-973B-9	Sequence 9, Appl
5	1047.8	93.6	1111	US-09-419-568F-9	Sequence 9, Appl
6	1047.8	93.6	1111	US-09-354-243B-9	Sequence 9, Appl
7	601.4	53.7	7445	US-09-178-973B-8	Sequence 8, Appl
8	601.4	53.7	7445	US-09-419-568F-8	Sequence 8, Appl
9	601.4	53.7	7445	US-09-354-243B-8	Sequence 8, Appl
10	555.2	49.6	5935	US-09-178-973B-17	Sequence 17, Appl
11	555.2	49.6	5935	US-09-419-568F-29	Sequence 29, Appl
12	555.2	49.6	5935	US-09-354-243B-29	Sequence 29, Appl
13	409.2	36.6	690	US-09-419-568F-24	Sequence 24, Appl
14	409.2	36.6	690	US-09-354-243B-24	Sequence 24, Appl
15	126	11.3	4797	US-09-419-568F-25	Sequence 25, Appl
16	126	11.3	4797	US-09-354-243B-25	Sequence 25, Appl
17	59.4	5.3	678	US-07-867-106-2	Sequence 2, Appl
18	51.8	4.6	678	US-07-991-867B-23	Sequence 23, Appl
19	51.8	4.6	678	US-08-107-755A-23	Sequence 23, Appl
20	51.8	4.6	678	US-08-544-332-23	Sequence 23, Appl
21	51.8	4.6	678	US-09-370-861A-23	Sequence 23, Appl
22	51.8	4.6	6768	US-08-107-755A-1	Sequence 1, Appl
23	51.8	4.6	8457	US-07-991-867B-1	Sequence 1, Appl
24	51.8	4.6	8457	US-08-544-332-1	Sequence 1, Appl
25	51.8	4.6	8457	US-09-370-861A-1	Sequence 1, Appl
26	51.4	4.6	168575	US-09-426-290-1	Sequence 1, Appl
27	51.2	4.6	20674	US-09-641-638-651	Sequence 651, App

C 28	50.8	4.5	837	4	US-08-998-416-288	Sequence 288, App
C 29	50.8	4.5	7218	1	US-08-232-463-14	Sequence 14, Appl
C 30	50.6	4.5	4526	1	US-07-855-412B-4	Sequence 4, Appl
C 31	50.6	4.5	4526	2	US-08-308-887A-4	Sequence 4, Appl
C 32	50.6	4.5	4526	3	US-08-881-094-4	Sequence 4, Appl
C 33	49.6	4.4	4526	3	US-08-998-416-1137	Sequence 1137, Ap
C 34	49.2	4.4	731	1	US-08-451-405A-2	Sequence 2, Appl
C 35	49.2	4.4	8920	2	US-08-446-855A-1	Sequence 1, Appl
C 36	49.2	4.4	8920	2	US-08-150-741-1	Sequence 1, Appl
C 37	48.2	4.3	615	4	US-08-998-416-1137	Sequence 186, App
C 38	48.2	4.3	615	4	US-08-998-416-1137	Sequence 1137, Ap
C 39	48.2	4.3	837	4	US-08-998-416-288	Sequence 288, App
C 40	47.2	4.2	1689	1	US-07-991-867B-41	Sequence 41, Appl
C 41	47.2	4.2	1689	2	US-08-544-332-41	Sequence 41, Appl
C 42	47.2	4.2	1689	4	US-09-370-861A-41	Sequence 74, Appl
C 43	47.2	4.2	1947	4	US-09-370-861A-74	Sequence 36, Appl
C 44	47	4.2	665	2	US-08-883-795A-36	Sequence 124, App
C 45	47	4.2	12793	4	US-09-004-838-124	

ALIGNMENTS

RESULT 1	US-09-178-973B-7	Sequence 7, Application US/09178973B
Patent No. 6274710		
GENERAL INFORMATION:		
APPLICANT: Dumontier, Laure		
APPLICANT: Louhed, Valérie		
APPLICANT: Renaud, Jean-Christophe		
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible		
TITLE OF INVENTION: (Type)		
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof		
FILE REFERENCE: LUD 5543		
CURRENT APPLICATION NUMBER: US/09/178, 973B		
CURRENT FILING DATE: 1998-10-26		
NUMBER OF SEQ ID NOS: 17		
SEQ ID NO 7		
LENGTH: 1119		
TYPE: DNA		
ORGANISM: Mus musculus		
US-09-178-973B-7		
Query Match	100.0%; Score 1119; DB 4; Length 1119;	
Best Local Similarity	100.0%; Pred. No. 1.8e-273;	
Matches 1119; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
1	TAACAGGCTCTCTCTCACTTATCACTTGATGCGATCTCTGATGCTGTC	60
1	TAACAGGCTCTCTCTCACTTATCACTTGATGCGATCTCTGATGCTGTC	60
61	CTGCGAATATATATATTTTCTTATGGGATTTGGCCGACGCTGCTGCTTC	120
61	CTGCGAATATATATATTTTCTTATGGGATTTGGCCGACGCTGCTGCTTC	120
61	CTGCGAATATATATATTTTCTTATGGGATTTGGCCGACGCTGCTGCTTC	120
121	ATTGCTGTGGGCGCCAGAGCAATATCGCTGCGCCGCAACACCCGGTGCAAGTTG	180
121	ATTGCTGTGGGCGCCAGAGCAATATCGCTGCGCCGCAACACCCGGTGCAAGTTG	180
121	ATTGCTGTGGGCGCCAGAGCAATATCGCTGCGCCGCAACACCCGGTGCAAGTTG	180
181	GTGTCACCTTCAGACAGCCGATATGTCACCGACCTTTATCTGGCCAGAGGCC	240
181	GTGTCACCTTCAGACAGCCGATATGTCACCGACCTTTATCTGGCCAGAGGCC	240
181	GTGTCACCTTCAGACAGCCGATATGTCACCGACCTTTATCTGGCCAGAGGCC	240
241	AGCTTGCAGATTAACAACAGACGTCGGGCTCATCGGGAGAACTGTCGAGAGTC	300
241	AGCTTGCAGATTAACAACAGACGTCGGGCTCATCGGGAGAACTGTCGAGAGTC	300
241	AGCTTGCAGATTAACAACAGACGTCGGGCTCATCGGGAGAACTGTCGAGAGTC	300
301	AGTGTAAAGATCAGTCTGATGAAGAGAGTCTCACTTACCTGGAAGAGCTT	360
301	AGTGTAAAGATCAGTCTGATGAAGAGAGTCTCACTTACCTGGAAGAGCTT	360
301	AGTGTAAAGATCAGTCTGATGAAGAGAGTCTCACTTACCTGGAAGAGCTT	360
361	CTGCTCCCAATCAGACAGGTTCCAGCCCTTATGACAGAGAGTGTACTTCTGACC	420

Db 961 GTATACATTTTATTTATGAGTTTATTAATGATTTATTTATGAAAACATTAATCTGC 1020
Qy 1021 TATTGATTTTATTTATGAGCAAAATTAATTTATGACATTAATGAAACAGATATC 1080
Db 1021 TATTGATTTTATTTATGAGCAAAATTAATTTATGACATTAATGAAACAGATATC 1080
Qy 1081 TTAGGCTTTAATTAACACATGATATCATTAATAAAAAA 1119
Db 1081 TTAGGCTTTAATTAACACATGATATCATTAATAAAAAA 1119

RESULT 3
US-09-354-243B-7
Sequence 7, Application US/09354243B
Patent No. 6359117
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides
TITLE OF INVENTION: (TIFFs)
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 7
LENGTH: 1119
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-354-243B-7

Query Match 100.0%; Score 1119; DB 4; Length 1119;
Best Local Similarity 100.0%; Pred. No. 1,8e-273;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAAACAGGCTCTCTCTCACTTATCAACGTGTGCACTTGTGCGATCTGATGCTGTC 60
Db 1 TAAACAGGCTCTCTCTCACTTATCAACGTGTGCGATCTGATGCTGTC 60
Qy 61 CTGCAGAAATCTATGAGTTTTCCTTATGAGGAACTTTGCGCGACCTGCTTCTC 120
Db 61 CTGCAGAAATCTATGAGTTTTCCTTATGAGGAACTTTGCGCGACCTGCTTCTC 120
Qy 121 ATTGCGCTGTGGGCGCCAGAGGCAATGCGCTGCGCTCAACACCCGCTGCAAGCTTGAG 180
Db 121 ATTGCGCTGTGGGCGCCAGAGGCAATGCGCTGCGCTCAACACCCGCTGCAAGCTTGAG 180
Qy 181 GTGTCCAACTTCAGAGCGGCTACATGTCACCGCACCTTTATGCTGGGCAAGAGGCC 240
Db 181 GTGTCCAACTTCAGAGCGGCTACATGTCACCGCACCTTTATGCTGGGCAAGAGGCC 240
Qy 241 AGCCTTGAGATAACAACAACAAGCTGCTCATCGGAGAACTGTTCCAGAGATC 300
Db 241 AGCCTTGAGATAACAACAACAAGCTGCTCATCGGAGAACTGTTCCAGAGATC 300
Qy 301 AGTGTAAAGATCAGTGTCTCTGATGTAAGCAAGGTGCTCAACCTTCGGAAGAGTT 360
Db 301 AGTGTAAAGATCAGTGTCTCTGATGTAAGCAAGGTGCTCAACCTTCGGAAGAGTT 360
Qy 361 CTGCTCCCCAGTCAAGCAGGTTCCAGCTCACTGAGAGGAGGTAACCTTCTGACC 420
Db 361 CTGCTCCCCAGTCAAGCAGGTTCCAGCTCACTGAGAGGAGGTAACCTTCTGACC 420
Qy 421 AAATCTGAGCAATGAGCTCAGCTCTCTGATCAATGAGCGGTGACGACAAATCAGAG 480
Db 421 AAATCTGAGCAATGAGCTCAGCTCTCTGATCAATGAGCGGTGACGACAAATCAGAG 480
Qy 481 AATGTCAAGAGGCTGAAAGAGACAGTGAATAAAAGCTTGAAGAGAGATCAAGCGC 540

Db 481 AATGTCAAGAGGCTGAAAGAGACAGTGAATAAAAGCTTGAAGAGAGATCAAGCGC 540
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Db 541 ATTGGGGAACGTGACCTGCTGTTTATGTCCTGAGAAATGCTTGGCTCTGAGCGAGAA 600
Qy 601 AGCTGAAACAGAAAGACGCTCCCTCCGCTTCAAAAAGAAACAATAGATCCCTGAA 660
Db 601 AGCTGAAACAGAAAGACGCTCCCTCCGCTTCAAAAAGAAACAATAGATCCCTGAA 660
Qy 661 TGGACTTTTCTTAAGGAAAGTGAAGCTTAACCTCCATCATCTTAAGATTTTAC 720
Db 661 TGGACTTTTCTTAAGGAAAGTGAAGCTTAACCTCCATCATCTTAAGATTTTAC 720
Qy 721 ATGAAACCTGCTCAGTTGAAAAAAGAAATAGTGCAGTGTGTCATGAGACAGAGTA 780
Db 721 ATGAAACCTGCTCAGTTGAAAAAAGAAATAGTGCAGTGTGTCATGAGACAGAGTA 780
Qy 781 GACTTGATTAACCAAAAGATTCATTCATATTTATGTCACCTGATGATCAACAGAA 840
Db 781 GACTTGATTAACCAAAAGATTCATTCATATTTATGTCACCTGATGATCAACAGAA 840
Qy 841 AAATTAATGACTTTAAAAAATTGTTGAAAGAGGTTACCTCATCTTCTTGAAGAAA 900
Db 841 AAATTAATGACTTTAAAAAATTGTTGAAAGAGGTTACCTCATCTTCTTGAAGAAA 900
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Qy 1081 TTAGGCTTTAATTAACACATGATATCATTAATAAAAAA 1119
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RESULT 4
US-09-178-973B-9
Sequence 9, Application US/09178973B
Patent No. 6274710
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides
TITLE OF INVENTION: (TIFFs)
FILE REFERENCE: LUD 5543
CURRENT APPLICATION NUMBER: US/09/178,973B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-178-973B-9

Query Match 93.6%; Score 1047.8; DB 4; Length 1111;
Best Local Similarity 97.0%; Pred. No. 1.7e-255;
Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

Qy 3 AACAGGCTCTCTCTCACTTATCACTGTCAGTGTGCACTTGTGCGATCTGATGCTGCT 62
Db 1 AACAGGCTCTCTCTCACTTATCACTTGTGCACTTGTGCGATGCTGATGCTGCT 60

QY 63 GCAGAAATCTATGAGTTTTCCTTATGAGGGACTTTGCGCCGACAGCTGCTGCTCTCAT 122
DB 61 GCAGAAATCTATGAGTTTTCCTTATGAGGGACTTTGCGCCGACAGCTGCTGCTCTCAT 120
QY 123 TGGCCGTGAGGCGCCGAGGAGCAATGCGCTGCGCCGCAACACCCGGTGCAGCTGAGGT 182
DB 121 TGGCCGTGAGGCGCCGAGGAGCAATGCGCTGCGCCGCAACACCCGGTGCAGCTGAGGT 180
QY 183 GTCCAACTTCCAGCAGCCGTAACATGCTCAACCGCACCTTATGCTGGCCAGAGGCGCAG 242
DB 181 GTCCAACTTCCAGCAGCCGTAACATGCTCAACCGCACCTTATGCTGGCCAGAGGCGCAG 240
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DB 241 CCTTGCAATTAACAACACAGAGCTGCGGCTCATGCGGAGAAACCTGTTCCGAGAGTCAG 300
QY 303 TGGTAAAGTCAAGTGTACCTGATGAGAGAGTCTCAACCTTACCCCTGGAGAGCTTCT 362
DB 301 TGGTAAAGTCAAGTGTACCTGATGAGAGAGTCTCAACCTTACCCCTGGAGAGCTTCT 360
QY 363 GCTCCCCGAGTCAAGAGCTGCTCAACATGACAGAGTGTATCCTTCTGACCAA 422
DB 361 GCTCCCCGAGTCAAGAGCTGCTCAACATGACAGAGTGTATCCTTCTGACCAA 420
QY 423 ACTCAGCAATCAAGCTGCTGCTGTCACATCAAGCGGTGACGACAGAGATCCAGAGAA 482
DB 421 ACTCAGCAATCAAGCTGCTGCTGTCACATCAAGCGGTGACGACAGAGATCCAGAGAA 480
QY 483 TGTCAAGAGCTGAGAGAGAGAGAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAGCGCAT 542
DB 481 TGTCAAGAGCTGAGAGAGAGAGAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAGCGCAT 540
QY 543 TGGGGAAGTGAAGCTGCTGTTATGCTGAGAGAAAGCTGCTGCTGAGCGGAGAGAG 602
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QY 603 CTAGAAAGAGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662
DB 601 CTAGAAAGAGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
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DB 661 GACTTTTATCTTAAAGAGAGAGAGTGAAGAGTCAATCATCATTTAGAGAGATTTACAT 720
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DB 721 GAAAGCTGAGTCTGAGAGAGAGAGAGTGAAGAGTCAATCATCATTTAGAGAGATTTAG 780
QY 783 CTTGATTAACCAAGAGATTCATTTATGATGATGATGATGATGATGATGATGATGATGAT 842
DB 781 CTTGATTAACCAAGAGATTCATTTATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 843 ATATAGTACTTAAAGAGAGAGAGAGTGAAGAGTCAATCATCATTTAGAGAGATTTAG 902
DB 841 ATATAGTACTTAAAGAGAGAGAGAGTGAAGAGTCAATCATCATTTAGAGAGATTTAG 900
QY 903 CTATAGTACTTATTTCAATCAATCAATTTATATATATATATATATATATATATATATAT 962
DB 901 CTATAGTACTTATTTCAATCAATCAATTTATATATATATATATATATATATATATATAT 960
QY 963 ATATCAATTTATTTATGCTGAGTATTTATATATATATATATATATATATATATATAT 1022
DB 961 ATATCAATTTATTTATGCTGAGTATTTATATATATATATATATATATATATATATAT 1020
QY 1023 TTTATATTTT-AGTATAGGCAATTAATTTATGACAAATCAATATAGAGAAAGATATCT 1081
DB 1021 TTTATATTTTGAATATAGGCAATTAATTTATATATATATATATATATATATATATATCT 1080
QY 1082 TAGGCTTATATTAACAGATGATATCATAA 1112
DB 1081 TAGGCTTATATTAACAGATGATATCTATAA 1111

RESULT 5
US-09-419-568F-9
; Sequence 9, Application US/09419568F
; Patent No. 6331613
; GENERAL INFORMATION:
; APPLICANT: Dumoulier, Laure
; APPLICANT: Dumoulier, Jamila
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
; FILE REFERENCE: LUD 5543.2
; CURRENT APPLICATION NUMBER: US/09/419,568F
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US09/354,243
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 9
; LENGTH: 1111
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
US-09-419-568F-9
Query Match 93.6%; Score 1047.8; DB 4; Length 1111;
Best Local Similarity 97.0%; Pred. No. 1.7e-255;
Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;
QY 3 AACAGGCTCTCTCTCACTTATCAACTGTTGACACTTGTGCGATCTTGATGGCTCTCT 62
DB 1 AACAGGCTCTCTCTCACTTATCAACTTGTGACACTTGTGCGATCTTGATGGCTCTCT 60
QY 63 GCAGAAATCTATGAGTTTTCCTTATGAGGGACTTTGCGCCGACAGCTGCTGCTCTCAT 122
DB 61 GCAGAAATCTATGAGTTTTCCTTATGAGGGACTTTGCGCCGACAGCTGCTGCTCTCAT 120
QY 123 TGGCCGTGAGGCGCCGAGGAGCAATGCGCTGCGCCGCAACACCCGGTGCAGCTGAGGT 182
DB 121 TGGCCGTGAGGCGCCGAGGAGCAATGCGCTGCGCCGCAACACCCGGTGCAGCTGAGGT 180
QY 183 GTCCAACTTCCAGCAGCCGTAACATGCTCAACCGCACCTTATGCTGGCCAGAGGCGCAG 242
DB 181 GTCCAACTTCCAGCAGCCGTAACATGCTCAACCGCACCTTATGCTGGCCAGAGGCGCAG 240
QY 243 CCTTGCAATTAACAACAGAGCTGCGGCTCATGCGGAGAAAGCTGTTCCGAGAGTCAG 302
DB 241 CCTTGCAATTAACAACAGAGCTGCGGCTCATGCGGAGAAAGCTGTTCCGAGAGTCAG 300
QY 303 TGGTAAAGTCAAGTGTACCTGATGAGAGAGTGTCAACTTCAACCTTGGAGAGCGTCT 362
DB 301 TGGTAAAGTCAAGTGTACCTGATGAGAGAGTGTCAACTTCAACCTTGGAGAGCGTCT 360
QY 363 GCTCCCCGAGTCAAGAGCTGCTCAACATGACAGAGTGTATCCTTCTGACCAA 422
DB 361 GCTCCCCGAGTCAAGAGCTGCTCAACATGACAGAGTGTATCCTTCTGACCAA 420
QY 423 ACTCAGCAATCAAGCTGCTGCTGTCACATCAAGCGGTGACGACAGAGATCCAGAGAA 482
DB 421 ACTCAGCAATCAAGCTGCTGCTGTCACATCAAGCGGTGACGACAGAGATCCAGAGAA 480
QY 483 TGTCAAGAGCTGAGAGAGAGAGAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAGCGCAT 542
DB 481 TGTCAAGAGCTGAGAGAGAGAGAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAGCGCAT 540
QY 543 TGGGGAAGTGAAGCTGCTGTTATGCTGAGAGAAAGCTTGTGCTTGAAGAGAGAG 602
DB 541 TGGGGAAGTGAAGCTGCTGTTATGCTGAGAGAAAGCTTGTGCTTGAAGAGAGAG 600
QY 603 CTAGAAAGAGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662
DB 601 CTAGAAAGAGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

QY 663 GACCTTTTACTAAGAAAGTGAAGACTAACGTCATCATTAAGAAATTCACAT 722
DB 661 GACTTTTCTTAAGAAAGTGAAGACTTAACGTCATCATTAAGAAATTCACAT 720
QY 723 GAAACCTGGCTCAGTTGAAAAAGAAATAGTGTCAAGTTGTCATGAGACAGAGTGA 782
DB 721 GAAACCTGGCTCAGTTGAAAAAGAAATAGTGTCAAGTTGTCATGAGACAGAGTGA 780
QY 783 CTTGATTAACCAAGAAATTCATTAACATATTTTATTTGTCATGATGATACAAAGAAA 842
DB 781 CTTGATTAACCAAGAAATTCATTAACATATTTTATTTGTCATGATGATACAAAGAAA 840
QY 843 ATATAGTACTTTAAAAATTTGTTGAAGAGGTTCCCTCAATCCCTTAGAAAAAAG 902
DB 841 AGTATGACTTTAAAAATTTGTTGAAGAGGTTCCCTCAATCCCTTAGAAAAAAG 900
QY 903 CTTATGTAATCTCATTTCCATTCATCAATATTTTATATATATAGTTTATTTATTAAT 962
DB 901 CCTATGTAATCTCATTTCCATTCATCAATCTTTATATATATATATTTATTTATTAAT 960
QY 963 ATACATTTTATTTATGTCAGTTTATTAATATATATATATTTATTAAGAAACATTAATCTGCTA 1022
DB 961 ATACATTTTATTTATGTCAGTTTATTAATATATATATATTTATTAAGAAATTTATCTGATG 1020
QY 1023 TTGATATTTT-AGTATTAAGCAATTAATATTTATTAAGCAATTAATTAAGCAATTAATCT 1081
DB 1021 TTGATATTTTGAAGTATTAAGCAATTAATATTTATTAAGTATTAAGTATTAAGCAATTAATCT 1080
QY 1082 TAGGCTTTAATAAACAATGATATCATATAA 1112
DB 1081 TAGGCTTTAATAAACAATGATATCATATAA 1111

RESULT 6

US-09-354-243B-9
Sequence 9, Application US/09354243B
Patent No. 6359117
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Leunhed, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
TITLE OF INVENTION: (TTFs)
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-354-243B-9

Query Match 93.6%; Score 1047.8; DB 4; Length 1111;
Best Local Similarity 97.0%; Pmed. No. 1.7e-255;
Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;
QY 3 AACAGGCTCTCTCTCTCACTATCAACTGTGACACTTGTGCGATCTCTGATGGCTGCT 62
DB 1 AACAGGCTCTCTCTCTCACTATCAACTGTGACACTTGTGCGATCTCTGATGGCTGCT 60
QY 63 GCAGAAATCTATGAGATTTTCCCTTATGGGACTTTGGCCGCAAGCTGCTGCTTCTCAT 122
DB 61 GCAGAAATCTATGAGATTTTCCCTTATGGGACTTTGGCCGCAAGCTGCTGCTTCTCAT 120
QY 123 TGCCCTGTGGGCCCAAGGCAATATGCGTGCCTCAACACCCGGGTGAAGCTTGAGGT 182
DB 121 TGCCCTGTGGGCCCAAGGCAATATGCGTGCCTCAACACCCGGGTGAAGCTTGAGGT 180

QY 183 GTCCAACTTCACAGACCGGTACATGTCACACCGCACTTTATGTCGGCCAGAGGCCAG 242
DB 181 GTCCAACTTCACAGACCGGTACATGTCACACCGCACTTTATGTCGGCCAGAGGCCAG 240
QY 243 CTTGAGATTAACACACAGAGGTCGGCTCATTCGGGAGAAATCTGTTCCAGAGTCA 302
DB 241 CTTGAGATTAACACACAGAGGTCGGCTCATTCGGGAGAAATCTGTTCCAGAGTCA 300
QY 303 TGTCTAAAGATCAAGTCTTACCTGATGAAGAGGTCCTCAACTTCACCTCGAAGAGCTTCT 362
DB 301 TGTCTAAAGATCAAGTCTTACCTGATGAAGAGGTCCTCAACTTCACCTCGAAGAGCTTCT 360
QY 363 GCTCCCCGACGACAGAGGTCACGCTTCCAGCTTCAATGACAGAGGTCCTTCTGACCA 422
DB 361 GCTCCCCGACGACAGAGGTCACGCTTCCAGCTTCAATGACAGAGGTCCTTCTGACCA 420
QY 423 ACTCAGCAATCAAGCTCAGCTCCTGTCACATCAAGCTGACAGACAGAAATCCAGAGAA 482
DB 421 ACTCAGCAATCAAGCTCAGCTCCTGTCACATCAAGCTGACAGACAGAAATCCAGAGAA 480
QY 483 TGTCAAGAGCTGAAGAGACAGTGAAGAAAGCTTGAAGAGTGAAGATCAAGCCGAT 542
DB 481 TGTCAAGAGCTGAAGAGACAGTGAAGAAAGCTTGAAGAGTGAAGATCAAGCCGAT 540
QY 543 TGGGGAATCGACCTGCTTTATGTCCTGAGAAATGCTTGGCTGAGCCGAGAGAG 602
DB 541 CGGGGAATCGACCTGCTTTATGTCCTGAGAAATGCTTGGCTGAGCCGAGAGAG 600
QY 603 CTGAAAAAGAAAGAACTGCTCCTTCTGCTTCAAAAAAGAAACATTAAGTCCCTGATG 662
DB 601 CTGAAAAAGAAAGAACTGCTCCTTCTGCTTCTTCAAAAAAGAAACATTAAGTCCCTGATG 660
QY 663 GACTTTTCTTAAGAAAGTGAAGGCTAAAGCTTCAATCATCATTAAGAAATTCACAT 722
DB 661 GACTTTTCTTAAGAAAGTGAAGGCTAAAGCTTCAATCATCATTAAGAAATTCACAT 720
QY 723 GAAACCTGGCTCAGTTGAAAAAGAAATAGTGTCAAGTTGTCATGAGACAGAGTGA 782
DB 721 GAAACCTGGCTCAGTTGAAAAAGAAATAGTGTCAAGTTGTCATGAGACAGAGTGA 780
QY 783 CTTGATTAACCAAGAAATTCATTAACATATTTTATTTGTCATGATGATACAAAGAAA 842
DB 781 CTTGATTAACCAAGAAATTCATTAACATATTTTATTTGTCATGATGATACAAAGAAA 840
QY 843 ATATAGTACTTTAAAAATTTGTTGAAGAGGTTCCCTCAATCCCTTAGAAAAAAG 902
DB 841 AGTATGACTTTAAAAATTTGTTGAAGAGGTTCCCTCAATCCCTTAGAAAAAAG 900
QY 903 CTTATGTAATCTCATTTCCATTCATCAATATTTTATATATATATTTATTTATTAAT 962
DB 901 CCTATGTAATCTCATTTCCATTCATCAATCTTTATATATATATTTATTTATTAAT 960
QY 963 ATACATTTTATTTATGTCAGTTTATTAATATATATATTTATTAAGAAACATTAATCTGCTA 1022
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QY 1023 TTGATATTTT-AGTATTAAGCAATTAATATTTATTAAGCAATTAATTAAGCAATTAATCT 1081
DB 1021 TTGATATTTTGAAGTATTAAGCAATTAATATTTATTAAGTATTAAGTATTAAGCAATTAATCT 1080
QY 1082 TAGGCTTTAATAAACAATGATATCATATAA 1112
DB 1081 TAGGCTTTAATAAACAATGATATCATATAA 1111

RESULT 7

US-09-178-973B-8
Sequence 8, Application US/09178973B
Patent No. 6274710
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Leunhed, Jean-Christophe
APPLICANT: Renauld, Jean-Christophe


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; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factors
; TITLE OF INVENTION: (Title)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543
; CURRENT APPLICATION NUMBER: US/09/178,973B
; CURRENT FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 8
; LENGTH: 7445
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-178-973B-8

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[illegible]

Query Match	53.7%	Score 601.4	DB 4	Length 7445
Best Local Similarity	99.8%	Pred. No. 2,4e-14		
Matches 602	Conservative	0	Mismatches 1	Indels 0
			Gaps	0

Qy	510	AAACCTTGAGAGAGAGTGGAGAGATCAAGAGCATTTGGGGAACTGGACCTGCTGTTATATC	569
Db	6535	ATACCTTGGAGAGAGTGGAGAGATCAAGAGCATTTGGGGAACTGGACCTGCTGTTATATC	6599
Qy	570	TCTGAGAAATGCTTGGCTCTGAGCGGAGAGAGACTTGAAGAACTGCTCTCTTCT	629
Db	6595	TCTGAGAAATGCTTGGCTGCTGAGCGGAGAGAGAGACTTGAAGAACTGCTCTCTTCT	665
Qy	630	GCCTTCTTAAAAAGAACAAATAGATCCCTGAAATGCACTTTTCTAATAAGAAAGTGAGAA	689
Db	6655	GCCTTCTTAAAAAGAACAAATAGATCCCTGAAATGCACTTTTCTAATAAGAAAGTGAGAA	6719
Qy	690	GCTAACGTCATCATCATTTAGAAAGATTTACATGAAACCTGGCTCAGTTGAAAAAGAAAA	749
Db	6715	GCTAACGTCATCATCATTTAGAAAGATTTACATGAAACCTGGCTCAGTTGAAAAAGAAAA	6779
Qy	750	TAGTGTCAAGTTGTTCATGAGACGACGAGTGATCTTGATACCAACAAAGATTCATTGACA	809
Db	6775	TAGTGTCAAGTTGTTCATGAGACGACGAGTGATCTTGATACCAACAAAGATTCATTGACA	6839
Qy	810	ATATTTTATGTCACTGATGATACACAGAAAAATTAAGTCTTTAAAAAATTTGTTGAA	869
Db	6835	ATATTTTATGTCACTGATGATACACAGAAAAATTAAGTCTTTAAAAAATTTGTTGAA	6889
Qy	870	AGAGAGTTACCTTCATTCCTTTAGAAAAAAAAGCTTATGAACTTCATTTCCATATCCAA	929
Db	6895	AGAGAGTTACCTTCATTCCTTTAGAAAAAAAAGCTTATGAACTTCATTCATATCCAA	6959
Qy	930	TATTTTATATATGTAAGTTTATTTATATATAGTATACATTTTATTTATATGTCAGTTTATA	989
Db	6955	TATTTTATATATGTAAGTTTATTTATATATAGTATACATTTTATTTATATGTCAGTTTATA	7019
Qy	990	ATATGAGATTTTATATAGAAACATTAATGCTATGATATTAGTATAGGCAAAATATA	1049
Db	7015	ATATGAGATTTTATATAGAAACATTAATGCTATGATATTAGTATAGGCAAAATATA	7079
Qy	1050	TTTATGACAAATACATGAGAAACAAGATATCTTAAGCTTTAATAAACAATGATATCAT	11099
Db	7075	TTTATGACAAATACATGAGAAACAAGATATCTTAAGCTTTAATAAACAATGATATCAT	7139
Qy	1110	AAA 1112	
Db	7135	AAA 7137	

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RESULT 9
US-09-354-243B-8
; Sequence 8, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
; APPLICANT: Dumoulier, Laure
; APPLICANT: Louned, Jamila
; APPLICANT: Renaud, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
; TITLE OF INVENTION: (TIS)

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;; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
;; FILE REFERENCE: LUD 5543.1
;; CURRENT APPLICATION NUMBER: US/09/354,243B
;; CURRENT FILING DATE: 1999-07-16
;; PRIOR APPLICATION NUMBER: US09/178,973
;; PRIOR FILING DATE: 1998-10-26
;; NUMBER OF SEQ ID NOS: 29
;; SEQ ID NO 8
;; LENGTH: 7445
;; TYPE: DNA
;; ORGANISM: Mus musculus
;; FEATURE:
US-09-354-243B-8

Query Match 53.7%; Score 601.4; DB 4; Length 7445;
Best Local Similarity 99.8%; Pred. No. 2.4e-142;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 510 AAAGCTTGAGAGAGTGAAGATCAAGCGATGGGGAACCTGCTGTTATGTC 569
DB 6535 ATAGCTTGAGAGAGTGAAGATCAAGCGATGGGGAACCTGCTGTTATGTC 6594
QY 570 TCTGAGAAATGCTGCTGCTGAGCGAAGAGCTGAGAAAGAGAACTGCTCCT 629
DB 6595 TCTGAGAAATGCTGCTGCTGAGCGAAGAGCTGAGAAAGAGAACTGCTCCT 6654
QY 630 GCCTTCTAAAAAGAAACAATAGATCCCTGAATGACTTTTCTAATAAGAAAGTGA 689
DB 6655 GCCTTCTAAAAAGAAACAATAGATCCCTGAATGACTTTTCTAATAAGAAAGTGA 6714
QY 690 GCTAACGTCATCATATTAGAAAGATTCAACATGAACCTGCTCAGTTGAAAAAGAAA 749
DB 6655 GCCTTCTAAAAAGAAACAATAGATCCCTGAATGACTTTTCTAATAAGAAAGTGA 6714
QY 6715 GCTAACGTCATCATATTAGAAAGATTCAACATGAACCTGCTCAGTTGAAAAAGAAA 6774
DB 750 TAGTGTCAAGTGTCCATGAGACGAGGTAGCTGATPACACAAAGATTCATTGACA 809
QY 6775 TAGTGTCAAGTGTCCATGAGACGAGGTAGCTGATPACACAAAGATTCATTGACA 6834
DB 750 TAGTGTCAAGTGTCCATGAGACGAGGTAGCTGATPACACAAAGATTCATTGACA 809
QY 810 ATATTTTATTTGTCACGTGATGATACACAGAAAAATATGACTTTAAAAATTTGTTGAA 869
DB 6835 ATATTTTATTTGTCACGTGATGATACACAGAAAAATATGACTTTAAAAATTTGTTGAA 6894
QY 870 AGAGGTTACCTCTCATCTCTTTAGAAAAAAGCTTATGTAATCTTCATTCATTCACAA 929
DB 6895 AGAGGTTACCTCTCATCTCTTTAGAAAAAAGCTTATGTAATCTTCATTCATTCACAA 6954
QY 930 TATTTTATATATGTAAGTTTATTTATTAAGATACATTTATTTATGTCAGTTATTA 989
DB 6955 TATTTTATATATGTAAGTTTATTTATTAAGATACATTTATTTATGTCAGTTATTA 7014
QY 990 ATATGATTTATTTATTAAGAAACATTTATGCTATGATATTTAGTAAGGCAATATTA 1049
DB 7015 ATATGATTTATTTATTAAGAAACATTTATGCTATGATATTTAGTAAGGCAATATTA 7074
QY 1050 TTATGACAAATACTATGAGAAACAGATATCTTAGGCTTTAATTAACACATGATATCAT 1109
DB 7075 TTATGACAAATACTATGAGAAACAGATATCTTAGGCTTTAATTAACACATGATATCAT 7134
QY 1110 AAA 1112
DB 7135 AAA 7137

RESULT 10
US-09-178-973B-17

;; Sequence 17, Application US/09178973B
;; Patent No. 6274710
;; GENERAL INFORMATION:
;; APPLICANT: Dumoutier, Laure
;; APPLICANT: Louhed, Jamila
;; APPLICANT: Renaud, Jean-Christophe
;; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
;; TITLE OF INVENTION: (Tlfs)

;; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
;; FILE REFERENCE: LUD 5543
;; CURRENT APPLICATION NUMBER: US/09/178,973B
;; CURRENT FILING DATE: 1998-10-26
;; NUMBER OF SEQ ID NOS: 17
;; SEQ ID NO 17
;; LENGTH: 5935
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-09-178-973B-17

Query Match 49.6%; Score 555.2; DB 4; Length 5935;
Best Local Similarity 96.0%; Pred. No. 1e-130;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

QY 510 AAAGCTTGAGAGAGTGAAGATCAAGCGATGGGGAACCTGCTGTTATGTC 569
DB 5221 ATAGCTTGAGAGAGTGAAGATCAAGCGATGGGGAACCTGCTGTTATGTC 5280
QY 570 TCTGAGAAATGCTGCTGCTGAGCGAAGAGCTGAGAAAGAGAACTGCTCCT 629
DB 5281 TCTGAGAAATGCTGCTGCTGAGCGAAGAGCTGAGAAAGAGAACTGCTCCT 5340
QY 630 GCCTTCTAAAAAGAAACAATAGATCCCTGAATGACTTTTCTAATAAGAAAGTGA 689
DB 5341 GCCTTCTAAAAAGAAACAATAGATCCCTGAATGACTTTTCTAATAAGAAAGTGA 5400
QY 690 GCTAACGTCATCATATTAGAAAGATTCAACATGAACCTGCTCAGTTGAAAAAGAAA 749
DB 5401 GCTAACGTCATCATATTAGAAAGATTCAACATGAACCTGCTCAGTTGAAAAAGAAA 5460
QY 750 TAGTGTCAAGTGTCCATGAGACGAGGTAGCTGATPACACAAAGATTCATTGACA 809
DB 5461 TAGTGTCAAGTGTCCATGAGACGAGGTAGCTGATPACACAAAGATTCATTGACA 5520
QY 810 ATATTTTATTTGTCACGTGATGATACACAGAAAAATATGACTTTAAAAATTTGTTGAA 869
DB 5521 ATATTTTATTTGTCACGTGATGATACACAGAAAAATATGACTTTAAAAATTTGTTGAA 5580
QY 870 AGAGGTTACCTCTCATCTCTTTAGAAAAAAGCTTATGTAATCTTCATTCATTCACAA 929
DB 5581 AGAGGTTACCTCTCATCTCTTTAGAAAAAAGCTTATGTAATCTTCATTCATTCACAA 5640
QY 930 TATTTTATATATGTAAGTTTATTTATTAAGATACATTTATTTATGTCAGTTATTA 989
DB 5641 TATTTTATATATGTAAGTTTATTTATTAAGATACATTTATTTATGTCAGTTATTA 5700
QY 990 ATATGATTTATTTATTAAGAAACATTTATGCTATGATATTT-AGTATAGGCAATAT 1048
DB 5701 ATATGATTTATTTATTAAGAAACATTTATGCTATGATATTTAGTATTAAGCAATAT 5760
QY 1049 ATTTAGCAATACTATGAGAAACAGATATCTTAGGCTTTAATTAACACATGATATCA 1108
DB 5761 ATTTAGCAATACTATGAGAAACAGATATCTTAGGCTTTAATTAACACATGATATCA 5820
QY 1109 TAAA 1112
DB 5821 TAAA 5824

RESULT 11
US-09-419-568F-29

;; Sequence 29, Application US/09419568F
;; Patent No. 6331613
;; GENERAL INFORMATION:
;; APPLICANT: Dumoutier, Laure
;; APPLICANT: Louhed, Jamila
;; APPLICANT: Renaud, Jean-Christophe
;; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
;; FILE REFERENCE: LUD 5543.2
;; CURRENT APPLICATION NUMBER: US/09/419,568F
;; CURRENT FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 29
LENGTH: 5935
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-419-568F-29

Query Match 49.6%; Score 555.2; DB 4; Length 5935;
Best Local Similarity 96.0%; Pred. No. 1e-130;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

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QY 510 AAAGCTGGAGAGAGAGATCAAGGCGATTGGGGAACTGACCTGCTTTATATGC 569
DB 5221 ATAGCTGGAGAGAGAGAGATCAAGGCGATTGGGGAACTGACCTGCTTTATATGC 5280
QY 570 TCTGAGAAATGCTTGCCTGCTGAGGAGAAAGCTAGAAAAGAAAGAACTGCTCTTCT 629
DB 5281 TCTGAGAAATGCTTGCCTGCTGAGGAGAAAGCTAGAAAAGAAAGAACTGCTCTTCT 5340
QY 630 GCCTCTTAAAAAGAAAGAAAGCTGCTGATGAACTTTTCTTAAAGAAAGTGAACA 689
DB 5341 GCCTCTTAAAAAGAAAGAAAGCTGCTGATGAACTTTTCTTAAAGAAAGTGAACA 5400
QY 690 GCTAACGCCATCATCATTAAGATTCACATGAAACCTGGCTCAGTTGAAAAAGAAA 749
DB 5401 GCTAACGCCATCATCATTAAGATTCACATGAAACCTGGCTCAGTTGAAAAAGAAA 5460
QY 750 TAGTGTCAAGTGTCCATGAGACAGAGGTAGACTTGAATTAACCAAGAAATTCATTGACA 809
DB 5461 TAGTGTCAAGTGTCCATGAGACAGAGGTAGACTTGAATTAACCAAGAAATTCATTGACA 5520
QY 810 ATATTTTATGTCTACTGATGATACACAGAAAAATATGTAATTTTAAAAATTTGTTGAA 869
DB 5521 ATATTTTATGTCTACTGATGATACACAGAAAAATATGTAATTTTAAAAATTTGTTGAA 5580
QY 870 AGAGAGTACCTCTCATCTCTTAAAGAAAAAGCTTATGTAATTCATTCATTCATTCACA 929
DB 5581 AGAGAGTACCTCTCATCTCTTAAAGAAAAAGCTTATGTAATTCATTCATTCATTCACA 5640
QY 930 TATTTTATATATGTAAGTTTATTTATTAAGTATACATTTTATTTATGTCAGTTTATTA 989
DB 5641 TATTTTATATATGTAAGTTTATTTATTAAGTATACATTTTATTTATGTCAGTTTATTA 5700
QY 990 ATATGATTTTATTTATAGAAACATTATCTGTAATGATATTT-AGTATAGGCAAAATAT 1048
DB 5701 ATATGATTTTATTTATAGAAACATTATCTGTAATGATATTTAGATATTAACAAATATAT 5760
QY 1049 ATTATGACATTAATCTATGAGAAACAGATATCTTGGCTTTATTAACACATGATATCA 1108
DB 5761 ATTATGATTAATTAATCTATGAGAAACAGATATCTTGGCTTTATTAACACATGATATCA 5820
QY 1109 TAAA 1112
DB 5821 TAAA 5824
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RESULT 12
US-09-354-243B-29
Sequence 29, Application US/09354243B
Patent No. 6359117
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louned, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides (TIFs)
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.1

CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 29
LENGTH: 5935
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-354-243B-29

Query Match 49.6%; Score 555.2; DB 4; Length 5935;
Best Local Similarity 96.0%; Pred. No. 1e-130;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

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QY 630 GCCTCTTAAAAAGAAAGAAAGCTGCTGATGAACTTTTCTTAAAGAAAGTGAACA 689
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QY 690 GCTAACGCCATCATCATTAAGATTCACATGAAACCTGGCTCAGTTGAAAAAGAAA 749
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QY 750 TAGTGTCAAGTGTCCATGAGACAGAGGTAGACTTGAATTAACCAAGAAATTCATTGACA 809
DB 5461 TAGTGTCAAGTGTCCATGAGACAGAGGTAGACTTGAATTAACCAAGAAATTCATTGACA 5520
QY 810 ATATTTTATGTCTACTGATGATACACAGAAAAATATGTAATTTTAAAAATTTGTTGAA 869
DB 5521 ATATTTTATGTCTACTGATGATACACAGAAAAATATGTAATTTTAAAAATTTGTTGAA 5580
QY 870 AGAGAGTACCTCTCATCTCTTAAAGAAAAAGCTTATGTAATTCATTCATTCATTCACA 929
DB 5581 AGAGAGTACCTCTCATCTCTTAAAGAAAAAGCTTATGTAATTCATTCATTCATTCACA 5640
QY 930 TATTTTATATATGTAAGTTTATTTATTAAGTATACATTTTATTTATGTCAGTTTATTA 989
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QY 990 ATATGATTTTATTTATAGAAACATTATCTGTAATGATATTT-AGTATAGGCAAAATAT 1048
DB 5701 ATATGATTTTATTTATAGAAACATTATCTGTAATGATATTTAGATATTAACAAATATAT 5760
QY 1049 ATTATGACATTAATCTATGAGAAACAGATATCTTGGCTTTATTAACACATGATATCA 1108
DB 5761 ATTATGATTAATTAATCTATGAGAAACAGATATCTTGGCTTTATTAACACATGATATCA 5820
QY 1109 TAAA 1112
DB 5821 TAAA 5824
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RESULT 13
US-09-419-568F-24
Sequence 24, Application US/09419568F
Patent No. 6331613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louned, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides (TIFs)
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/419,568F

/ CURRENT FILING DATE: 1999-10-18
/ PRIOR APPLICATION NUMBER: US09/354,243
/ PRIOR FILING DATE: 1999-07-16
/ PRIOR APPLICATION NUMBER: US09/178,973
/ PRIOR FILING DATE: 1998-10-26
/ NUMBER OF SEQ ID NOS: 29
/ SEQ ID NO 24
/ LENGTH: 690
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
US-09-419-568F-24

Query Match 36.6%; Score 409.2; DB 4; Length 690;
Best Local Similarity 76.1%; Pred. No. 3e-94;
Matches 504; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 9 CTCCTCTCACTTATCACTGTTGACACTTGTGCGATCTGTATGAGTGTCTCTGAGAA 68
DB 29 CTCCTTCCCAAGCACAGTGTGCTGAGTTAGATTGTCTGCAATGGCCGCTGAGAA 88
QY 69 ATCTATGATTTTCCCTTATGAGGACCTTGGCCGACGCTGCTTCTCTGAGCCCT 128
DB 89 ATCTGAGACTCTTCTTATGAGGACCTGCGCACAGCTGCTCTCTCTGAGCCCT 148
QY 129 GTGGGCCCCAGAGGCAATGCGCTGCGCTCAACACCCGCTGCAAGCTTGAAGTTCGA 188
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QY 189 CTTCAGAGCCGATACATGTCACACGCACTTTATGCTGGCCAAAGAGCCGACCTTGC 248
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DB 509 AAGGCTGAAGAGACAGTGAATAAGCTTGAAGAGTGAAGATCAAGGCGATTGGGGA 568
QY 549 AAGGCTGAAGAGACAGTGAATAAGCTTGAAGAGTGAAGATCAAGGCGATTGGGGA 608
DB 569 ACTGAGTTGCTGTTATGCTCTGAGAAATGCTGCAATTGACAGAGCAAGGCTGAAA 628
QY 609 AAGGAGAACTGCTCTCTGCTTCTTAAAGAAATGATGATGCTGAAATGCACTTT 668
DB 629 AATGATTAATAACCCCTTCTCTGCTGAAATTAATAATTAATGATGATGATGAT 688
QY 669 TT 670
DB 689 TT 690

RESULT 14
US-09-354-243B-24
/ Sequence 24, Application US/09354243B
/ Patent No. 6359117
/ GENERAL INFORMATION:
/ APPLICANT: Dumoulier, Laure
/ APPLICANT: Louhed, Tamila

/ APPLICANT: Renaud, Jean-Christophe
/ TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
/ TITLE OF INVENTION: (Tlfe)
/ FILE REFERENCE: LUD 5543.1
/ CURRENT APPLICATION NUMBER: US/09/354,243B
/ CURRENT FILING DATE: 1999-07-16
/ PRIOR APPLICATION NUMBER: US09/178,973
/ PRIOR FILING DATE: 1998-10-26
/ NUMBER OF SEQ ID NOS: 29
/ SEQ ID NO 24
/ LENGTH: 690
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
US-09-354-243B-24

Query Match 36.6%; Score 409.2; DB 4; Length 690;
Best Local Similarity 76.1%; Pred. No. 3e-94;
Matches 504; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 9 CTCCTCTCACTTATCACTGTTGACACTTGTGCGATCTGTATGAGTGTCTCTGAGAA 68
DB 29 CTCCTTCCCAAGCACAGTGTGCTGAGTTAGATTGTCTGCAATGGCCGCTGAGAA 88
QY 69 ATCTATGATTTTCCCTTATGAGGACCTTGGCCGACGCTGCTTCTCTGAGCCCT 128
DB 89 ATCTGAGACTCTTCTTATGAGGACCTGCGCACAGCTGCTCTCTCTGAGCCCT 148
QY 129 GTGGGCCCCAGAGGCAATGCGCTGCGCTCAACACCCGCTGCAAGCTTGAAGTTCGA 188
DB 149 CTGTGATACAGGAGGAGGAGCTGCGCCATCACTGAGCTTGAACAAGTTCGA 208
QY 189 CTTCAGAGCCGATACATGTCACACGCACTTTATGCTGGCCAAAGAGCCGACCTTGC 248
DB 209 CTTCAGAGCCCTTATATCAACACGCACTTATGCTGGCTTGAAGAGCTTGTGCG 268
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DB 569 AAGGAGAACTGCTCTCTGCTTCTTAAAGAAATGATGATGCTGAAATGCACTTT 628
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DB 629 AATGATTAATAACCCCTTCTCTGCTGAAATTAATAATTAATGATGATGATGAT 688
QY 669 TT 670
DB 689 TT 690

RESULT 15
US-09-419-568F-25
/ Sequence 25, Application US/09419568F

Patent No. 6331613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
TITLE OF INVENTION: (Title) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 25
LENGTH: 4797
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-419-568F-25

Query Match 11.3%; Score 126; DB 4; Length 4797;
Best Local Similarity 71.7%; Pred. No. 2.5e-22;
Matches 165; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
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DB 29 CTCCTTCCCAAGTACAGAGTGTGCTGAGTAGAATGTGTGCAATGGCCGCTGCAGAA 88
QY 69 ATCTATGAGTTTTCCTTATGGGGAAGCTTGGCCGCGAGCTGCTGCTTCTCATTTGCCCT 128
DB 89 ATCTGTAGCTCTTCTTATGGGGAAGCTTGGCCGCGAGCTGCTGCTTCTTGGCCCT 148
QY 129 GTGGGCCAGAGGCAATGCGCTGCGCTCAACACCCGCTGCAAGTTGAGGTGTCCAA 188
DB 149 CTGTGTACAGGAGAGAGAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAACTCCA 208
QY 189 CTTCCAGAGCCGTATCATGTCAACCGCACCTTTATGCTGSCCAAGAGG 238
DB 209 CTTCCAGAGCCGTATCATCAACCGCACCTTCTATGCTGCTAAGAGG 258

Search completed: July 19, 2003, 19:46:43
Job time : 38.2798 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:03:00 ; Search time 12472.3 Seconds

(without alignments)
17372.171 Million cell updates/sec

Title: US-09-751-797-8

Perfect score: 7445 1 gctatcaccgtccttaagat.....gatttaattatcgttat 7445

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Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: gb_hcg:*

3: gb_in:*

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5: gb_ov:*

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22: em_ov:*

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25: em_pl:*

26: em_ro:*

27: em_seg:*

28: em_un:*

29: em_vl:*

30: em_hcg_hum:*

31: em_hcg_inh:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pin:*

35: em_hcg_rod:*

36: em_hcg_mam:*

37: em_hcg_vit:*

38: em_sy:*

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40: em_hcgo_mus:*

41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	7445	100.0	7445	6 AR165227	AR165227 Sequence
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3	7441.8	100.0	7445	6 AX459954	AX459954 Sequence
4	7426	99.7	8370	10 MMU294727	AJ294727 Mus muscu
5	4245.2	57.0	5935	6 AR165224	AR165224 Sequence
6	4245.2	57.0	5935	6 AR201417	AR201417 Sequence
7	4245.2	57.0	5935	6 AX459988	AX459988 Sequence
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9	1197.6	16.1	133899	2 AC111483	AC111483 Rattus no
10	1081	14.5	8393	9 AF387519	AF387519 Homo sapi
11	1079.4	14.5	133350	9 AC022511	AC022511 Homo sapi
12	929.6	12.5	5397	9 HSA277248	AJ277248 Homo sapi
13	686	9.2	4797	6 AR201415	AR201415 Sequence
14	686	9.2	4797	6 AX459972	AX459972 Sequence
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17	601.4	8.1	1119	6 AX459953	AX459953 Sequence
18	601.4	8.1	1121	10 MMU2949491	AJ294941 Mus muscu
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ALIGNMENTS

RESULT 1

AR165227

LOCUS AR165227 7445 bp DNA linear PAT 17-OCT-2001

DEFINITION Sequence 8 from patent US 6274710.

ACCESSION AR165227

VERSION AR165227.1 GI:16238720

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 7445)

AUTHORS Dumoutier L., Louhed J. and Renaud J.-C.

TITLE Antibodies which specifically bind T cell inducible factors (Tifs)

JOURNAL Patent: US 6274710-A 8 14-AUG-2001;

FEATURES Location/Qualifiers

source 1. 7445
/organism="unknown"
BASE COUNT 2058 a 1570 c 1597 g 2220 t
ORIGIN

Query Match 100.0%; Score 7445; DB 6; Length 7445;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1921 ACACCTAAACAGTAAAGACTCAGACCTCTACAGCAATCATGCTGTGATACCATGCTA 1980
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Oy 2041 CTCACCTATCAACTGTGTCACCTGTGGGATCTGTGATGGCTGTCTGCAAAATCTATG 2100

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DEFINITION Sequence 8 from patent US 6359117.
ACCESSION AR201398
VERSION AR201398.1 GI:20252286
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Dumoutier, L., Louhed, J. and Renaud, J.-C.
TITLE Isolated nucleic acid molecules which encode T cell inducible factors (Tfns), the proteins encoded, and uses therefor
JOURNAL Patent: US 6359117-A 8 19-MAR-2002;
FEATURES
source 1. 7445
BASE COUNT 2058 a 1570 c 1597 g 2220 t
ORIGIN
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Qy	1621	TCTACTACGGCAAAAGCCATGAGCTTTCTTTGAAAACCGTGTTAGAAGATTTCTGGGATTT	1680
Db	1621	TCTACTACGGCAAAAGCCATGAGCTTTCTTTGAAAACCGTGTTAGAAGATTTCTGGGATTT	1680
Qy	1681	GTCGCAAAAAGCACTTGTGTGGCCCTCACCGTGAAGTTTTAGGGAAGATTCCTCCATCTCT	1740
Db	1681	GTCGCAAAAAGCACTTGTGTGGCCCTCACCGTGAAGTTTTAGGGAAGATTCCTCCATCTCT	1740
Qy	1741	CAAGGTGGGAAGGCTTGGAGGTGTCTGTGGGCTCTATAGGAGGTGTAGTACTTCTC	1800
Db	1741	CAAGGTGGGAAGGCTTGGAGGTGTCTGTGGGCTCTATAGGAGGTGTAGTACTTCTC	1800
Qy	1801	AGAAACAGACTGGAAAATAGATATGTCTGATGTCTATCATTCACAAATACCAAAA	1860

Db	1801	AGAMGACGAGCTGCAAAATTGATATATGTCTGATGTCAATATATCTACAAATACCAAAAA	1860
Qy	1861	ACCCTGCTGCCGATGCGTATTAAGAAGACNACTTCTGCTCTCCCATCACAAGCAG	1920
Db	1861	ACCCTGCTGCCGATGCGTATTAAGAAGACNACTTCTGCTCTCCCATCACAAGCAG	1920
Qy	1921	ACACCTAAACAGGTAAAGCACTCAGACCTCTACAGACATCATCTGTTGGTACCATGCTA	1980
Db	1921	ACACCTAAACAGGTAAAGCACTCAGACCTCTACAGACATCATCTGTTGGTACCATGCTA	1980
Qy	1991	CCCGAGCAAGCTGCCCCCTGATGTTTTGGCTTTTGGCTCTCTCACTAAAGGCTCTCT	2040
Db	1991	CCCGAGCAAGCTGCCCCCTGATGTTTTGGCTTTTGGCTCTCTCACTAAAGGCTCTCT	2040
Qy	2041	CTCATCTTAACACTGTGACCTGTGCGATCTGTATGAGTGTCTCTGCAAAATCTATG	2100
Db	2041	CTCATCTTAACACTGTGACCTGTGCGATCTGTATGAGTGTCTCTGCAAAATCTATG	2100
Qy	2101	AGTTTTTCCCTTAATGAGGACCTTTGGCCGCGACGTGCTGCTTCTCATTTGCCCTGTGGCC	2160
Db	2101	AGTTTTTCCCTTAATGAGGACCTTTGGCCGCGACGTGCTGCTTCTCATTTGCCCTGTGGCC	2160
Qy	2161	CAGAGAGCAAAAGCCCTGCGCGTCAACACCGGTGAAGCTTGAGGGTCCAACTTCAG	2220
Db	2161	CAGAGAGCAAAAGCCCTGCGCGTCAACACCGGTGAAGCTTGAGGGTCCAACTTCAG	2220
Qy	2221	CAGCGTACATGTCNAACCGCACCTTTATGCTGCGCAAGAGGTAGACGTCACTCTTT	2280
Db	2221	CAGCGTACATGTCNAACCGCACCTTTATGCTGCGCAAGAGGTAGACGTCACTCTTT	2280
Qy	2281	CTCTCCATACCGCCTTGCCATTTCTCTGAAGCACTTGCAACTCTTTAGGGGCGCTTTA	2340
Db	2281	CTCTCCATACCGCCTTGCCATTTCTCTGAAGCACTTGCAACTCTTTAGGGGCGCTTTA	2340
Qy	2341	TCTCCGAGGTCTCACTACCTATGTTTTCTGTCTCTTTAGAGACTCTTTAAGACTGGGT	2400
Db	2341	TCTCCGAGGTCTCACTACCTATGTTTTCTGTCTCTTTAGAGACTCTTTAAGACTGGGT	2400
Qy	2401	CTTTTCTAATTTCTAATTTCAAGGTCTCAGAGCCATTTCCATCTTGAGCCTTCAGACACA	2460
Db	2401	CTTTTCTAATTTCTAATTTCAAGGTCTCAGAGCCATTTCCATCTTGAGCCTTCAGACACA	2460
Qy	2461	TATACTGAATTTTATCTACAGAGCGCATTTAGAAAGCCACCGACATGCAATACTTTC	2520
Db	2461	TATACTGAATTTTATCTACAGAGCGCATTTAGAAAGCCACCGACATGCAATACTTTC	2520
Qy	2521	CATTTCTCTGTGCTCTCTTCTGAACCTCATCTCTTGGCTACTCCTGAAACCCACTGCG	2580
Db	2521	CATTTCTCTGTGCTCTCTTCTGAACCTCATCTCTTGGCTACTCCTGAAACCCACTGCG	2580
Qy	2581	GACATACATCTTACTACTACAGGCTTTCTTCCATCTCCTTGACCCAGGCACTTAGGGT	2640
Db	2581	GACATACATCTTACTACTACAGGCTTTCTTCCATCTCCTTGACCCAGGCACTTAGGGT	2640
Qy	2641	TTTCTCTCTTTAGGCGCAGCCTTGACATAAACAACAAGCCTCGGCTCATCGGGAGA	2700
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Qy	2701	AACTGTTCCGAGAGTCAAGTGAAGTCTCACTGTGATGACAGGGCTACCTGCGGAGC	2760
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Qy	2761	TGCTGACCTCTCGGGATAGTCTGAAGTAAACCCCTGCTCTTTGTCTTACTCTGACG	2820
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Qy	2821	CTAAAGATCAGTCTACTGATGAACAGGCTGCTCAACTCACCTGAAAGAGCTTCTGC	2880
Db	2821	CTAAAGATCAGTCTACTGATGAACAGGCTGCTCAACTCACCTGAAAGAGCTTCTGC	2880
Qy	2881	TTCCCAAGTACAGAGTTTCAGCCCTCATCTGAGAGGTGTATCTTTCTTACCAAAAC	2940
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 RESULT 3
 AX459954 7445 bp DNA linear PAT 08-JUL-2002
 LOCUS Sequence 8 from Patent W00210393.
 DEFINITION AX459954
 ACCESSION AX459954
 VERSION AX459954.1 GI:21725690
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 Dumoutier, L. and Renaud, J.C.
 Isolated nucleic acid molecules which encode a cell inducible
 factor, or interleukin-21, the proteins encoded, and uses thereof
 Patent: W0 0210393-A 8-07-FEB-2002;
 JOURNAL LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
 FEATURES
 source
 1. 7445
 Location/Qualifiers
 BASE COUNT 2059 a 1568 c 1597 g 2221 t
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 Best Local Similarity 100.0%; Pred. No. 0;
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 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 5935)
 AUTHORS Dumoulier, L., Louhed, J., and Renaud, J.-C.
 TITLE Isolated nucleic acid molecules which encode T cell inducible factors (TIFs), the proteins encoded, and uses therefor
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RESULT 7
AX459988 5935 bp DNA linear PAT 08-JUL-2002
LOCUS AX459988
DEFINITION Sequence 42 from Patent WO0210393.
ACCESSION AX459988
VERSION AX459988.1 GI:21725722
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Dumoutier, L. and Renaud, J.C.
TITLE Isolated nucleic acid molecules which encode t cell inducible factors, or interleukin-21, the proteins encoded, and uses thereof
JOURNAL Patent: WO 0210393-A 42 07-FEB-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
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/db xref="taxon:10090"
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ORIGIN
Query Match 57.0%; Score 4245.2; DB 6; Length 5935;
Best Local Similarity 88.3%; Pred. No. 0;
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 Db 1372 AGAGGAGGAGGGGCTCAGACACACACACCATATAGGCACTTGAATAGGTCAACAAG 1431
 QY 3111 CTTTGGCTTCAATTGATTAATCTTGAATTTGTATGATGATGAACTTTATTTGTTTATC 3170
 Db 1432 CTTTGGCTTCAATTGATTAATCTTGAATTTGTATGATGATGAACTTTATTTGTTTATC 1491
 QY 3171 CATGAAAGAAATCACTCAAAATCTGTATGATGAGAAAGATGTTGGAAACGAAAAAG 3230
 Db 1492 CATGAAAGAAATCACTCAAAATCTGTATGATGAGAAAGATGTTGGAAACGAAAAAG 1551
 QY 3231 CCTAGATAGAGAAACAGATCTGCTGATAGTACTTAT----GGGGAGAGCAGGGGGG 3286
 Db 1552 CCTAGATAGAGAAACAGATCTGCTGATAGTACTTATGAGGGGGGGGGGGGAGGGGGG 1611
 QY 3287 AATTCACCTGAGTACAAATCTTGTGGGAGAGAAATCCATGATGACAAATCTTGTG 3346
 Db 1612 AATTCACCTGAGTACAAATCTTGTGGGAGAGAAATCCATGATGACAAATCTTGTG-- 1669
 QY 3347 GCATGAGATCCATGATGACAAATCTTGTGGGGGAGAGAAATGCAACAGCAAAAT 3406
 Db 1670 -----GGGGAGAGATGGCAAGCAAGCAAAAT 1697
 QY 3407 TGAAGGGA---AGAGATGAGAGAGGCTCATGTTGGGGGTGTAAGAGTCACTCC-TT 3462
 Db 1698 TGAAGGGAAGAGAGATGAGAGAGGCTCATGTTGGGGGTGTAAGAGTCACTCC-TT 1757
 QY 3463 TTCCATGTATGAGAGATTAGAAAAACAGATGTGTGAGTTGATGTCTTCAGACACCCC 3522

Db 1758 TTCCATGTATGAGAGATTAGAAAAATCAGTGTGTGATGTGATGATCTTCAGACACCCC 1817
 QY 3523 CAATATGAAACATATCCAGAGAGCGGGAGACTGTGGAGACCTGGCAATTAGGGA 3582
 Db 1818 AA-----CTATGCAAGTGTGGAGACCTGGCAATTAGGGA 1855
 QY 3583 GGCGGGCTTTTACACAGAGAACTTTATGCTCATCTGTGTCTACACTCCACCTTGG 3642
 Db 1856 GGCGGGCTTTTACACAGAGAACTTTATGCTCATCTGTGTCTACACTCCACCTTGG 1915
 QY 3643 ATGAGGTTCACTCAGGTTTGTGTTCTACCCGTTCTGCTTACTGCTGAAACCTTCACTAG 3702
 Db 1916 ATGAGGTTCACTCAGGTTTGTGTTCTACCCGTTCTGCTTACTGCTGAAACCTTCACTAG 1975
 QY 3703 ATTCCCAAGACGAGGACAGCTCTCTGTATGAGGAGGACCTGGATTTCACTGCTAG 3762
 Db 1976 ATTCCCAAGACGAGGACAGCTCTCTGTATGAGGAGGACCTGGATTTCACTGCTAG 2035
 QY 3763 AGAAGAAATAGCTCAGAGAACTTATGCTCAACGTGAAATCTAGTCAACAGCGGGCAAAA 3822
 Db 2036 AGAAGAAATAGCTCAGAGAACTTATGCTCAACGTGAAATCTAGTCAACAGCGGGCAAAA 2095
 QY 3823 TGACTGAAGCCTCTATTCACAGTGAACGCTCACCTGCTCAGATATACTGAGTATGG 3882
 Db 2096 TGACTGAAGCCTCTATTCACAGTGAACGCTCACCTGCTCAGATATACTGAGTATGG 2155
 QY 3883 GCTCCACCGATTAAGTTCTTGTATGATGATGCTGTTTATTTTACAGACATCAGCCGT 3942
 Db 2156 GCTCCACCGATTAAGTTCTTGTATGATGATGCTGTTTATTTTACAGACATCAGTGT 2215
 QY 3943 GACGACAGAAATCAGAGATGTCAAGAGCTGAAAGGAGACAGTGAAGAAAGTACTA 4002
 Db 2216 GACGACAGAAATCAGAGATGTCAAGAGCTGAAAGGAGACAGTGAAGAAAGTACTA 2275
 QY 4003 TTGGCAAGCCACATATCTAAGCCATCTAGTAGAGACGTTGGGATTTCTTCTGCTTC 4062
 Db 2276 TTGGCAAGCCACATATCTAAGCCATCTAGTAGAGACGTTGGGATTTCTTCTGCTTC 2335
 QY 4063 CCAATCCCTTCTACTTGTATTAATTTTGAAGCTGTCTACTATCTGGTCCATTAAGT 4122
 Db 2336 CCAATCCCTTCTACTTGTATTAATTTTGAAGCTGTCTACTATCTGGTCCATTAAGT 2395
 QY 4123 CTTAGCTCAGCTGTATCTAGCTGAGTCTATAGATCTTTCATCTGTGTCTAAATTTGTA 4182
 Db 2396 CTTAGCTCAGCTGTATCTAGCTGAGTCTATAGATCTTTCATCTGTGTCTAAATTTGTA 2455
 QY 4183 AGTCAAAATTTGAGCTAGACAGAAAGCTTATGCTCAGCCAGTCTCATGAGCACTTGCTG 4242
 Db 2456 AGTCAAAATTTGAGCTAGACAGAAAGCTTATGCTCAGCCAGTCTCATGAGCACTTGCTG 2515
 QY 4243 GAGGATGGCTGTGACAGATCAATGCTAGAAAGCAGCATCCGATTCAGCTCTGCA 4302
 Db 2516 GAGGATGGCTGTGACAGATCAATGCTAGAAAGCAGCATCCGATTCAGCTCTGCA 2575
 QY 4303 CTTGCTAGTGGCCATGTATTAATCTTGTGCTTGTATTAAGTATTTGGAAAGCAGTTC 4362
 Db 2576 CTTGCTAGTGGCCAGGTATTAATCTTGTGCTTGTATTAAGTATTTGGAAAGCAGTTC 2635
 QY 4363 CCAGGACCTTACATATCTGAAGAACATGATGAAACCTTGAAGAGCTGGGCAAACT 4422
 Db 2636 CCAGGACCTTACATATCTGAAGAACATGATGAAACCTTGAAGAGCTGGGCAAACT 2695
 QY 4423 TACTAGATATATTTTGAAGCTATTAAGGAGTCTGAAATGTGGCAAAATCAACC 4482
 Db 2696 TACTAGATATATTTTGAAGCTATTAAGGAGTCTGAAATGTGAATCAATCAACC 2755
 QY 4483 AGAATACACAAAGAGCTGATTTGCAATAGGACAAAGATTTAGAACTCTGAT 4542
 Db 2756 AGAATACACAAAGAGCTGATTTGCAATAGGACAAAGATTTAGAACTCTGAT 2815
 QY 4543 AATAGCTATCATTTAATTAATATAGGCTATATA---TATATTTAAGATTAACA 4598

Db 2816 AACAGCTCATCTTAATTAATAATAGTCTATTTAGCTGCTTAATTTAGATTAAACA 2875
 QY 4599 CAAGATGATAGAGCTCCCAATTTTACTTGCCCTGTTTCAAAAGATAAAAATACAGTC 4658
 Db 2876 CAAGATGATAGAGCTCCCAATTTTACTTGCCCTGTTTCAAAAGATAAAAATACAGTC 2935
 QY 4659 ATGATTAATTAATAGTCTAATAAGATAGATAGAAACCTTCTTCTTACTTTTACTCT 4718
 Db 2936 ATAGATTAATTAATAGTCTAATAAGATAGATAGAAACCTTCTTCTTACTTTTACTCT 2995
 QY 4719 TCATTTCTTAGT-----TTTTTTTTCTTCAACCTGATCAAGCACTAGTAAAGACCT 4773
 Db 2996 TCATTTCTTAGTAAATTTTCTTCTTCAACCTGATCAAGCACTAGTAAAGACCT 3055
 QY 4774 ATCTGCTGAGCTATTATATGACTTTACAGCAACCAATTTGCTGTGTGCTCTTTGG 4833
 Db 3056 ATCTGCTGAGCTATTATATGACTTTACAGCAACCAATTTGCTGTGTGCTCTTTGG 3115
 QY 4834 GGAAGGAAACAGATAGCAGAGGCTCAGGCTAGCAAGTCT-GACTGCTCTTAAAGCCAG 4892
 Db 3116 GGAAGGAAACAGATAGCAGAGGCTCAGGCTAGCAAGTCTGACTCAACTTAAAGCCAG 3175
 QY 4893 AGGCTGTGTTATATACAGAAAGTGAAGCTCTTGCAAGTGGGTGTGTTAATATCA 4952
 Db 3176 AGGCTGTGTTATATACAGAAAGTGAAGCTCTTCAAGTGGGTGTGTTAATATCA 3235
 QY 4953 GAAACAGAAAGGCTCCGTTGATGGAATTAATCAGTAAAGATCTACCTTATCTC---CT 5009
 Db 3236 GAAACAGAAAGGCTCCGTTGATGGAATTAATCAGTAAAGATCTACCTTATCTCCTTCT 3295
 QY 5010 TCTATGAACTTAAATCGTCTCTTTTCTTGTGTGATGAGCTGATAAACACTTGTTTTC 5069
 Db 3296 TCTATGAAAGCTTAAACCGTCTCTCTCTTGTGTGATGAGCTGATAAACACTTGTTTTC 3355
 QY 5070 TTTTGAAGTGTATAGCTTTTGTAGATTTTGTAGTCTTCCAGTCTTGTGTAGAGGTTT 5129
 Db 3356 TTTTGAAGTGTATAGCTTTTGTAGATTTTGTAGTCTTCCAGTCTTGTGTAGAGGTTT 3415
 QY 5130 GTTACCTTGACACCTGGGCTTGATGATGTTAGATGCCAAGGACACACTTGTGAATGCT 5189
 Db 3416 GTTACCTTGACACCTGGGCTTGATGATGTTAGATGCCAAGGACACACTTGTGAATGCT 3475
 QY 5190 GTTAAAAAGTTATTATTCATTTACTTTGTCTTTGAAAAGTGAACCGTGTGTGAAGA 5249
 Db 3476 GTTAAAAAGTTATTATTCATTTACTTTGTCTTTGAAAAGTGAACCGTGTGTGAAGA 3535
 QY 5250 AACTACAGAGATGTGTCTCTGTAGAAAACCTTTTTCCTTAAAGCCATATA 5309
 Db 3536 AACTACAGAGATGTATCTCTGTAGAAAAC-TTTTTTTCCCTTAAAGCCATATA 3594
 QY 5310 TCCACTTTCAGTCACTTTGACTTTTATTCACATGCTGTGACATGAAAGAGTGTTAGGCC 5369
 Db 3595 TCCACTTTCAGTCACTTTGACTTTTATTCACATGCTGTGACATGAAAGAGTGTTAGGCC 3654
 QY 5370 CGCTCTCATGCTCTGTGAAAAGCACCAATAGGGGAAGATGTATGTGTGAATACTGT 5429
 Db 3655 CGCTCTCTGCTCTGTGAAAAGCACCAATAGGGGAAGATGTATGTGTGAATACTGT 3714
 QY 5430 ACCGCGAAGGAACTGTGTAGAGCTCCCCGAAAGCACCAAGGTGTTAAGTAGAACA 5489
 Db 3715 ACTGCGAAGGAACTGTGTGTGAGAGCTCCCCGAAAGCACCAAGGTGTTAAGTAGAACA 3774
 QY 5490 GTTCCAGGGGTGGCTCATGTATATGATAGTGAACAGAGCGAGGGGAAGTAAAGTCAAAAGTT 5549
 Db 3775 GTTCCAGGGGTGGCTCATGTATATGATAGTGAACAGAGCGAGGGGAAGTAAAGTCAAAAGTT 3834
 QY 5550 TCATAGGATCCGAGATCTTAAAGATTAACAATAAGCTGTGGCTTCATTAACAAGGAAG 5609
 Db 3835 TCATAGGATCTTAAGTCTTAAAGATTAACAATAAGCTGTGGCTTCATTAACAAGGAAG 3894
 QY 5610 TCTGGGAAGGCAAG---TGAAGGGAATGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGG 5666
 Db 3895 TCTGGGAAGGCAAGCATTGAAGGGAAGTGAAGGGAAGGGAAGGGAAGGGAAGGGAAGG 3952

QY 5667 CTGGAACAGCTTAAATCTCTTACCAAGCATTTTCTTGGAAACAATCTAGA---GCT 5722
 Db 3953 TTTGAAAAGCTTAAATCTCTTACCAAGGATTTTCTTGGAGGATCTTAAACAAGGCT 4012
 QY 5723 AGTGAATTAAGT-GATTGCAAGGGGACTTGTGCTTGGCAATTGAATCTGGGTTTGTCTC 5781
 Db 4013 GGTGATTAAGTGTGATCGCAAGAGGACTTGTGCTTGGCAATTGAATCTGGGTTTGTCTC 4072
 QY 5782 TCCATTGAGTGTGAAGCGTCAACC-TTTTAACTCCGATGAGAGGGAAGAAAGGAGT 5840
 Db 4073 TCCATTGAGTGTGAAGCGTCAACCCTTTTAACTCCGATGAGAGGGAAGAAAGGAGT 4132
 QY 5841 GTTATGACTCTTACCTGAGTTTATCTAGTTTACGCAATGGAACAGACACTCGGACCTC 5900
 Db 4133 GTTATGACTCTTACCTGAGTTTATCTAGTTTACGCAATGGAACAGACACTCGGACCTC 4192
 QY 5901 CTCTTGAC-----AAAAAATGGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5950
 Db 4193 CTCTTGACAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 4252
 QY 5951 TTAAGAAAGACA----- 5963
 Db 4253 TTAAGAAAGACAAGGCACTGAGCATGTGTGCCCATGCTTTAATCCAGCATTTGGAG 4312
 QY 5964 ----- 5963
 Db 4313 GCAAGGCAAGTGAATTTCTAATTCAGGCCAGCTGTCTACAAAGTGAATTCAGGA 4372
 QY 5964 ----- 5963
 Db 4373 CAGCAGGCTATACAGAGAAACCTGTCTCGGAAAAAAGAAAAAAGAAAAAAG 4432
 QY 5964 ----- 5963
 Db 4433 AAAAGAGAAAG 4492
 QY 5964 ----- 5963
 Db 4493 GAG 4552
 QY 5964 ----- 5963
 Db 4553 GAG 4612
 QY 5964 -----GGCAAGCCCGACACATGGAT 5985
 Db 4613 AAGAGAAAAAAGAAAAAAGAAAAAAGCAAGCAAGCACTGGCAAGCACTGGCAAG 4672
 QY 5986 TGAATGTGGCTTTTGAAGTCAAGGCTTTTGAAGTGAAGTCAATCAATGATGATCATGG 6045
 Db 4673 CGTATGTGGCTTTTGAAGTCAAGGCTTTTGAAGTGAAGTCAATCAATGATGATCATGG 4732
 QY 6046 TCAAGTGAAGGCTTCTGTCAAGGCTTGTCAAGGCTTGTCAAGTGTCAAGTGTCAAG 6105
 Db 4733 TCAAGTGAAGGCTTCTGTCAAGGCTTGTCAAGGCTTGTCAAGTGTCAAGTGTCAAG 4792
 QY 6106 TCTCAATCACTTCTGTCAAGGCTTGTCAAGGCTTGTCAAGGCTTGTCAAGGCTTGTCAAG 6165
 Db 4793 TCTCAATCACTTCTGTCTGTGTCAAGGCTTGTCAAGGCTTGTCAAGGCTTGTCAAG 4852
 QY 6166 CCCCACATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 6225
 Db 4853 CCCCACATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4912
 QY 6226 GATCTATGTGCTATTTGCAAGGCTTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 6285
 Db 4913 GATCTATGTGCTATTTGCAAGGCTTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 4972
 QY 6286 TATGGGTGGAATGCAAGTATATAGGAGATGCTGTGGGTGCTTAAAGTCAAGGAAG 6345
 Db 4973 TATGGGTGGAATGCAAGTATATAGGAGATGCTGTGTGCTTAAAGTCAAGGAAG 5031

QY 6346 CATGATTTTAAAGGCTTGGGCAATCATATTATTAATCTCATGCTTAAATAATCAATTATGTTGA 6405
 Db 5032 CATGATTTTAAAGGCTTGGGCAATCATATTATTAATCTCATGCTTAAATAATCAATTATGTTGA 5091
 QY 6406 TTATATATCTTTTGAAGAGGCTATCTGGTTTGGTGTCTGAGCAAGCAAAAGTCAACC 6465
 Db 5092 TTATCAATCTTTTGAAGAGGCTATCTGGTTTGGTGTCTGAGCAAGCAAAAGTCAACC 5151
 QY 6466 AGCTCTTCTTCACTGTAACCACTTTAAGAAATGCTACCTGCTCAATTTGGTTTGTATT 6525
 Db 5152 AGCTCTTCTTCACTGTAACCACTTTAAGAAATGCTACCTGCTCAATTTGGTTTGTATT 5211
 QY 6526 CTATATTTTCATAGCTTGGAGAGAGTGAAGATCAAGCGATTGGGAACTGACCTGCT 6585
 Db 5212 CTATATTTTCATAGCTTGGAGAGAGCGGAGAGATCAAGCGATTGGGAACTGACCTGCT 5271
 QY 6586 GTTATATGCTCTGAGAAATGCTTGGCTGTGAGCGAGAAAGAAAGCTAGAAAGAAAGAACTG 6645
 Db 5272 GTTATATGCTCTGAGAAATGCTTGGCTGTGAGCGAGAAAGAAAGCTAGAAAGAAAGAACTG 5331
 QY 6646 CTCTCTCTGCTCTTCAAAAAAGCAATTAACATCCCTGAATGACCTTTTCTTAAAGGA 6705
 Db 5332 CTCTCTCTGCTCTTCAAAAAAGCAATTAACATCCCTGAATGACCTTTTCTTAAAGGA 5391
 QY 6706 AAGTGAAGAGCTAACTGTCATCATATTAGAAGATTTTCAATGAACCTGCTGAGTTGA 6765
 Db 5392 AAGTGAAGAGCTAACTGTCATCATATTAGAAGATTTTCAATGAACCTGCTGAGTTGA 5451
 QY 6766 AAAAGAAATATGTCATAGTTGTCATGAGACCCGAGGTAGACTTGTATTAACCAAAAGAT 6825
 Db 5452 AAAAGAAATATGTCATAGTTGTCATGAGACCCGAGGTAGACTTGTATTAACCAAAAGAT 5511
 QY 6826 TCATGACAAATATTTTATGTCATGATGATACAGAAAGAAATTAAGTACTTTAAAGAA 6885
 Db 5512 TCATGACAAATATTTTATGTCATGATGATACAGAAAGAAATTAAGTACTTTAAAGAA 5571
 QY 6886 TTGTTTGAAGAGGTTACCTCTCATTCCTTTAGAAAAAGCTTATGTTAACTTCAATTC 6945
 Db 5572 TTGTTTGAAGAGGTTACCTCTCATTCCTTTAGAAAAAGCTTATGTTAACTTCAATTC 5631
 QY 6946 CATATCCAAATTTTATATATGTAAGTTATTTTATTAAGTATTAACATTTTATTAATGTC 7005
 Db 5632 CATATCCAAATTTTATATATGTAAGTTATTTTATTAAGTATTAACATTTTATTAATGTC 5691
 QY 7006 AGTTATTAATATGATTTATTTATAGAAACATTAATGCTATGATTAATTT-AGTATTAAG 7064
 Db 5692 AGTTATTAATATGATTTATTTATAGAAATTAATGCTATGATTAATTTAGATTAATTA 5751
 QY 7065 GCAAAATATATTTTATGACAAATTAATGAGAAACAAATATCTTAGGCTTTAATTAACACA 7124
 Db 5752 GCAAAATATATTTTATGATTAATTAATGAGAAACAAATATCTTAGGCTTTAATTAACACA 5811
 QY 7125 TGAATATCATTAATCTTCTGCTGTAATTTTCTCCCTTAATTAATCAACATTAACATCA 7184
 Db 5812 TGAATATCATTAATCTTCTGCTGTAATTTTCTCCCTTAATTAATCAACATTAACATCA 5871
 QY 7185 TCATCATCATTAACCAATCATTTTCATGATTTCAAGTTCAGCCCATTTATATAGTTTAAA 7244
 Db 5872 TCATCATCATTAACCAATCATTTTCATGATTTCAAGTTCAGCTTCAATATTAATCTGTAAG 5931
 QY 7245 GTTG 7248
 Db 5932 TTG 5935

RESULT 9
 AC111483 133899 bp DNA linear HTG 13-JUL-2002
 LOCUS Rattus norvegicus clone CH230-87D20, *** SEQUENCING IN PROGRESS
 DEFINITION *** 70 unordered pieces.
 ACCESSION AC111483.2 GI:21736032
 VERSION AC111483.2
 KEYWORDS HTG; HTGS_PHASE1.

SOURCE

Norway rat.
 Rattus norvegicus

REFERENCE

1 (bases 1 to 133899)
 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,

Alsbrooks, S.L., Amaralunga, H.C., Aye, J.R., Ayele, M., Banks, T.,
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 Weinstein, G., and Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 133899)
 Morley, K.C.
 Direct Submission
 Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 133899)
 Morley, K.C.
 Direct Submission
 Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 12, 2002 this sequence version replaced gi:18701248.

Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 Project Information
 Center project name: GMKX
 Center clone name: CH230-87D20
 Sequencing vector: Plasmid
 Chemistry: Dye-terminator Big Dye 100% of reads
 Assembly program: Phrap, version 0.990329

COMMENT

On Jul 12, 2002 this sequence version replaced gi:18701248.

Consensus quality: 69386 bases at least Q40
 Consensus quality: 74271 bases at least Q30
 Consensus quality: 78120 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
 (see http://www.hbrc.bcm.tmc.edu/docs/genbank_draft_data.html)

NOTE: This is a 'working draft' sequence. It currently
 consists of 70 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1	1029	1128:	contig of 1028 bp in length
*	1129	2454:	contig of 1326 bp in length
*	2455	2554:	gap of unknown length
*	2555	3691:	contig of 1137 bp in length
*	3692	3791:	gap of unknown length
*	3792	4827:	contig of 1036 bp in length
*	4828	4927:	gap of unknown length
*	4929	6022:	contig of 1095 bp in length
*	6033	6122:	gap of unknown length
*	6133	7635:	contig of 1513 bp in length
*	7636	7735:	gap of unknown length
*	7736	8825:	contig of 1090 bp in length
*	8826	8925:	gap of unknown length
*	8926	10599:	contig of 1574 bp in length
*	10560	10599:	gap of unknown length
*	10600	11629:	contig of 1030 bp in length
*	11630	11729:	gap of unknown length
*	11730	12994:	contig of 1265 bp in length
*	12995	13094:	gap of unknown length
*	13095	14397:	contig of 1303 bp in length
*	14398	14497:	gap of unknown length
*	14498	15583:	contig of 1086 bp in length
*	15584	15683:	gap of unknown length
*	15684	16679:	contig of 1196 bp in length
*	16680	16879:	gap of unknown length
*	16881	18514:	contig of 1535 bp in length
*	18515	18614:	gap of unknown length
*	18615	19735:	contig of 1121 bp in length
*	19736	19835:	gap of unknown length
*	19836	20551:	contig of 1116 bp in length
*	20552	21051:	gap of unknown length
*	21052	22262:	contig of 1175 bp in length
*	22263	22326:	gap of unknown length
*	22327	23339:	contig of 1613 bp in length
*	23940	24039:	gap of unknown length
*	24040	25111:	contig of 1072 bp in length
*	25112	25114:	gap of unknown length
*	25212	26491:	contig of 1280 bp in length
*	26492	27834:	gap of unknown length
*	26532	27934:	contig of 1243 bp in length
*	27835	27934:	gap of unknown length
*	27935	29575:	contig of 1641 bp in length
*	29576	29575:	gap of unknown length
*	29676	31127:	contig of 1452 bp in length
*	31128	31127:	gap of unknown length
*	31282	32866:	contig of 1639 bp in length
*	32867	32866:	gap of unknown length
*	32967	34471:	contig of 1505 bp in length
*	34472	34571:	gap of unknown length
*	34572	35881:	contig of 1410 bp in length
*	35882	36081:	gap of unknown length
*	36082	37443:	contig of 1362 bp in length
*	37444	38778:	gap of unknown length
*	38779	38878:	gap of unknown length
*	38879	41118:	contig of 2440 bp in length
*	41139	41118:	gap of unknown length
*	41315	43315:	contig of 1797 bp in length

*	43216	44315	gap of unknown length
*	44316	44358	contig of 1643 bp in length
*	44395	445058	gap of unknown length
*	45059	44619	contig of 1761 bp in length
*	46820	46319	gap of unknown length
*	46920	48452	contig of 1533 bp in length
*	48453	48552	gap of unknown length
*	48553	50853	contig of 2301 bp in length
*	50854	50953	gap of unknown length
*	50954	53024	contig of 2071 bp in length
*	53025	53124	gap of unknown length
*	53125	54165	contig of 1041 bp in length
*	54166	54265	gap of unknown length
*	54266	55580	contig of 1315 bp in length
*	55581	55680	gap of unknown length
*	55681	57173	contig of 1493 bp in length
*	57174	57273	gap of unknown length
*	57274	59644	contig of 2371 bp in length
*	59645	59744	gap of unknown length
*	59745	61544	contig of 1800 bp in length
*	61545	61644	gap of unknown length
*	61645	62787	contig of 1143 bp in length
*	62788	62887	gap of unknown length
*	62888	64902	contig of 2015 bp in length
*	64903	65002	gap of unknown length
*	65003	66388	contig of 1286 bp in length
*	66289	66388	gap of unknown length
*	66389	68342	contig of 1954 bp in length
*	68343	68442	gap of unknown length
*	68443	70210	contig of 1768 bp in length
*	70211	70310	gap of unknown length
*	70311	72481	contig of 2071 bp in length
*	72382	72481	gap of unknown length
*	72482	73978	contig of 1497 bp in length
*	73979	74078	gap of unknown length
*	74079	75795	contig of 1717 bp in length
*	75796	75895	gap of unknown length
*	75896	77662	contig of 1767 bp in length
*	77663	77662	gap of unknown length
*	77763	79097	contig of 1335 bp in length
*	79098	79187	gap of unknown length
*	79198	80903	contig of 1706 bp in length
*	80904	81003	gap of unknown length
*	81004	82877	contig of 1874 bp in length
*	82878	82977	gap of unknown length
*	82978	85665	contig of 2888 bp in length
*	85666	85965	gap of unknown length
*	85966	88565	contig of 2690 bp in length

Query Match	16.1%	Score 1197.6;	DB 2;	Length 133899;
Best Local Similarity	75.0%;	Pred. No. 2.6e-24;		
Matches 1894;	Conservative 0;	Mismatches 410;	Indels 221;	Gaps 23;

QY	4430	GAGGATTTTGGACCTCAATTAAGAGAGCGCTGGAATGGGCAATCA--CCGGAATA	4488
Db	38966	GAGTGTGTTTGACCTCGTAATCTAGTCTGAAATGAGCCAAACCCCGAGACA	39025
QY	4489	ACAACAAAAGCGTGAATTTGCAATAGACAAGTATTTAGATCATGTGATTTATAC	4548
Db	39026	GCAACAGAAAGACCTGATGTTTGGCATGAGATGAATGTTTAGAATCCTGATTTCTAAAC	39085
QY	4449	TATCATCTTAAATTTAAATATAGGC---CTATATATATTTTAAAGTTTAAACAAGAT	4605
Db	39086	TATCATCTTAAATTTAAATATAGGCTTTAAATAGCTACCTTAATTTAGGATTTAAAGCAAGAT	39145
QY	4606	GGATAGCGCTCCCAATTACTTGCGCTGGTTCCAAAGAGATAAATAATCAGTCATGATT	4665
Db	39146	GGATTAACCTCCGAGTTTCTGTACCTGGTTTCAATAGATTAATAAATATCAGTCATGGTT	39205
QY	4666	AATTAATGTGTCAATGAAGATATAGATGAAACCTTCTCTTAATCTTTACTCTATATTC	4725
Db	39206	CATTGACGTATATGGAAGTAGAGGTGGAATCTTTTCTCTTAATCTTTTACATCAATTC	39265

QY	4726	TTACTTTTTTTTTTCTCAACCCCTGATCAAGCACAAGTAAAGCACTATCTGCTGAG	4785
Db	39266	TTAA--TTTTTTCCTTCAACCCCTGATCAAGCACAAGTAAAGCACTATCTGCTGAG	39322
QY	4786	CTATTATATGCTTTTACAGCAAAACAATTGCTGTGTGGCTCTTTGGGAGAGGAACAG	4845
Db	39324	CTATTGTAAGACTTCAAGCAAAAGCATTTGTGTGTGCCCTCTTTGGGAGAGGAAC	39388
QY	4846	GATAGCAGAGAGGCTCAGGCTAGCAAGTCTGACTTTGGCCCTTAAAGCCAGAGGCATGTTGAT	4905
Db	39383	-TTAGCAGAGAGGCAAGGTCAGCAAGACAGACTCAACCTTAAAGCCAGAGGCATGATTGAC	39444
QY	4906	AGCAGAGAAATGAGGCTTTCCGAAATGGGTGTGCTTAAGTATCAAGAACAGAAAGGC	4965
Db	39442	AGCAGTAAATGATGCTCTTTGCAAGTGGGTGTGCTTAAGTACTCAAAACAAAAGGC	39500
QY	4966	TCCAGTTGATGGAATTATCAGTAAGATATCAACCCCTAT-----CTCCCTCATC	5015
Db	39502	TCCAGTTGATGCACTTATCAGTAAATATATCTATCTTATTTCTTATCTCTTCTTCATC	39566
QY	5016	GAACCTAAATGCTCTCTTTTCTTGTGTGTAAGGCTGATAAACACACTTGTCTTTCTTTGA	5075
Db	39562	AAACCTAAATATCTCTCTCTCTTGTGTGTGATGTGATTAACAAGACTGTTTTATTTCA	39622
QY	5076	GTTTTCATGCTTTGTAGATTTTGTAGTGTCTGTCCAGTTCTTGTTAAGGCTTTTACC	5135
Db	39622	ATGTTTCATGCTTTGTGAAGCTTTTCAAGTCTGTCCAGTCTCTTTTAAAGCTTTTGTGAGC	39682
QY	5136	TTGACACCTGGGCTTGATGTGTACATGCCAAGACACACACTTCTGAATGCCGTGTAA	5195
Db	39682	TCGACACATGGGCTTGATGTGCACACAGCCACAGAGGCAACAGCTTCCAGATGCTTACGA	39744
QY	5196	AAGGTTATTTATTCATTTACTTTGTCTTTTGGAAAGTGAAGCGTGTGTGAAGAAATCA	5255
Db	39742	AAGCTATATATTCATTTACTTTGTCTTTGGAAAGTGAAGATGATGAGTAAGAAAGATCTCA	39800
QY	5256	---CAGGATGTGTCTCTGTAGAAAATTTTTTTTCCCTTAAATGCTATATCC	5312
Db	39802	CATCATGAGATGTAGCTCTGTAGAAAATTTTTTTT---CTTAAAGCTATATCTCT	39858
QY	5313	ACTTCAGTCAACTTGTGACTTTTATACATGCTGTCAATGAAAGATGTTTGGCCCGC	5372
Db	39857	ACTTTCATCAACCTCTATCTTTACACATGCTCCCCATG-----GGAAGAG	39900
QY	5373	TCTCATGCGCTCTGGGAAAAGCACCATATAGGGAGAGATGTTATGCTGAGAAATCTGAC	5432
Db	39905	TGTTTAGGCTCTAGAAAAGACCAACAGGGGAGAGATGTTATGACAGAAATCTGATA	39966
QY	5433	GGCAGGAACTGCTCAGAGCTCCCCGAGAACCAACAAGTGTATAGTAGAACAATC	5492
Db	39965	GGCAGGGGAA-----ACTATGACAGCTCTGGATAGCA	39999
QY	5493	CAGGCTGGGCTCATGTATAAGATGGAACAGAGGAGGAAAGATAACTCAAAAGTTCA	5552
Db	39998	GAGGCTGGGCTCATGTAGAGAAATAGGAGAAAGATG---AGATTACTCAAAAGTTCA	40005
QY	5553	TAGGCTCCGAGTCTTTAAAGATACAAATATAGC-TGCTTGGGCTTCATACAAAGGAATGC	5611
Db	40055	AAGGTTGTGTGTCTTTAAGTACAAATATAGCATGCGTGGGCACTCTTACAGAAAGTCA	40111
QY	5612	TGGGAGGACGCAAGTGAAGGAGAAATGAAAGGAAAA---AAACAATGTAGAGACT	5668
Db	40115	TGGGAGGCCCAAGGTGAGAGAGGAGGCTGCAAGGAAAAAGAAACAATGTAGAGATT	40177
QY	5669	TGAAGATTAACAATCTCTTACAGACATTTTTCTTGGACAAATCTAGAA---GGTAG	5724
Db	40175	TGAAGATGTCAAAATCTCTCCTGTGAGGATTTTTCTTGGACAAATCTAGAACAGGGTAG	40233
QY	5725	TGATTTAGTGAATTCAGAGGAGACTTGTCTTGCAATTTGAAATCTGGGTTTTGTCTCTCC	5784
Db	40235	TAGATTTAGTGAATG-GGGACACAGTGTCTTGTCTTTGAAATTTGGGTTTTGTCTCTCC	40299
QY	5785	ATTGAGTTGAAGGCTACCCCTTTTACCTCGAATGAGAGAGAAAAAGGGGTGTTA	5844

Db	40294	ATTGAGGTTGAGAGCTTCAACATTTTACTCTT--AATGAAAGAGAAAGAAAGAGTTTA	40355
Qy	5845	TGACTCTTACCTGAGTTTACTAGTTTACGCAATGAAACAGACTCGGACCTTCCT	5904
Db	40352	TGATTCTTACTCTAATGTGACAT-----	40374
Qy	5905	TGACAAAAAAATGAAACCTGTGTTTGCTGTTGTTCTTTGTTTAAGAAAGACAG	5964
Db	40375	-----	40378
Qy	5965	GCAAGCCGACACATGAGTGTGAATGTGGGTCTTTGAGTCAGAGCTTTGAGTTAGCA	6024
Db	40375	-----AATGTGCTCTTTGAGTCAGAGATTTTGAGTTGAATG	40411
Qy	6025	CTCATCAATAGTTGATCATGTCAGGTGAGGGCTACCTGTGAGCCGAGCCCTGTCGC	6084
Db	40411	CTGCGCAATAGTTGATCATGTCAGGTGAGGGCTCATGTCAGGTGAGCTCTA-----	40465
Qy	6085	TTGCGACTTAAACATCTCCAGGTCAGATACCTTCTGCTACTTACAGACAGTTAGAGCT	6144
Db	40466	---GCACCTTAAACATCTCCAGGTCCTAGATGGCTTCCTGTGCTTAGACAGTTAGAGG	40522
Qy	6145	TGACCAAAACCTTTTTTCCAAACCC-----CACTAAATTAATGCAAAAACAGTGT	6199
Db	40523	TGACCAAAACCTTTTTTCCAAACCCCACTAAATTTACTTTTAATGCAATATACCTGTG	40581
Qy	6200	AATTTGTGGGATACAGTGTATTAATGATCTAATGTGTCATTTGCAAGGTTCAATAGA	6259
Db	40583	AGTTTAATGGATACAGTGCATTAATGATCTAATGTATACATATGCAAGTTCAACAGG	40644
Qy	6260	TAGATTAATAGGCCCATCAACAGCTTTATGGGTGTAATGCAATATATAGGTAGTG	6319
Db	40643	CGAATTAATAGTCCCATCACAGAGCTCCCTGTGTGTAATGCAATATATATATAT	40699
Qy	6320	CCGTGTGTCTCTTAAAGTCAAGAAAGGATATTTAAGCTTGGGCAATCATATTATA	6379
Db	40699	GGTATGTGTCTTAAAGTCAAGAAAGGATCTTTAAGGCTTTGGCAACCATATGTG	40755
Qy	6380	CTCATGTCAAAAATACATTTATGTTGATTTAATCTTTTAGAAGAGCTGATCTTGTT	6439
Db	40759	TTCACTACTAAAAAT-CATTATGTTGATTAATTTTAAGABAAGCTGATCTTGTT	40811
Qy	6440	TTGTGTCTCAGCAAGCAATGTCAACAGCTCTTTCTAATCTGTGACCATTTAGAAAATGC	6499
Db	40818	TTGTGTCTCAGCAAGCAATGTGTGTCTCTTCCAGTAGTACTTCTTAAGAAAGTGA	40877
Qy	6500	TACCTGTGCTCAATTTGGTTGTATTTCTTAATTTTCATAGCTTGAGAGAGTGGAGATC	6559
Db	40878	CACATATGTCTCAATTCAGTTGTGTTCTTAATTTTCAAGCTTGAGAGATGGAGATTT	40933
Qy	6560	AAGCGATTTGGGGAACTGGAACCTGCTGTTATGTCTCTGAGAATGCTTCCGTGACGC	6619
Db	40938	AAGCGATCGGGAACTGGAATCTGCTGTTTATGTCTCTGAGAAACGTTTGGCTGAGAA	40999
Qy	6620	AGAGAAAGCTAAGAAACGAAAGACTGCTCTCTCTCTTAATAAAGAACTAATAGATC	6679
Db	40998	AG-AGAGCTAAGAAATGAGCAACTTACCTTCTGCTGCTTTAAGAAATTAATAATTC	41058
Qy	6680	CTGTAATGCACTTTTATCTTAAGAGAAAGTGAAGCTAACCTCCATCATCATTAAGAG	6739
Db	41057	CCTGAATGCACTTTTATCTTAAGAGAAATGAGAGCTTAACCTCCATCATCATTAAGAG	41111
Qy	6740	TTTCAATGAAACCTGCGCTAGTTGAAAAAAGAAATAGTCAAGTTGCTCATGAGCA	6799
Db	41117	CTTCAATGAAACCTGTTTCAAGTTGAAAAAAGAAATCATGTCAATGCTGCAAGCA	41177
Qy	6800	GAGGTAGACTGATTAACCAAAAGATTCATTGCAATATTTTATTTGTCACTGATGATCA	6859
Db	41177	GAGGTAGACTGATTAACCAAAAGATTTAGTGAATATTTTACTGTCATGATGAT-CA	41233
Qy	6860	ACAGAAAAATATGTACTTTAAAAATTTGTTGAAGAGAGTTAACCCTCAATTCCTTAG	6919

Db	41235	ATAGAAATATGATTTTAAATTTGTAATTCACAAGAGATACCTCTCTCTTAA	41294	variation	1121	/frequency="0.03"	
OY	6920	AAAAA	6924	variation	1165	/replace="G"	
Db	41295	AAAAA	41299	variation	1412	/frequency="0.43"	
				variation	1500	/replace="A"	
				variation	1500	/frequency="0.13"	
				variation	1500	/replace="T"	
				variation	1500	/frequency="0.01"	
				variation	1500	/replace="T"	
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				variation	1500	/replace="T"	
				variation	1500	/frequency="0.01"	
				variation	1500	/replace="A"	
				variation	1500	/frequency="0.10"	
				variation	1500	/replace="G"	
				variation	1500	/gene="IL22"	
				variation	1500	/join(2056, .6841)	
				variation	1500	/product="interleukin 22"	
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				variation	1500	/protein_id="AAK62468.1"	
				variation	1500	/db_xref="GI:14423571"	
				variation	1500	/translation="MAALQKSVSFFLNGTLATSCLLLIALLIVGGGAAPFISHCKELDK SNFOOPYITNRTFMILAKESLADNNTVRLIGKTLFGVSVSEKCYLKKOVLNFTLEB VLPFSDPFCPOVMOEVPFLRLSNRLSTCHIEGDDLHIQNNVOKLKOTVKKLGSSE IKAIGELDLFMSLRNACI"	
				variation	1500	/gene="IL22"	
				variation	1500	/frequency="0.01"	
				variation	1500	/replace="A"	
				variation	1500	/gene="IL22"	
				variation	1500	/frequency="0.02"	
				variation	1500	/replace="G"	
				variation	1500	/gene="IL22"	
				variation	1500	/frequency="0.01"	
				variation	1500	/replace="G"	
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				variation	1500	/frequency="0.45"	
				variation	1500	/replace="A"	
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				variation	1500	/frequency="0.05"	
				variation	1500	/replace="A"	
				variation	1500	/gene="IL22"	
				variation	1500	/frequency="0.35"	
				variation	1500	/replace="C"	
				variation	1500	/gene="IL22"	
				variation	1500	/frequency="0.02"	
				variation	1500	/replace="T"	
				variation	1500	/gene="IL22"	
				variation	1500	/frequency="0.01"	
				variation	1500	/replace="A"	

variation	4156	/gene="IL22"	/frequency="0.01"	/replace="C"
repeat_region	4234	/rpt_family="MIR3"	/rpt_type="dispersed"	
variation	4290	/gene="IL22"	/frequency="0.19"	/replace="C"
repeat_region	4303	/rpt_family="MIR"	/rpt_type="dispersed"	
variation	4497	/gene="IL22"	/frequency="0.05"	/replace="C"
variation	4561	/gene="IL22"	/frequency="0.05"	/replace="A"
variation	4615	/gene="IL22"	/frequency="0.02"	/replace="C"
variation	4723	/gene="IL22"	/frequency="0.47"	/replace="A"
variation	4829	/gene="IL22"	/frequency="0.01"	/replace="T"
variation	5064	/gene="IL22"	/frequency="0.01"	/replace="G"
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variation	5241	/gene="IL22"	/frequency="0.01"	/replace="G"
variation	5358	/gene="IL22"	/frequency="0.04"	/replace="C"
variation	5382	/gene="IL22"	/frequency="0.15"	/replace="A"
variation	5389	/gene="IL22"	/frequency="0.01"	/replace="T"
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	Query Match	Similarity	Score	1081	DB 9	Length	8393
	Best local	56.7%	Pred.	No. 1.7e-219			
	Matches 3680	Conservative	0	Mismatches 2300	Indels	509	Gaps 71
Oy	1080	TATCCATCTATATAGATGTTATTGAGGCTCATTTTAAATAATATTTTGAGACTATG	1139				
Db	1105	TATACACACATATATAGTGTATATAGGATTTATTTGGAAATATATATGTTGACGCTGTG	1164				
Oy	1140	-----CTTGACACAGTAAATGTCAGAAATTGCAAAATGATATATATTTTATTTT	1193				

Db	1165	TGAAGTGAAGATTAGGTAAATTTTAAAGTGAACCTATATCAACGGTAATCTTTATATTT	1224
Oy	1194	AAAAAATCTATGCTT-----AAAATGCTATTAAGATTGTCTACACCGATTTTCCAA	1248
Db	1225	AAAAAAAGTTTACTGTTAAGAAAAAAGAGATCAGATTTTCAAGCATTAATTACAA	1284
Oy	1249	CTTAAGTGAACCTTGCGTATGATTTCAACCTTGATATTCATCTACCAATAC-AGTCTC	1307
Db	1285	CTTAAGTGAATATGATTAATTAATCAATTAATCAATTTTAAGATAATTTACTTCCGC	1344
Oy	1308	TGAACCAAGACATCTCTGGCAATGGAGCGTGAAGAAAGCCAACTCTTAATTA	1367
Db	1345	TTAATTTGTAATGATCTTAAATAATTTCTCAAAAAGGAGAAACAAATTAATTAGTTA	1404
Oy	1368	AAAAAAACAGCTAGTATTAGTTTGAATTTGCATTTACTATAAA-----AAATAGA	1417
Db	1405	GCCAAAGACGATATTTTGAACATTAAGCTGTTTGAATTCAGCATGTTTAAATAATGA	1464
Oy	1418	GATATTAATTTATTTAAATAATGAATATATCTCCAAAGTTTCAATTAAGCTTATTTCAAG	1477
Db	1465	GATAAATTTATTTAATTAATAG-AATAGCTGTAGTGTGATACCATTAATTAAGCTTAAAG	1523
Oy	1478	CACGAATATTAAGACACGGGTCTTTAATTTCTGCTACTCTTAAGATTAAGATCTAT	1537
Db	1524	CAGAGATATTAAGACATGGGTCTTTTTCGTATCACTTCCAAATGAGATTAAGATCTAT	1583
Oy	1538	GAAGTTGGTGGAAAAATGAGTCCGTGACCAAAAAGCTGACTCAATTAAGCTACGGAGATCA	1597
Db	1584	AAAGCTGTAGAAAAATGATCGCTGACCAAAAAGCTTACTCAGCCACTATAGAGATCA	1643
Oy	1598	AAGCTGCTCTACTCAATCAGAA-TCATAAGGCCAAAGCCATGGCTTTCTTTGAAA--	1654
Db	1644	AAACATTTTATCTAAATATCTGAACCTCTACTAAGCAAAAACATATGTCTTTGAAAAAT	1703
Oy	1655	---CCGTGTTAAGAAATTTCTGGGATTTGTGTCCAAAAGCACTTGTTGGCCCTCACCG	1711
Db	1704	ATGTAGGATTAAAGAAATTTCTGGGATTTGTGTGTA--TACCTCCGGGCTCTTAATAG	1762
Oy	1712	TGACGTTTAAAGGAAGACTTCCCATCTCTCAAGGTGGGAAAGGCTTGGAGGTGTGCTTG	1771
Db	1763	TGAGCTTTTAAAGGAAAACCTTGACATCTC--AAGGTGAAGATATAGAGGTGTGTTTG	1819
Oy	1772	TGGCTCTCTATAGTGTAGTACTTCTCAGAAACAGAGACTGGAAAAATAGATATGCT	1831
Db	1820	TGGGCTCTGTGTGTAGTGTGCTTCTCAGAAACAGTACTGGAAATTAAGATATGCT	1879
Oy	1832	GATGTCATATTCATCAACATACCAAAAAACCTGTGTCTCCCATGGCTATTAAGACAGC	1891
Db	1880	GATGTCATATTTTTCACAACT--TAAAAAAGTCAGATCTCTGGGGCTATTAAGACAGC	1937
Oy	1892	AACTTTCGCCCTCCCATCAACACAGACACCTAAACAGGTAAAGCACTCAGACCTCTA	1951
Db	1938	AGCTTCTACCTTCCCCGTCACACACAGAAATTTTCAAGAACAGTAAAGCTTTCCGCAACT	1997
Oy	1952	CAGACAA--TCATGTGCTTGGTACACATGCTACCCGAGCAATGCTCCCTGATGTTTT	2009
Db	1998	TGATACAAATGGTATAGTTTGTATGAATAATCTTGAACAAATTTGTTCCTTCAAGTGTG	2057
Oy	2010	GCTTTTGTCTGTCACTAACAGGCTCTCTTCACTTATCACTGTTAGACATTTGTGCG	2069
Db	2058	TTGCAACCAAGTTCTCTTCCC-----CAGTCAACCAAGTTGCTGAGTATGAAT	2105
Oy	2070	ATCTCTGATGGCTGCGCCGACGAATCTATAGTTTTTCCCTTAATGGGAACTTTGGACGC	2129
Db	2106	GTCGTCAATGGCCCGCTCGACGAATCTGTAGCTTTTCTTTATGGGAACTCTGGACAC	2165
Oy	2130	CAGCTGCTGCTTCTCATTTGCTGCGGTGGGCCCAAGAGCAATGCGTGCCTCCCTCAAC	2189
Db	2166	CAGCTGCTCTCTTCTCTTGGCCCTCTTGATGAAGAGAGACAGTGGGCCCATCAAGCTC	2225
Oy	2190	CCGGTCAAGCTTGAAGTGTCAATCTTCAGACCGCTACATGCTCAACCGCACTTTAT	2249

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences. Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintain sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

----- Summary Statistics -----

Contig length: 150667
Phrap values in estimate: 149705
Average error rate (BCM-Phrap estimate): 1.52849e-05
Fraction of Phrap values less than 40: 0.0163588
Number of consensus changing edits: 83
Number of N's in consensus: 0

----- Consensus changing edits -----

Position	Original+Context	Edited+Context
7824	tattatcatat(n)nnngtatact	tattatcatat(g)tggtatcat
7825	atataatatin(n)ngtatact	atataatatin(t)tggtatcat
7826	tatatatatin(n)ngtatact	tatatatatin(g)tggtatcat
7827	tatatatatin(n)ngtatact	tatatatatin(g)tggtatcat
7855	atatatcatgc(n)acatttata	atatatcatgc(t)tggtatcat
8162	agacacattt(n)tgagttgga	agacacattt(t)tgagttgga
10049	tgagacatc(n)cnmngnm	tgagacatc(a)ccgagttga
10051	ggcagatcnc(n)nnmngnm	ggcagatcnc(c)tgagttgga
10053	gcagatcnc(n)nnmngnm	gcagatcnc(t)tgagttgga
10054	gcagatcnc(n)nnmngnm	gcagatcnc(g)tgagttgga
10055	gacatcnc(n)nnmngnm	gacatcnc(a)tgagttgga
10057	gacatcnc(n)nnmngnm	gacatcnc(g)tgagttgga
10058	gacatcnc(n)nnmngnm	gacatcnc(t)tgagttgga
10059	gacatcnc(n)nnmngnm	gacatcnc(c)tgagttgga
10060	gacatcnc(n)nnmngnm	gacatcnc(g)tgagttgga
10061	gacatcnc(n)nnmngnm	gacatcnc(a)tgagttgga
10062	gacatcnc(n)nnmngnm	gacatcnc(t)tgagttgga
10064	gacatcnc(n)nnmngnm	gacatcnc(c)tgagttgga
10065	gacatcnc(n)nnmngnm	gacatcnc(g)tgagttgga
10066	gacatcnc(n)nnmngnm	gacatcnc(a)tgagttgga
10067	gacatcnc(n)nnmngnm	gacatcnc(t)tgagttgga
10068	gacatcnc(n)nnmngnm	gacatcnc(c)tgagttgga
10069	gacatcnc(n)nnmngnm	gacatcnc(g)tgagttgga
10070	gacatcnc(n)nnmngnm	gacatcnc(a)tgagttgga
10071	gacatcnc(n)nnmngnm	gacatcnc(t)tgagttgga
10072	gacatcnc(n)nnmngnm	gacatcnc(c)tgagttgga
10073	gacatcnc(n)nnmngnm	gacatcnc(g)tgagttgga
10074	gacatcnc(n)nnmngnm	gacatcnc(a)tgagttgga
10075	gacatcnc(n)nnmngnm	gacatcnc(t)tgagttgga
10076	gacatcnc(n)nnmngnm	gacatcnc(c)tgagttgga
10077	gacatcnc(n)nnmngnm	gacatcnc(g)tgagttgga
10078	gacatcnc(n)nnmngnm	gacatcnc(a)tgagttgga
10079	gacatcnc(n)nnmngnm	gacatcnc(t)tgagttgga
10080	gacatcnc(n)nnmngnm	gacatcnc(c)tgagttgga
10081	gacatcnc(n)nnmngnm	gacatcnc(g)tgagttgga
10082	gacatcnc(n)nnmngnm	gacatcnc(a)tgagttgga
10083	gacatcnc(n)nnmngnm	gacatcnc(t)tgagttgga
10084	gacatcnc(n)nnmngnm	gacatcnc(c)tgagttgga
10085	gacatcnc(n)nnmngnm	gacatcnc(g)tgagttgga
10086	gacatcnc(n)nnmngnm	gacatcnc(a)tgagttgga
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Db	7036	GATGTCATATATTTTCACAAT - - TAAAAAAAAGTCAGATCTCTGGGGCTATTAAGACAGC	6979
Qy	1892	AATCTTGACCTCTCCCATCACAACAGAGACACCTAAACAGGTAAAGCACTCAGACTCTA	1951
Db	6978	AGCTTCTTACCTTCCCGTCACAAAGCAGATTTTCAAGAACAGGTAAAGCTTTCCGCAAACT	6919
Qy	1952	CAGACAA - - TCATCTGCTTGGTACATGCTACCCGAGAACATGCTCCCTGATGTTTTT	2009
Db	6918	TGATACAAATGTTAGTTAGTTAGTAATACTTTGACATAATTTGTTCTTCAAGTTGTC	6859
Qy	2010	GCTTTTGTCTCTTCACTAACAGGCTCTCTCTCACTTATCAACTGTTAGACATTGTGCG	2069
Db	6858	TTGCACACAGGTTCTCTCC-----CAGTCAACAGTTGCTCGAGTTAGATT	6811
Qy	2070	ATCTCTGATGGCTGCTCCGACGAATACTATAGTTTTCCCTTAAGGGACCTTTGGGCGC	2129
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Qy	2130	CAGCTGCTGCTTCTCATTTGCTGTGGGCCGACAGAGCAAAATGCGTGCCTGCTCAACAC	2189
Db	6750	CAGCTGCTCTCTTCTCTTGCGCCCTCTTGATGACAGAGACAGCTGGGCCATCACTC	6691
Qy	2190	CCGGTGCAGCTTGAAGTGTCCAACTTCACAGACCGGTATCTGTCAACCGCACTTTAT	2249
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Db	6630	GCTGGCTTAGAGGATACATCTCAATCTCTCTCTTCTGCTGATGATCTACTTGAATCC	6571
Qy	2286	CATACCGGCTTGCATTTTCTGTAGACACTTGCAAACTCTTAAGGGGCGCTTATCTCC	2345
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QY 4014 CAATPACTAAGCAATTCAGT--GAGCGTGGGATTTCTTCTGCTCCAGTCCCT 4971
DB 4850 CAATGCTAATGCTATGCAATGAGAGACAAATGTTGTTTCTTCTTCTTCTTCTTCC 4791
QY 4072 TCTACTTTGTATATTTATTTGACTGTCTACTATCTGCTCACTTACTGCTTACTGCTC 4131
DB 4790 ATCACTTTGTATTTTCACTTATGTTCTCTACACAGGCGCATTA-----CTTGGTGT 4735
QY 4132 ACCGTATCTAGCTGGGTCTATGATTTTCAATCTGTGTCTAATTT--GTATGTCAC 4188
DB 4734 CTGTGTATGTATATATCTATATCTATGATGCTAGTTCCTCAATCTTCAATTTGTAG 4675
QY 4189 AATTCGAGCTGAGAAAGCTTAGCTCAGCCAGCTCATGAGCACTTGTGAGAGAT 4248
DB 4674 AATTCGAGCTGAGTGGATCTTGAAGTCTTGTATGATCACTTCACTTCTGAGGAT 4615
QY 4249 GAGCTGTGACAGATCAATCTAGAGACAGATCCCTGATTTCCAGCTGTGACTTG-C 4307
DB 4614 GGTGAGTGGCAGATATGAGGCTGAATGAGGTCTCTGATCCCAAGCCAGCACTTTTC 4555
QY 4308 CTGTGTGCTATGTATTACTTTGGCTTATTAATTAATTTGGAAA--GCCAGTTCCCA 4365
DB 4554 CCGGTGTGTATAGATTAATTTTGTATCAATTAATTTCTTGAAGAAATTTTCAATTCCTA 4495
QY 4366 CGGACCAATTAATCTGAGAAACCATGATTTGAAAATAGAAA-----GCTGGGCAACAA 4421
DB 4494 TTAATCTATGATTAATCTGAGAAAGTATCTGTTTAAAAACAAAAATGCTTATGCGCAAT 4435
QY 4422 TTAATAGATGATTTTGAAGCTTATTAACGAGTGTCTGAATGTGGCAAAATCAAC 4481
DB 4434 TTAATTAAGTCACTTTGAAGTATTAATGATGCTTTTGAAGCTTGAAGATTAATCT 4375
QY 4482 CAGATTAACAACAAAGCTGATTTGCAATAGCAAGTATTTGAATCACTGTAT 4541

DB 4374 CAGAACATGAGAAAAAGATGACTGTGATATAGGCTTAATTTCTGGA-----GTAA 4322
QY 4542 TAAATGCTATCACTTAATTAATAATAGGCGCTATATATATTTATGATTTAAACAA 4601
DB 4321 TAAACACTATTTTGAATATATATATCTATGATATGATTTTAAAGCA 4262
QY 4602 GAGTGAATGCTCCCAATTTACTGGCTGTTCATAAAGTAAAAATATCAATG 4661
DB 4261 GAGCAGACAAC-CCGATCTCTTTTATAGAGTTCAAAATGAGTAAAAATATAGTAA 4203
QY 4662 GATTAATTAATGATGATAGATGATGAGATGGAACCTTCTTACTTTTACCTCA 4721
DB 4202 GATTTATTAATGATTAATGAGTGAATGGAATGGAATTTTCTTCTCTTCCCA 4143
QY 4722 -----TTCTTATGTTTTTTTTTCTTCAACCTGTATCAAGCCATTAAGACCT 4773
DB 4142 TCAAGACTTCAATCTACTTTCTTCTTCACTCCCTCAAAATCCCTAGGAGCATTT 4083
QY 4774 ATCTGTGTAGCTATTAATATGACTTTACAGAAACATGCTGTGTGCTCTTTGG 4833
DB 4082 ATCAATGTGGGCTGTGTATCAATTTCTATAGTGAATGATACATCAATGCGCTATTGG 4023
QY 4834 GGAAGGAAACAGATATGACGAGGCTCAGAGCTAGCAAGTCTAGCTTGGCCCTAAAGCAG 4893
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QY 4954 AAACAGAAAGCTCCGTTGATGATTAATATCACTAAG-----TATCTACCTTA 5003
DB 3905 AAACATGAAGGCTCCAGTATGAAATTTTCACTAACAAGCTTAATCTTATCCCTT 3846
QY 5004 TCTCTCTATGAACTTAATGCTCTCTTTCTGTGTGTAGTGTGATTAACACACT 5063
DB 3845 TTTCCCTCTGACTTTTAAAAAGGTTCTTCTGACATCAATTAATGAGTGTACT 3786
QY 5064 GTT--TTCTTTGAGTGTATGAGCTTGTATGATTTTATGCTGTGCAAGTCTTGT-- 5119
DB 3785 GTTCTCTCTTGTATATGAAAGCTTGTATGTTTAAATTTGAAGCCAGTCTCTTG 3726
QY 5120 TGAAGGTTGTACCTTGACCTGAGCTTGGGCTTGAATGATGCCAAAGCACACTT 5179
DB 3725 TTAATGAATATATATATGACATGAGGCTGAATGATGACATGACAGACAAAGCATG 3666
QY 5180 CTGAATGCTGTGTAAAGTATATATCTTACT-----TTGTCTTGGAAAGT 5231
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QY 5232 GAAGGCTGTGAGAAAGACTCAGAGAGATGTGTCTGTAGAGAAACTTTTCTT 5291
DB 3605 GAAATGTGAGAGAGAAATCTATGATG-----ATCTGTGT 3569
QY 5292 CCCCTTAATGCTTATATCACTTCACTCA--ACTTGACTTTATACATGCTGTCT 5348
DB 3568 GATTTTCAAGACTTATATCACTTTTGAAGAAATCAATTTATTTGCAATGGGTTGCC 3509
QY 5349 ACATGAAGAGTGTAGGCGGCTCTATGCTCTGGGAAAAAGCAATAGGGGAAG 5408
DB 3508 ATGTGAAGAGTATATCTTTTGTGTGAGCTTCAAGAAAGCA--CAGAGAGGAGAGC 3450
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QY 5463 -----GACCACCAAGGTTTATAGTGAAGACGTCAGGCTGCTCAT 5506
DB 3389 GGTTTTGGAGCATTAATTTCCCTCTTGTGGGGGTAAAGAGACGAGGTTGTGTAT 3330
QY 5507 GTATATGATGAGACAGAGCGAGGAGATTAAGCTTCAAGTTTCTAGAGTCC--GAGT 5565

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 QY 2529 TGTGCTCTCTGTAATCATACTCTCTGGCTACTC----- 2565
 Db 1137 TGTGATGTTTCTAACTCATGCACACATTCGAAATTCGCTTTAGTCTTATGATGTTG 1196
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 Db 1197 CTCTGGGAGACGGGATGGGACATGCTATGATTAATTTTTTTTCTATTTGCTCAAT 1256
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 QY 3446 GTGAAAGGTCACTCTTTTCCATGTGATGAGAGATTAAGAAAAACA-CTGTGATAGTT 3504
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QY 3933 CATCAGCGGTGACAGCAGACATCCAGAAAGATGACAGAGGCTGAAGAGACAGTGA 3992
DB 1941 TATTGAAGGTGATGACTCTCATATCCAGGAATGTGCAAAAGCTGAAGAGACAGTGA 2000
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DB 2061 TTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2120
QY 4111 GTCCTACTGCTTACTGCTGACGCTGATCTAGCGGTGCTAATCTTCAATCTG 4170
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QY 4171 TCTAATTT-----GTAACTCAATTTCTGAGCTAGCAGAAAGCTTGTGCTGAGTCTC 4227
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DB 2237 ATTAACCTCAGATTTGCGGATGCTCAGTGCAGAGATAGGCTAGATCAGATCTCTG 2296
QY 4288 ATTCCAGCTGAC- TTGCTAGGCGCATGTGTAACTTTGCTGCTGATTAAGTAT 4346
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QY 4641 AAGATTAATATCACTGATGATTAATTAATGATGATGATGATGATGATGATGATGATG 4700
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QY 5723 AGTGAATTAAGTGAATGAAG 5782


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Db 2537 AATTTCTGGA-----GTATTAACACTTATTTGATGATGATGATGATGATGATGATGATGATGAT 2589
Qy 4581 TATATTAAGATTAACACAGAGGTGATGCTCCCAATTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4640
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Qy 4641 AGAGTAAATATCAGTATGATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 4700
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Qy 4701 TTTCTTACTTTTACTTGA-----TTTCTTGTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 4752
Db 2709 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2768
Qy 4753 TCAAGCAGTATGAGACCTATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4812
Db 2769 ACAATTCCTAGGAGATTTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2828
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QY	4933	TGGGTGTGCTTAAAGTAATCAGAAAACAGAAAGGCTCCGGTTAGTGAATTATCAGTAAGA-	4991
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Db	3066	CATCATTTAATGAGGTGACGTGTTCTTCTCTTGAATAATGGAAGCTTTGTAGTTTAA	3125
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Db	3126	TTGTGAAGCCAGATCTCTGTGTATAGAACTATTATCTAGACATGGAAGGCTGATGTTA	3185
QY	5159	GCATGCCAAGGCAACACTTCTGATATGCCCTGTGTAAGGTTATTAATTCATTTACT--	5215
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QY	5486	AACAGTCCAGGCTGGGCTCATGTAAATAGATGGAACAGAGGAGGAAGATAGCTTACA	5545
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QY	5603	AAGGAAGCTGGGAAGCAGCAAGTGAGAGGGAATGAAAAGGAAAAACAGATGTAG	5662
Db	3641	AAAAGATATGGAAGG-----TAAAGGGCGGAAGAAACAGAAAAAGGAAG	3688
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Db	3749	ATTAGTTTAGAGGAATTTTCAGTAGGGAATGCTTTTCACTTGAATTTGGGTTTCTCT--T	3805
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Db	3862	TAGGACCTATATCTGGTTTCTATTACTAAAGCAGTGGAAAAAGACTTATTTGGTATTT	3921
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Db	3922	TTCCACAAAAAGTAAAAACCTTTCTTTTACTGTGTCAAAAAGGTGGAAATAGAAAAAG	3981
OY	5963	AGGCAAAAGCCGACCATGGGTGAATGTGGGTCTTTAGTCAAGCCTTTTGAGTTGAG	6022
Db	3982	CCTTAATGATATGGTGAATACATGTTCAAAAGTCATTGAGTGAAGATGTTTTTAATCAG	4041
OY	6023	CACATCATCAATAGTT-----GATCATGGTCAAGGTGGAGGGC	6058
Db	4042	GAGTGTCMAATCTTGGCTTCCCTGGACCACTTGAAGAATTTGTTGGTACACAT	4101
OY	6059	TACCTGTAGGCGAGCCCTGTGGCTTGGCACTTAATCATCTCCAGGCTCAGATACCT	6118
Db	4102	AAAAATACAGAACATAGCTGATAGCTTAAAAAGTCAATGATAAATCTCATCTGTTT	4151
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Db	4162	TAAAGAGTTTATGAATTTCTGTAGGGTGATTCAAAGCTGCTGTGGGCATGTGGGC	4221
OY	6164	-----AACCCCACTAAATTAATTGACAAAAGACTGTGAATTTG	6205
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OY	6404	GATATTATATCTTTTAAGAGAGGTGATCTGTGTTTGGGCTCACCAAGCAATGCA	6463
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OY	6644	TGCTCTTCCGCTTCTAAAAAGAAATTAAGATCCCTGAATGAGACTTTT	6695
Db	4746	TAAACCCCTTCCCTGTAGAAATTAACATTTAGATGCCCCAAGCAATTTTT	4797

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LOCUS	AR165226
DEFINITION	Sequence from patent US 6274710.
ACCESSION	AR165226
VERSION	AR165226.1
KEYWORDS	GI:16238719
SOURCE	Unknown.
ORGANISM	Unknown.
	DNA
	linear
	PAT 17-OCT-2001

Unclassified.

REFERENCE 1 (bases 1 to 1119)

AUTHORS Dumoutier, L., Louhed, J. and Renauld, J.-C.

TITLE Antibodies which specifically bind T Cell inducible factors (TIFs)

JOURNAL Patent: US 6274710-A 7 14-AUG-2001;

FEATURES Location/Qualifiers

SOURCE 1..1119

/organism="unknown"

BASE COUNT 352 a 233 c 232 g 302 t

ORIGIN

Query Match

8.1%; Score 601.4; DB 6; Length 1119;

Best Local Similarity 99.8%; Pred. No. 2.1e-117;

Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB	510	AAAGCTGGAGAGAGATCAAGGCGATTGGGGAAGCTGAGCTGCTTTATGTC	569
QY	6595	TCTGAGAAATGCTTGGCTGAGGAGAGAGAGCTAGAAAAGCTGCTTCTCT	6654
DB	570	TCTGAGAAATGCTTGGCTGAGGAGAGAGAGCTAGAAAAGCTGCTTCTCT	629
QY	6655	GCCCTTAAAGAAACAATAAGATCCCTGAATGGAATTTTACTAAAGAAAGTGAA	6714
DB	630	GCCCTTAAAGAAACAATAAGATCCCTGAATGGAATTTTACTAAAGAAAGTGAA	689
QY	6715	GCTAAGCGTCATCATATTAGAGATTACATGAACCTGGCTCAGTTGAAAAGAAA	6774
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DB	750	TAGTCAAGTTGTCATGAGACAGAGTAGACTGTGATTAACCAAAAGATTGACA	809
QY	6835	ATATTTTATGTCATGATGATACACAGAAAAATATGTAATTTTAAAAATGTTGAA	6894
DB	810	ATATTTTATGTCATGATGATACACAGAAAAATATGTAATTTTAAAAATGTTGAA	869
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DB	870	AGGAGGTACCTCATCTCTTTAGAAAAAAGCTTATGTAATTTTATTCATATCCAA	929
QY	6955	TATTTATATATGTAAGTTTATTTATTAAGTATACATTTTATTTATGTCAGTTATTA	7014
DB	930	TATTTATATATGTAAGTTTATTTATTAAGTATACATTTTATTTATGTCAGTTATTA	989
QY	7015	ATATGATTTTATTTATAGAAATTTATGCTATTTGATTTAGTATAGGCAATATA	7074
DB	990	ATATGATTTTATTTATAGAAATTTATGCTATTTGATTTAGTATAGGCAATATA	1049
QY	7075	TTTATGACATATACATGAGAAACAAGATATCTTAGGCTTTATTAACAACATGATATCAT	7134
DB	1050	TTTATGACATATACATGAGAAACAAGATATCTTAGGCTTTATTAACAACATGATATCAT	1109
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DB	1110	AAA 1112	

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Job time : 12624.3 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:06:30 ; Search time 6517.75 Seconds

(Without alignments)
18499.535 Million cell updates/sec

Title: US-09-751-797-8

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estlin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_hiv: *
20: em_gss_dln: *
21: em_gss_vit: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rtd: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	554.4	7.4	700	11	AK005228 Mus muscu
2	519.8	7.0	562	17	AZ449260 IM0247J21
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4	149	2.0	149	17	AZ895851 RPT-24-2
5	113	1.5	534	17	AQ762065 HS_3136_B
6	110.4	1.5	377	17	AQ212781 HS_3118_B

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87.6	86.6	84.2	84	84	83.8	83.6	83.2	83	82.6	82.2	81.6	81.4	80.8	80.8	80.8	80.8	80.6	80.6	80.4	80.4	80.2	79.8	79.8	79.4	79.4	79.4	79.4	79.4	79.4	79.4	78.8	78.8	78.6	78.6	78.6	78.4	78.2	78	
1.2	1.2	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1
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ALIGNMENTS

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LOCUS
DEFINITION
Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500012D04;interleukin 10-related T cell-derived inducible factor, full insert sequence.
ACCESSION
AK005228
VERSION
AK005228.1 GI:12837639
KEYWORDS
HTC; CAP trapper.
SOURCE
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clone:1500012D04.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
REFERENCE
1
Garnica, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
JOURNAL
MEDLINE
PUBMED
10349636
AUTHORS
Garnica, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komuro, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PUBMED
11042159

clone UUCG1M0247J21 F, DNA sequence.
ACCESSION AZ449260
VERSION AZ449260.1 GI:10602872
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 562)
Islam, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Dunam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A.,
and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddum@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0247 Row: J Column: 21
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 562.
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/clone="UUCG1M0247J21"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gb]|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 119 a 155 c 116 g 172 t
ORIGIN

Query Match 7.0%; Score 519.8; DB 17; Length 562;
Best Local Similarity 97.5%; Pred. No. 3.6e-94;
Matches 549; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 2350 GTCCACACTACTGTTTCTGCTCTTTAGAGATC-TTTAAGACGCGGCTTTTCT 2408
DB 1 GTCCACACTACTGTTTCTGCTCTTTAGAGATC-TTTAAGACGCGGCTTTTCT 60
QY 2409 ATTCTATTCAAGGCTCAGAGACATTTCCATCTTGAGACACATATATCGA 2468
DB 61 ATTCTATTCAAGGCTCAGAGACATTTCCATCTTTGGCCTTCAGATACATATACGA 120
QY 2469 ATTTATCTACAGAGGCGCATTTAGAAAGCACCAGACATGCAATCTTCATTTCTC 2528

DB 121 ATTTATCTACAGAGGCGCATTTAGAAAGCACCAGACATGCAATCTTCATCTC 180
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DB 181 TGTGCTCTCTTCTGAACTCACTCTCTGCTACTCTCTGAGACCACTGCGGACATACA 240
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DB 241 TCTCTACTTACAGGCTTTTCTTCATCTCTCTGCTACTCTCTGAGACCACTGCGGACATACA 300
QY 2649 TTTGAGGCGGCTCTGAGATTAACAACAAGACAGCTCCGCTCATCTGCGGAGAACTGTC 2708
DB 301 TTTGAGGCGGCTCTGAGATTAACAACAAGATCTCCGCTCATCTGCGGAGAACTGTC 360
QY 2709 CGAGAGCTCACTGTAAGTCTCTCACTGTAAGAGAGGCTTACCTGCGGAGCTGAGAC 2768
DB 361 CGAGAGCTCACTGTAAGTCTCTCACTGTAAGAGAGGCTTACCTGCGGAGCTGAGAC 420
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RESULT 3
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DEFINITION AV030414.1 GI:4829962
ACCESSION AV030414
VERSION AV030414.1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
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1 (bases 1 to 256)
AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Kono, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara,
A., Hayatsu, N., Horii, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
Kikuchi, N., Kojima, Y., Matsuyama, T., Natsushima, H., Oda, H., Owa, C.,
Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara,
Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y., Tomioka, N.,
Watanabe, S., Yamane, M., Yamamura, T., Yokota, T., Yoshino, M.,
Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
TITLE RIKEN Mouse ESTs
JOURNAL Unpublished (1999)
COMMENT Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermolabile and thermostable activation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
location/Qualifiers
1..256
/organism="Mus musculus"
/strain="C57BL/6J"

BASE COUNT	88 a	29 c	41 g	98 t
ORIGIN				
Query Match	2.3% Score 173; DB 9; Length 256;			
Best Local Similarity	90.3%; Pred. No. 2.6e-24;			
Matches 196; Conservative	0; Mismatches 20; Indels 1; Gaps 1;			
Oy	6917 TAGAAAAAAGCTTATGTAAGTCTTATTCATATTCATATTTTATATATGTAAGTTAT 6976			
Db	40 TGGGGAGTACCCATATGTCATTTCTTTCCATACCGATACCTATATATATGTAAGTTAT 99			
Oy	6977 TTATATATAGATATACATTTTATTTATATGTCAGTTATTTATATATGTAAGTTAT 7036			
Db	100 TTATATATAGATATATATTTTATTTATATGTCAGTTATTTATATATGTAAGTTAT 159			
Oy	7037 ATTATCTGCTATGATATATTT-AGTATTAAGGCATAATATTTATGACATTAAGTAA 7095			
Db	160 ATTATCTGATGTGATATTTTGGATTAAGCAATAATATTTATGATATATTAACATATAA 219			
Oy	7096 ACAAGATATCTTAGGCTTTAATTAACACATGATATC 7132			
Db	220 ACAAGATATCTTAGGCTTTAATTAACACATGATATC 256			
RESULT 4				
LOCUS	A2895851 149 bp DNA linear GSS 05-MAR-2001			
DEFINITION	RPCI-24-211K19.TV RPCI-24 Mus musculus genomic clone RPCI-24-211K19			
ACCESSION	A2895851			
VERSION	A2895851			
KEYWORDS	GSS.			
ORGANISM	house mouse.			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 149)			
AUTHORS	Zhao, S., Niemann, W., Malek, J., Shatsman, S., Akintet, B., Levina, M., Tesgaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E., Russell, D., de Jong, P. and Fraser, C.M.			
TITLE	Mouse BAC End Sequences from Library RPCI-24			
JOURNAL	Unpublished (1999)			
COMMENT	Other_GSSs: RPCI-24-211K19.TV Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.choi.org/bacpac/orderingframe.html). BAC end page: http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html Plate: 211 row: K column: 19			

FEATURES	Seg primer: SP6
source	Class: BAC ends
	Location/Qualifiers
	1. 149
	/organism="Mus musculus"
	/strain="C57BL/6J"
	/db_xref="taxon:10090"
	/clone="RPCT-24-21K19"
	/clone_11b="RPCT-24"
	/sex="Male"
	/cell_type="Spleen/Brain"
	/note="Vector: pTRABAC1; Site 1: BamH1; Site 2: BamH1; RPCT-24 Mouse BAC library produced by Pieter de Jong. The library was cloned in the pTRABAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
BASE COUNT	49 a 24 c 18 g 58 t
ORIGIN	
Query Match	2.0%; Score 149; DB 17; Length 149;
Best Local Similarity	100.0%; Pctd. No. 1.9e-19;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1155 TGTGAGCAATTACCAATGATGTATTTATTTATTTAAAAAATCTATGCTTAAAT 1214
Db	1 TGTGAGCAATTACCAATGATGTATTTATTTATTTAAAAAATCTATGCTTAAAT 60
Oy	1215 GTCTATAGATTTGTCACACCGATTTTCCAACTTAACCTGACCTTGCTATGATTTT 1274
Db	61 GTCTATAGATTTGTCACACCGATTTTCCAACTTAACCTGACCTTGCTATGATTTT 120
Oy	1275 AACCTTGATTTGCATCTACCATTAACG 1303
Db	121 AACCTTGATTTGCATCTACCATTAACG 149
RESULT 5	
AQ762065	534 bp DNA linear GSS 28-JUL-1999
LOCUS	HS 3136 B1 H07 T7C CIR Approved Human Genomic Sperm Library D Homo
DEFINITION	sapiens genomic clone Plate=136 Col=13 Row=P, DNA sequence.
ACCESSION	AQ762065
VERSION	AQ762065.1 GI:5640181
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
	1 (bases 1 to 534)
	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
	Hood L.
	Sequence-tagged connectors: A sequence approach to mapping and
	scanning the human genome
	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
JOURNAL	99380589
MEDLINE	Contact: Mahairas GG, Wallace JC, Hood L
COMMENT	High Throughput Sequencing Center
	University of Washington
	401 Queen Anne Avenue North, Seattle, WA 98109, USA
	Tel: (206) 616-3618
	Fax: (206) 616-3887
	Email: jwallace@u.washington.edu
	Clones may be purchased from Research Genetics (info@resgen.com).
	BAC end Web Server: http://www.htsc.washington.edu
	Plate: 3136 Row: P Column: 13
	Seq primer: T7
	Class: BAC ends
	High quality sequence stop: 534.
FEATURES	Location/Qualifiers
source	1. 534
	/organism="Homo sapiens"
	/db_xref="taxon:9606"


```

/clone="Plate=3136 Col=13 Row=P"
/sex="male"
/clone_11b="CIT Approved Human Genomic Sperm Library D"
/notes="Organ: sperm; Vector: pBelOBA11; BAC Clones in
E-Coli DH10B"
BASE COUNT      171 a      84 c      104 g      170 t      5 others
ORIGIN

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Query Match      1.5%; Score 113; DB 17; Length 534;
Best Local Similarity 61.3%; Pred. No. 2.7e-12;
Matches 288; Conservative 0; Mismatches 166; Indels 16; Gaps 6;

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OY 4245 GGATGCTGTCAGCAGATGCTAATGCTAGAGACAGATCCCTGATCCCGACGCTGCAC- 4303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 68 GGATGCTGTCAGCAGATGCTAATGCTAGAGATGCTGCTGATCCCGACGCTGCAC 127
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 4304 TTGCTAGTGGCCATGCTAATTAATCTTGGCTGATTAAGTATTTGGGAAG--CCAGTT 4361
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 128 TTTCGGGGTGTAGACAGATTAGTTTGTGACATTAATCTTGGGAATTTTCAGATT 187
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 4362 CCCACGACCTAATATATGTAAGAACCATGCAATGAAACTAGAAAGCTGGGCA---C 4417
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 188 CCTATTGACTCATGTAATCTGAAGAGTCTGTTTAAACAGAAAGATGCTATGGGC 247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 4418 AAATCTAGAGATGATTTTGAAGTCAATTAACGAGTCTGAAATGTCGCAAAATC 4477
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 248 AAATTTATTTGAAGTCAATTTTGAAGTCAATTAATGATTTGTAACCTTGGAAATA 307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 4478 AACCCAGATTAACAACAAAGAGCTGATTTGCAAAATAGACAAGATTTAGATCACTG 4537
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 308 AACTCAGAACATGAGAAAGAGCTGACCTGCAATATAGGGCTAATTTCTGCA----- 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 4538 GTATTATATGCTATCATCTTAATTAATAATAGGGCTAATATATATTTAAGATTAAAC 4597
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 361 GTAATTAACAATTAATTTGAATTCATATATCTATCAGATATGATATATAGTTTAA 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 4598 ACAAGATGATAGCTCCCAATTTACTGGCTGTTTCAAAAGATTAATATCAT 4657
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 421 GCAAGACGACGACACCC-CGATCTCTTTATACACCTTCMAATAGGTAAAAATATAGT 479
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 4658 CATGATTAATATATAGTGCATGAAAGATGAGATGAAACCTTTCTCT 4707
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 480 NAGAATTTATTAAGT-AAATGAGATCTGAATTTGTAGACTTTCTTT 528
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 6
AQ012781      377 bp      DNA      linear      GSS 18-SEP-1998
LOCUS      HS_3118_B2_B08_MR_CIT Approved Human Genomic Sperm Library D Homo
DEFINITION      sapiens genomic clone Plate=3118 Col=16 Row=D, DNA sequence.
ACCESSION      AQ012781
VERSION      AQ012781.1 GI:3623982
KEYWORDS      GSS.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 377)
AUTHORS      Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

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```

TITLE      Sequence-tagged connectors: A sequence approach to mapping and
JOURNAL      scanning the human genome
MEDLINE      Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
COMMENT      Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector

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Plate: 3118 row: D column: 16
Class: BAC ends
High quality sequence stop: 377.
Location/Qualifiers

```

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FEATURES
source
1..377
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3118 Col=16 Row=D"
/clone_11b="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/notes="Organ: sperm; Vector: pBelOBA11; BAC Clones in
E-Coli DH10B"
BASE COUNT      119 a      60 c      80 g      118 t
ORIGIN

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```

Query Match      1.5%; Score 110.4; DB 17; Length 377;
Best Local Similarity 63.2%; Pred. No. 9.6e-12;
Matches 220; Conservative 0; Mismatches 121; Indels 7; Gaps 3;

```

```

OY 4194 TGGAGCTAGCAGAAAGCTTAGCTCAGCCAGTCTCATGACACTTCTCGAGAGATGCTT 4253
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 TAGAAGCTGTGGGATCTTACCTGTCTAGTCATTAACCTCAGATTCTGGGATGTC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 4254 GTGACAGAGTCATGCTAGAGACAGACATCCCTGATCCAGCTCTGCAC--TTGCTAGT 4312
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 GTGCGAGATATGAGGCTAGATGACAGTCTCTGATATCCAGACGACACTTTCCGGT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 4313 GGCATGTGTATTAATCTTTGGCTGATTAAGTATTTGGGAAA--GCCAGTTCCACGAG 4370
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 GGTGATACAGATTATTTTGTGATCATTATTTAGGGAATTTTCAGATTCTTATGAC 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 4371 CTACATTAATCTGAAGAACCATGATTTGAAACTAGAAA---GCTGGCACAACCTACT 4426
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 TCATGTAATCTGAAGAAAGTACTTGTTTAAACAGAAAGATGCTATGGGCAATTTAT 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 4427 AGAGATGATTTTGGCTCATTAACGAGTCTGAAATGTCGCAAAATCAACCCAGA 4486
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 TGAAGTCAATTTTGAAGTCAATTAATGATTTGCTTTGAAACTTGGAGATTAATCAGAA 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 4487 TAACAACAAAGAGCTGATTTGCAATATAGACAAATTTAGAAATCA 4534
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 301 CAATGAGCAAGAGCTGACCTGATATAGGGCTAATTTCTGAGATTA 348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 7
AQ104025/c      389 bp      DNA      linear      GSS 28-AUG-1998
LOCUS      HS_3108_B1_C01_T7_CIT Approved Human Genomic Sperm Library D Homo
DEFINITION      sapiens genomic clone Plate=3108 Col=1 Row=F, DNA sequence.
ACCESSION      AQ104025
VERSION      AQ104025.1 GI:3478961
KEYWORDS      GSS.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 389)
AUTHORS      Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

```

```

TITLE      Sequence-tagged connectors: A sequence approach to mapping and
JOURNAL      scanning the human genome
MEDLINE      Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
COMMENT      Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector

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Plate: 3108 row: F column: 1

```


Class: BAC ends
High quality sequence scop: 389.

FEATURES
Location/Qualifiers

source

1..389
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate3108 Col=1 Row=F"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC clones in E-Coli DH10B"

BASE COUNT 119 a 86 c 65 g 118 t 1 others
ORIGIN

Query Match 1.2%; Score 87.6; DB 17; Length 389;
Best Local Similarity 64.0%; Pred. No. 3.7e-07;
Matches 165; Conservative 0; Mismatches 89; Indels 4; Gaps 2;

QY 3782 AATCTAGCTCAACGTAATCTAGCTCAGCGGCGCAAAATGACTGAAACGCTCTATTTC 3841
|||||
DB 291 AATCTAGCTCACTGTAATCTAGCTCATTTGTG--CAAAATTACTAAGAGCTTTATTTC 235
|||||

QY 3842 CAGTGAACGCTCAGCTGCCTCAGATATACAGGATTTGGGCTCCACCGGATAAGATT 3901
|||||
DB 234 CAGGTGAATTTGCTTACTTCTTCACTGCGGTGTGAGGTTATTAAGTTTACGACACATTT 175
|||||

QY 3902 CTGTTAGTGA-CTCTGCTTTTATTTTTCAGACATCAGCGGTGACGACCAAGACATCCAG 3960
|||||
DB 174 AAGATAGTATGCTTCTGTTATTTTATAGCATATTGAAGGTGATGACCTGCATATCCAG 115
|||||

QY 3961 AAGATGTCAAGAGGTGAGGACAGTGAAGGTAAGTCTTTGGCAAGCCACATACT 4020
|||||
DB 114 AGGAATGTGCAAAAGGTGAAGACACAGTGAAGGTAAGTCTGATCTGTCATGTT 55
|||||

QY 4021 AAGCATTCAGTAGGAGA 4038
|||||
DB 54 AAGTCATGCATAGGAGA 37
|||||

RESULT 8
BI301790 626 bp mRNA linear EST 20-JUL-2001
LOCUS
DEFINITION UI-R-DL0-cin-d-08-0-UI-s1 UI-R-DL0 Rattus norvegicus cDNA clone
BI301790
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 626)
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized rat tongue library cDNA library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.reagen.com) The following repetitive

elements were found in this cDNA sequence: 12-236, >B3SINE/B2
311-349, >U2HERNA
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
Location/Qualifiers

1..626
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-DL0-cin-d-08-0-UI"
/clone_lib="UI-R-DL0"
/dev_sflag="ADULT"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-DL0
library is a non-normalized Rat Tongue library constructed
in pT7T3D-Pac vector according to the procedure described
by Bonaldo, Lennon & Soares (Genome Research Genome 6:
791-806, 1996). The oligonucleotide used to prime first
strand synthesis contained the sequence tag GCCGA between
the Not I cloning site and dT18 stretch.
TAG LIB=UI-R-DL0
TAG TISSUE=rat tongue
TAG_SEQ=GCCGA"

BASE COUNT 142 a 149 c 135 g 200 t
ORIGIN

Query Match 1.2%; Score 86.6; DB 13; Length 626;
Best Local Similarity 65.3%; Pred. No. 5.4e-07;
Matches 143; Conservative 0; Mismatches 74; Indels 2; Gaps 1;

QY 370 TGTTTTATCTTTTATTAATAATTCACACATCAGTGTGTCAGAGCTGTTTACC 429
|||||
DB 4 TTTTATTTTATTTTGAATAATGAAAAAATTTATTTATGTTATGTTGCTTTTCC 63
|||||

QY 430 CACATGTATGCTGTGTCACCAAGTCTGCTGTGTTGGGCGCAAGACAGACAGAG 489
|||||
DB 64 TGGATGTATGCTGTGCAACCGTATGTGCGGGTCCCTATGAGGCCGAAGAGGATT 123
|||||

QY 490 GATGCGCTGACCGAGTACAGATGTTGTGACCCACATGAGATGCTGGAGTTAG 549
|||||
DB 124 GATCTACTGCACTGAGATTACAGGAGTTTAAGCCACATGTGGTGTAGGATTGA 183
|||||

QY 550 ACCGAGTCTCTCAGAAAGTGCAGAAATGCTTTAACCA 588
|||||
DB 184 GCCCAGGTCTCTACAAAGGC--CAAGTCTTTAACCA 220
|||||

RESULT 9
BF416659 448 bp mRNA linear EST 28-NOV-2000
LOCUS
DEFINITION UI-R-CA0-bku-d-01-0-UI-s1 UI-R-CA0 Rattus norvegicus cDNA clone
BF416659
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 448)
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565

The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized rat tongue library cDNA library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.reagen.com) The following repetitive

Email: msosares@blue.ueg.uiowa.edu
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized cerebellum library cDNA library preparation. M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com). The following repetitive elements were found in this cDNA sequence: 33-240, >B3HSINE/B2 284-313, >ID RNHSINE/ID 349-391, >PB1D7HSINE/Alu
 Seq primer: M13 Forward
 POLYA=yes

FEATURES

source

Location/Qualifiers

1..448
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UT-R-CAO-bku-d-01-0-UT"
 /clone_1lb="UT-R-CAO"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The UT-R-CAO library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratseq.uiowa.edu. The subtraction has been previously described in (Bonaldi, Lemon and Soares, Genome Research 6:791-806, 1996)
 TAG LIB=UI-R-CAO
 TAG TISSUE=cerebellum
 TAG_SEQ=CGAAGC

BASE COUNT 93 a 85 c 97 g 172 t 1 others
 ORIGIN

Query Match 1.1%; Score 84.2; DB 12; Length 448;
 Best Local Similarity 61.8%; Pred. No. 1.7e-06;
 Matches 134; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 370 TGTTTTAACTTTTATTAATTCACACATCATGTTGTGCAAGTCTGTTTCCACC 429
 DB 1 TTTTATTTTATTTTATTAATTAAGACTTTATTTATTTGTAATTTTGGCC 60
 QY 430 CACATGATATGTCGTCACCAAGTGTGCTGCTTGGGGGAGAGAGAGAGAG 489
 DB 61 TGCATGTACGTACGTATCCATGTGATGATGTTGGCATAGTAGAAGACGGTGG 120
 QY 490 GGTGCTCTGCAACCGAGTCAAGATGTTGTGAGCACCATAGAGATGCTGGAGTTAG 549
 DB 121 GATCACTGAGAGTGGAGTTACGACAGTGTGGAGCGCCATGTGGTACTAGGAATTGA 180
 QY 550 ACCCAGGTCTCTCAGAAAGTGCAGCAATGCTTTTAC 586
 DB 181 ACCCAGATCTCTGAAAGAGCAGCCAGTGTCTTAC 217

RESULT 10

BO561085/c

LOCUS BO561085 262 bp mRNA linear EST 20-JUN-2002

DEFINITION H4068B12-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone

BO561085 H4068B12 5', mRNA sequence.

ACCESSION BO561085

VERSION BO561085.1 GI:21461970

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 262)
 Vanburen,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., Martin P.R., Stagg,C.A., Bassey,U., Aliba,K., Hamatani,T., Kargul,G.J.,

TITLE Luo, A.G. and Ko, M.S.H.
 JOURNAL Assembly, verification, and initial annotation of NIA 7.4K mouse cDNA clone set
 COMMENT Unpublished (2002)
 Other ESTs: H4068B12-3
 Contact: Yong Qian
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
 Email: cdna@gsun.gsc.nia.nih.gov
 This clone set has been freely distributed to the community. Please visit http://lgsun.gsc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
 Plate: H4068 row: B column: 12
 Seq primer: -21M13 Reverse
 High quality sequence stop: 262
 POLYA=no.

FEATURES

source

Location/Qualifiers

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 /strain="C57BL/6"
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 /db_xref="taxon:10090"
 /clone="H4068B12"
 /clone_1lb="NIA Mouse 7.4K cDNA Clone Set"
 /sex="mixed"
 /dev_stage="mixed"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."
 BASE COUNT 83 a 58 c 58 g 63 t
 ORIGIN

Query Match 1.1%; Score 84; DB 14; Length 262;
 Best Local Similarity 64.8%; Pred. No. 2.1e-06;
 Matches 158; Conservative 0; Mismatches 80; Indels 6; Gaps 2;

QY 377 ATCTTTTATTAATTAATTCACACATCATGTTGTGCAAGTCTGTTTCCACCACAT 436
 DB 250 ACCGGTTTAAATTTTGTAGATTATTTATGTGATGAATTTTACCTGCATAT 191
 QY 437 ATGTCTGTGACCAAGTGTGCTGCTGCTTGTGGGGCAGAGAGAGAGAGAGAG 494
 DB 190 ATGTATGTGACCAAGTGTGATGCTTATGTTGTGGAGTCAAGAGAGAGTCTAGATCC 131
 QY 495 CCTGGACCGAGTCAAGATGTTGTGAGCACCATGAGATGCTGGAGTTAGACCA 554
 DB 130 CTTAGACTGTGATTAACATGCTGTGACCACTGTGGTTTGGAAATGAACCA 71
 QY 555 GGTCTCTCAGAAAGTCAAGATGCTTTAACACACGAGCATTTCTCTCCAGCCC 614
 DB 70 GGTCTCTCAGAAAGTCAAGATGCTTTATCTA---CAGAGCTGTCTCTTTCAGCCC 15
 QY 615 CAAC 618
 DB 14 CAAC 11

RESULT 11

BB346070/c

LOCUS BB346070 645 bp mRNA linear EST 24-OCT-2001

DEFINITION BB346070 RIKEN full-length enriched, 10 days neonate cerebellum Mus musculus cDNA clone B930060A17.3', mRNA sequence.

BB346070 BB346070 GI:16405012

ACCESSION BB346070

VERSION BB346070.2 GI:16405012

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 645)
 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagata,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda


```

TAG_TISSUE=cerebellum
TAG_SEQ=CGGAAC"

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1.18; Score 83.8; DB 10; Length 453;
C1 0.0; Desc 3 10-05.

servative 0; Mismatches 82; Indels 0; Gaps 0;

Qy	432	CATGATATGTCCTGTCACCAAGTGTGCTGCTGCTTGTGGGGGCAGAGACGAGAGAGG	491
Db	62	CATGACGTACAGTATGCATGTGATAGTTTGGCATAGGTGCAGAGACGGTGGGGA	121

Qy	492	TGCCCTGGACCGGAGTCACGGATGGTGTGTGAGCCACATAGAGTCTGGGAGTTAC	551
Db	122	TCACCTGAGACTGGAGTTACAGACAGTGTGTAGCCCGCATATGGGTCTAGGAGTTGAC	181

Qy 552 CCAAGTCCCTCCAGAAGTCGACCAAATGCTCTTAAC 586
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 CCAGTCCCTCTCGAAGACGACGCCAGTGTCTTAGC 216

RESULT 13				
BG800654				
LOCUS	551 bp	mRNA	linear	EST 20-DEC-2001
DEFINITION	0051-46 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,			
	mRNA sequence.			

VERSION	BG800654.1	GI:17947515
KEYWORDS	EST.	
SOURCE	house mouse.	

Eukaryota; Metazoa;	Chordata;	Cranialta;	Vertebrata;	Euteleostomi;
Mammalia;	Eutheria;	Rodentia;	Sctirognathi;	Muridae;
1 (bases 1 to 551)				Mus

TITLE Gene expression in the developing mouse retina by EST sequencing and microarray analysis
JOURNAL Nucleic Acids Res. 29 (24), 4983-4993 (2001).
URL <http://www.ncbi.nlm.nih.gov/PMCID/118600/>

Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA

FEATURES	Location/Qualifiers
Source	1. .551

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'organism="Mus musculus"
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/tissue_type="neural retina"
/dev stage="embryonic day 14.5 post-fertilization"
/notes="vector: pAMP10 (clon) : Cloned unidirectionally
primer: Oligo dT. RNA isolation: cytoplasmic RNA prep
(Pharmacia); Cloning technique: CUA Cloning (clonamp,
Life Technologies); Average insert size: 1.8 Kb;

```

BASE COUNT	ORIGIN
138 a	119 g
119 c	184 t

Insertion site: TAGTCACGAAATTCGAGTG--->. Other information regarding entire library may be found at http://pga.swmed.edu/Data/Libraries/microarray_cdna_library.htm.

Query Match	1.1%	Score 83.6	DB 12	Length 551
Best Local Similarity	64.0%	Pred. No. 2	2e-06	
Matches 142	Conservative 0	Mismatches 79	Indels 1	Gaps 1

QY 355 CTCGATGTTTAACTCTTTTATTAATAATTCACAAATCAGGTGTTTGCGAAGTCTGTT 424
 50 CCCAGTGTTTTACCAATTCTTATTATTAATTTATCCCATGATATGATGTT 109
 Db

425 TCACCCACATGTAATGCTGTGTGACCAAGAGCTGGCTGGTGTGGGGGCCAAGAGACG 484
 QY
 110 TC-CCTACATGTAATCTTTGCACCAATGTAATCTGTGTCTATTAAGAAGCTAGAAAG 168
 Db

Qy 485 GAGAGGGGTCCTCCGAGCACCAGGAGTCACCGATGCTGTGTGAGCCACCATATGAGGATCTCTGGGA 544

Db 169 GTTTGGATCTCCTCGAATATGGAATTACAGCAATTTGTAAGCAGCAGCATATTAAGTCCTGGGA 228

QY 545 GTTAGACCCAGGTCCTCCAGAGTGACGCAATGCTCTTAAC 586
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Db 229 ATTAAACCAGGTCTCCTTGGAA CAGCACGCCGGTGTCTTAAC 270

[illegible]

VERSION	AV293250.2	GI:16392512
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	<i>Mus musculus</i>	

REFERENCE
AUTHORS
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.
1 (bases 1 to 626)
Eukaryota; Metazoa;
Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Mus.

M. Koya, S. Matsuyama, I. Miyazaki, A. Nomura, K. Ono, H. Sasaki,
Ozaki, Y. Okido, T. Saito, R. Sakai, K. Sakai, K. Sano, H. Sasaki,
D. Shibata, K. Shinagawa, A. Shiraki, T. Sogabe, Y. Tanaka, T. Toyoi,
Tadamasa, K. Tagawa, A. Takahashi, F. Takeda, Y. Tanaka, T. Toyoi,

TITLE
 JOURNAL
 COMMENT
 On Nov 9, 1999 this sequence replaced gi:6307281
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 Unpublished (2001)
 Mutamalsu, M. and Nagashizaka, Y.
 Mutamalsu, M. and Nagashizaka, Y.

Laboratory for Genome Exploration Research Group, National Science Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Fax: 81-43-503-7210
 Email: genome-res@cc.riken.go.jp
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh

N., Kounouci, T., Okafor, I., Gargano, J., et al. (2006) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.*, 10 (10), 1617-1630 (2000)

MAEDA, M., OKAZAKI, Y., MURAMATSU, M., INOUE, Y., KIRA, A. and HAYASHIZAKI, Y.
RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11): 1757-1771 (2000)

, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanka, I., Atawa
, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

FEATURES

source location/Qualifiers

1.626
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head"
/sex="mixed"
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/dev_stage="6 days neonate"
/lab_host="DH10B"
/note="Site 1: SalI; Site 2: BamHI. cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3']. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATCTGAGTTAATTAAATTCCTCCCTCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified Bluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
BamHI"

BASE COUNT 224 a 123 c 102 g 177 t
ORIGIN

Query Match 1.1%; Score 83.2; DB 9; Length 626;
Best Local Similarity 67.3%; Pred. No. 2.6e-06;
Matches 132; Conservative 0; Mismatches 63; Indels 1; Gaps 1;

396 CACAAATCAGTGTGTCAGTCTGTTTCCACCATGATGTCGTGACCAAGTGC 455
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456 TGCCTGTGCTTGGGGGCAAGAGAGAGAGAGG-TGCCCTGGACCGAGTACGGA 514
205 TGCCTGTGCTGAGAGACACGAGAGAGAGGTCGTGATCCCTGGAGTCGAGATCA 146
515 TGGTTGTAGCCACATAGATGCTGGAGTTAGACCCAGGTCTCCAGAAATGACACA 574
145 TGGTTGTAGCCACATAGATGCTGGAGTTAGAACTAGAGCCCTCGAAGATCACA 86
575 AATGCTTTAACCACA 590
85 AGTGCTCTTAGGCCA 70

RESULT 15
AA833456/c 382 bp mRNA linear EST 23-FEB-1998
LOCUS A:833456

DEFINITION uc91a01.r1 Soares_NMPu Mus musculus cDNA clone IMAGE:1432968 5',
mRNA sequence.
AA833456
ACCESSION AA833456.1 GI:2907184
KEYWORDS EST.

SOURCE

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 382)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellendberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

THE MASHU-HMI MOUSE EST PROJECT
The Mashu-HMI Mouse EST Project
Unpublished (1996)
CONTACT: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

COMMENT

Email: mouseset@watson.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:917036
Putative full length read
vector to vector length is 470
Seq primer: -28m3 rev2 ET from Amersham
High quality sequence stop: 366.

FEATURES

source location/Qualifiers

1.382
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/db_xref="taxon:10090"
/clone="IMAGE:1432968"
/clone_lib="Soares_NMPu"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pTZ19-Pac (Pharmacia) with
a modified polylinker; 1st strand cDNA was prepared from
pregnant mouse uterus, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pTZ19
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."

BASE COUNT 114 a 80 c 82 g 106 t
ORIGIN

Query Match 1.1%; Score 83; DB 9; Length 382;
Best Local Similarity 64.1%; Pred. No. 3.1e-06;
Matches 125; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

396 CACAAATCAGTGTGTCAGTCTGTTTCCACCATGATGTCGTGACCAAGTGC 455
296 CATTATTACTTATGATGATGAGTGTGTTGCTGCACTAGACCTGTGACCACTGTG 237
456 TGCCTGTGCTTGGGGGCAAGAGAGAGAGAGGTCCTTGACCGAGTACGAT 515
236 TGCCTGTGCTGAGAGACACGAGAGAGAGGTCCTTGAGACTGGAGATACAGAT 177
516 GATTGTAGCCACCATGATGCTGGAGTTAGACCCAGGTCTCCAGAAATGACAGCA 575
176 GATTGTAGCCACCATGATGCTGGAGTTAGAACTAGAGCCCTCTGGAAGATCAGCA 117
576 AATGCTTTAACCACA 590
116 GTGCTCTTAGGCCA 102

Search completed: July 19, 2003, 19:39:07

Mon Jul 21 05:36:40 2003

Job time : 6522 secs

us-09-751-797-8.rst

Page 11

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:02:25 ; Search time 1021.03 Seconds
(without alignments)
16420.772 Million cell updates/sec

Title: us-09-751-797-8

Perfect score: 7445
Sequence: 1 gttcaccctgcttaagat.....gatttaactatggtcat 7445

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7445	100.0	7445	22	AA514859
2	7445	100.0	7445	24	AAAD27134
3	7441.8	100.0	7445	24	AAAD30628
4	7433	99.8	7444	21	AAA28816
5	4245.2	57.0	5935	21	AAA28818
6	4245.2	57.0	5935	22	AA514878
7	4245.2	57.0	5935	24	AAAD30660
8	4245.2	57.0	5935	24	AAAD27153
9	686	9.2	4797	22	AA514876

10	686	9.2	4797	24	AAAD30646	Human TIF genomic
11	686	9.2	4797	24	AAAD27151	Human T cell deriv
12	682.4	9.2	4796	21	AA28840	Human T cell induc
13	601.4	8.1	1119	21	AA28815	Murine T cell indu
14	601.4	8.1	1119	22	AA514858	Mouse cDNA encodin
15	601.4	8.1	1119	24	AAAD30627	Mouse TIF alpha CD
16	601.4	8.1	1119	24	AAAD27133	Mouse T cell deriv
17	598.2	8.0	1166	21	AA281774	Murine GIL-19 prot
18	555.2	7.5	1111	21	AA28817	Murine T cell indu
19	555.2	7.5	1111	22	AA514860	Mouse cDNA for T C
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21	555.2	7.5	1111	24	AAAD27135	Mouse T cell deriv
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ALIGNMENTS

RESULT 1	AA514859	standard; DNA; 7445 BP.
ID	AA514859	
AC	AA514859	
XX	AA514859	
DT	19-DEC-2001	(first entry)
XX	AA514859	
DE	Mouse partial genomic DNA for T cell derived inducible factor, TIFalpha.	
XX	AA514859	
KW	Mouse; T cell derived inducible factor; TIFalpha; ds; anti-allergic;	
KW	antisthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;	
KW	cancer; lymphoma; immune system disorder; allergy; asthma;	
KW	acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;	
KW	thyroiditis; melanoma; hepatoma.	
XX	AA514859	
OS	Mus musculus.	
XX	AA514859	
PN	US2001024652-A1.	
XX	AA514859	
PD	27-SEP-2001.	
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PF	29-DEC-2000; 2000US-0751797.	
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PR	18-OCT-1999; 99US-0419568.	
PR	26-OCT-1998; 98US-0178973.	
PR	16-JUL-1999; 99US-0354243.	
XX	AA514859	
PA	(DUMO/) DUMOUTIER L.	
PA	(LOUAH/) LOUAHED J.	
PA	(RENA/) RENAUD J.	
XX	AA514859	

PI Dumoutier L, Louahed J, Renaud J;
XX WPI; 2001-638496/73.
XX
XX New isolated nucleic acid molecules encoding T cell inducible factors,
PT useful as markers for expression or effect of interleukin (IL)-9 in a
PT subject and diagnosing susceptibility to asthma or allergy -
XX
XX Claim 1; Page 11-14; 26pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule, which encodes
CC a T cell derived inducible factor (TIF) which are upregulated by the
CC cytokine interleukin-9 (IL-9) and induce STAT transcription factor
CC activation. The TIF proteins (or their mutants) may be used to test IL-9
CC ant/agonists for their potency against lymphomas, immune system
CC disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
CC autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
CC or inhibit differentiation of tissue types in which they are active and
CC therefore be used to develop treatments for melanomas and hepatomas.
CC The present sequence a partial genomic sequence for mouse Tifalpa.
XX
SQ Sequence 7445 BP; 2058 A; 1570 C; 1597 G; 2220 T; 0 other;
Query Match 100.0%; Score 7445; DB 22; Length 7445;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GTTTATACCTGCTTAAAGATTCTTTATTTATTAATAAACTATTCTTAATAATGAAA 60
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DB 301 TCGACTGCCCACTCTACCTTGGGCTCTGATGGCCACCTTTCAACTTTGCAATTA 360
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QY 661 TTCACTACCTGCACTCTCCCTTGGCATCTTTCTGCAAGAAACCAAAAGCAAGAT 720
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DB 721 CCCCACTGCTTTGCTCTCTCAAGTGTGACCTCTCAACAGGTCAAGATTCTCCAGTGT 780
QY 781 CCCCTTAACACTTTCCCAAGTGTCTCTCAACATTTCTCCAGTGTCTCTCAACCTTT 840
DB 781 CCCCTTAACACTTTCCCAAGTGTCTCTCAACATTTCTCCAGTGTCTCTCAACCTTT 840
QY 841 CTCACATGCTCTTCAACATTTGATGATCTCAATAGCTAGAGGAGAAAGATCTCACACA 900
DB 841 CTCACATGCTCTTCAACATTTGATGATCTCAATAGCTAGAGGAGAAAGATCTCACACA 900
QY 901 GTGATTTTCAAGATCTGCGGCTTCTAGTCTAGATGATGAGGATTTGCTGCTGCTGAG 960
DB 901 GTGATTTTCAAGATCTGCGGCTTCTAGTCTAGATGATGAGGATTTGCTGCTGCTGAG 960
QY 961 AGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 961 AGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1021 GGATTCAGTGTACATACATGCAAAATCCAGATTTTGTAAATTTCTCTTCAACT 1080
DB 1021 GGATTCAGTGTACATACATGCAAAATCCAGATTTTGTAAATTTCTCTTCAACT 1080
QY 1081 ATCCATCTATATAGTATGTTATGATGCTCAATTTAAATAATATTTGAGCTTATGC 1140
DB 1081 ATCCATCTATATAGTATGTTATGATGCTCAATTTAAATAATATTTGAGCTTATGC 1140
QY 1141 TTGCACAGTAAATGTCAAGATTAAGCAATGATATGATTTATTTTAAATAA 1200
DB 1141 TTGCACAGTAAATGTCAAGATTAAGCAATGATATGATTTATTTTAAATAA 1200
QY 1201 TCTATGCTTAAATGTCTTATGATGCTCACTACGATTTTCCAACTTATCTGACC 1260
DB 1201 TCTATGCTTAAATGTCTTATGATGCTCACTACGATTTTCCAACTTATCTGACC 1260
QY 1261 TTGGCTATGATTTCAACCTTTGATTTGATCTACCATTAACAGTCTCTGACCAAGACAT 1320
DB 1261 TTGGCTATGATTTCAACCTTTGATTTGATCTACCATTAACAGTCTCTGACCAAGACAT 1320
QY 1321 TCTGTGCAATGGAGCTGTGAAGAAAGCCAACTTTTAAATAAATAAATAAATAA 1380
DB 1321 TCTGTGCAATGGAGCTGTGAAGAAAGCCAACTTTTAAATAAATAAATAAATAA 1380
QY 1381 GTTATAGTTAGATTTCCATATCTAATAAATAAATAAATAAATAAATAAATAAATAA 1440
DB 1381 GTTATAGTTAGATTTCCATATCTAATAAATAAATAAATAAATAAATAAATAAATAA 1440
QY 1441 AATATCTCCAACTTTCTAATAGGCTTATTTCAAGACAGAAATAGAGACAGGGTCT 1500
DB 1441 AATATCTCCAACTTTCTAATAGGCTTATTTCAAGACAGAAATAGAGACAGGGTCT 1500
QY 1501 TTTATTTCTGCTACTCTTAAAGATTAAGATTAAGATTTGAGGAAATAGTCTC 1560
DB 1501 TTTATTTCTGCTACTCTTAAAGATTAAGATTAAGATTTGAGGAAATAGTCTC 1560
QY 1561 GTGACCAAAAGCTGATCTAATAGCTAGCGGAGATTAAGAGCTCTCACTCAATAGAA 1620
DB 1561 GTGACCAAAAGCTGATCTAATAGCTAGCGGAGATTAAGAGCTCTCACTCAATAGAA 1620
QY 1621 TCTACTACGCAAGAGCATGCTTTTGAAGAACCGTGTGAAGATTTCTGAGATT 1680
DB 1621 TCTACTACGCAAGAGCATGCTTTTGAAGAACCGTGTGAAGATTTCTGAGATT 1680
QY 1681 GTGTGCAAAAGCACTTTGTTGCTCTACCGTGAAGCTTTTGAAGAACTTCCACTCT 1740
DB 1681 GTGTGCAAAAGCACTTTGTTGCTCTACCGTGAAGCTTTTGAAGAACTTCCACTCT 1740
QY 1741 CAAGTGGGAAGGCTTGAAGGCTGTCTTGGGCTCTCATGAGGATAGGATCTCTC 1800
DB 1741 CAAGTGGGAAGGCTTGAAGGCTGTCTTGGGCTCTCATGAGGATAGGATCTCTC 1800

QY 1801 AGAAGACAGACTGGAAATTGATATATGTCTGATGTCTATCTATCTTACAAATACCAAAAA 1860
DB 1801 AGAAGACAGACTGGAAATTGATATATGTCTGATGTCTATCTATCTTACAAATACCAAAAA 1860
QY 1861 ACCCTGGGTCGGCATGGCTTAATAAGAGCACTTGGCTCTCCCATCAAGCAGAG 1920
DB 1861 ACCCTGGGTCGGCATGGCTTAATAAGAGCACTTGGCTCTCCCATCAAGCAGAG 1920
QY 1921 ACACTTAACAGAGTACACTCAGACCTCTACAGACATCATCTGCTTGTATACATGCTA 1980
DB 1921 ACACTTAACAGAGTACACTCAGACCTCTACAGACATCATCTGCTTGTATACATGCTA 1980
QY 1981 CCGCAGCAATGCTCCCTGATGTTTTTGTGCTTTTGTCTCTCTCTCTCTCTCTCTCT 2040
DB 1981 CCGCAGCAATGCTCCCTGATGTTTTTGTGCTTTTGTCTCTCTCTCTCTCTCTCTCT 2040
QY 2041 CTCACCTATCACTGTTGACCTTGTGATCTCTGATGCTGTCTGACAGAAATCTATG 2100
DB 2041 CTCACCTATCACTGTTGACCTTGTGATCTCTGATGCTGTCTGACAGAAATCTATG 2100
QY 2101 AGTTTTCCCTTATGAGGACCTTTGAGCGCCAGCTGCTTCTCATTTGCCCTGTGGCC 2160
DB 2101 AGTTTTCCCTTATGAGGACCTTTGAGCGCCAGCTGCTTCTCATTTGCCCTGTGGCC 2160
QY 2161 CAGAGGCAAAATGCGCTGCCCTGCAACACCGGCTGCAAGCTTGAAGTGTCCAACTTCCAG 2220
DB 2161 CAGAGGCAAAATGCGCTGCCCTGCAACACCGGCTGCAAGCTTGAAGTGTCCAACTTCCAG 2220
QY 2221 CAGCGGTAATCTGTCACACCGCACTTTATGCTGGCCAAAGAGTACAGCTGATCTTT 2280
DB 2221 CAGCGGTAATCTGTCACACCGCACTTTATGCTGGCCAAAGAGTACAGCTGATCTTT 2280
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DB 2281 CTCCTCAATACCGGCTGCACTTTCTCTGAGACCTTGAAGCACTTGAAGGCGCTTTA 2340
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DB 2341 TCTCCGAGAGTCTCACTACCTATGTTTTCTGCTCTTTAGAGACTCTTTAAGAGTGGGT 2400
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DB 2401 CTTTTTCTATTTCTATTTCAAGGTCCTCAGACCACTTTCTATCTTGGCTTCAAGACCA 2460
QY 2461 TATACGAAATTTATCTACAGAGGCGCATTTAGAAGCCACCGACGATGCAATCTTTC 2520
DB 2461 TATACGAAATTTATCTACAGAGGCGCATTTAGAAGCCACCGACGATGCAATCTTTC 2520
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DB 2521 CATTTCTCTGCTCTCTTCTGAACTCATCTCTTGGCTACTCTTGAGACCGACTGCG 2580
QY 2581 GACATCATCTCTACTACAGGCTTTTCTTCATCTCTTGTACCCAGGCACTTAGGGT 2640
DB 2581 GACATCATCTCTACTACAGGCTTTTCTTCATCTCTTGTACCCAGGCACTTAGGGT 2640
QY 2641 TTTCTCTCTTCAAGGCGCTTGCAGATAACAACAGAGCTCGGGCTATCGGGAGGA 2700
DB 2641 TTTCTCTCTTCAAGGCGCTTGCAGATAACAACAGAGCTCGGGCTATCGGGAGGA 2700
QY 2701 AACTGTTCCGAGAGTCAAGTGAAGTCTCACTGATGATGACAGGCTAGCTGGGGAGC 2760
DB 2701 AACTGTTCCGAGAGTCAAGTGAAGTCTCACTGATGATGACAGGCTAGCTGGGGAGC 2760
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QY 2821 CTAAAGATCAGTGCATCTGATGAAGAGAGTGTCAACTTCACTCGGAGAGCGTTCTGC 2880
DB 2821 CTAAAGATCAGTGCATCTGATGAAGAGAGTGTCAACTTCACTCGGAGAGCGTTCTGC 2880

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DB 2881 TCCCCGATCAGACAGGTTCCAGGCCCTTACATGACAGAGGTGTATCTTTCTGACCAAC 2940
QY 2941 TCAGCAATCAGCTCAGCTCCGTGTATGATCTGACTCTGGGCTACCTATGCTCTCTCTT 3000
DB 2941 TCAGCAATCAGCTCAGCTCCGTGTATGATCTGACTCTGGGCTACCTATGCTCTCTCTT 3000
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DB 3001 CCTCTCTATTTCCAGTAAGAACCCGAGGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 3060
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DB 3061 GGGCTCAGACACCAACCATCATAGGCCACTTGAATAGTCACAAAAGGCTTGGCTTC 3120
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DB 3121 AATTGATTAATCTGATGATTTGATAGAGAACTTATTTGTTTATATCATGGAAGA 3180
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DB 3181 AATCACTCAAAATCTGTAGATGAGAAAGATGTTGGAAAGAAAAAGGCTATGATAGA 3240
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DB 3241 GAAAACAGATCTGCTGATATATGTTATGAGGAGAGCAGGGGCGATATCTCATGAGTA 3300
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DB 3301 CAAGTACTTGTGGGAGAGAAATCCACTAGTACAACTACTTGTGTGCAATGAGATCCAC 3360
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DB 3421 ATGAGAGAGGCTCAATGTTGGGGGTGTGAAGGTCACTCTTTTCCATGTGATGAGAGT 3480
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DB 3481 TAAGAAAAACAGGTGTGATGTTGATGTTCTTACAGAACCCCACTATGATGAATATCC 3540
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QY 3601 AGAAACTTTATGCTCATCTCTGTGTACACTCCCACTTTGATGAGGTTCAAGTCAAGT 3660
DB 3601 AGAAACTTTATGCTCATCTCTGTGTACACTCCCACTTTGATGAGGTTCAAGTCAAGT 3660
QY 3661 TTGCTTTCTACCGTCTTCTGTAAGTGTGAGAACTTCAAGTGAATTTCCCAAGAGGAG 3720
DB 3661 TTGCTTTCTACCGTCTTCTGTAAGTGTGAGAACTTCAAGTGAATTTCCCAAGAGGAG 3720
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DB 3721 CAGCTCTTCTGTAAGGAGGAGCCTGATTTTCAAGTGTCTAGAGAGGAAATAGCTCAGA 3780
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DB 3781 GAATCTAGGTCAGAGTGAATCTAGGTCACAGCGGGCAAAATAGCTGAACGCTGATTT 3840
QY 3841 CCAGGTAAAGGTACAGTGCCTCAGATATCTAGAGTATTTGGGCTCCCAACCGATAGAT 3900
DB 3841 CCAGGTAAAGGTACAGTGCCTCAGATATCTAGAGTATTTGGGCTCCCAACCGATAGAT 3900
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DB 3901 TCTGTATGATGATGCTGCTTTTATTTTACAGACATCAGCGGTGACACCAAGATCTCAG 3960
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Db 3961 AAGATATCGAAGAGCTGAAGAGACAGTGAAGAAAAGTACTATTGGCAACCCAAACT 4020
Qy 4021 AAGCATTCAGTAGAGACGCGGGGATTTCTTCTGCTTCCAGTCCCTTACTTGG 4080
Db 4021 AAGCATTCAGTAGAGACGCGGGGATTTCTTCTGCTTCCAGTCCCTTACTTGG 4080
Qy 4081 TAACTTTTATTTGACTTGTCTACTATCTGTCTGTCATTACTGCTTAGCTGACCTGTATC 4140
Db 4081 TAACTTTTATTTGACTTGTCTACTATCTGTCTGTCATTACTGCTTAGCTGACCTGTATC 4140
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Db 4141 TAGCTGGGCTATATGATCTTCAATCTGTCTTAATTTGATGCAAAATTGGAGCT 4200
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Db 4201 AGCAGAAAGCTTAGCTAGCGACGCTGATAGACGCTGCGAGGATGGCTGTGACAG 4260
Qy 4261 AGTCATGCTAGAGAGACGATCCCTGATTCGCCAGCTCTGCACTTGGCTAGTGGCCATGT 4320
Db 4261 AGTCATGCTAGAGAGACGATCCCTGATTCGCCAGCTCTGCACTTGGCTAGTGGCCATGT 4320
Qy 4321 GTAATTAATTGCTGCTGATTAAGTATTTGGGAAAGCCAGTTCCGACGGACTTACATATC 4380
Db 4321 GTAATTAATTGCTGCTGATTAAGTATTTGGGAAAGCCAGTTCCGACGGACTTACATATC 4380
Qy 4381 TGAAGAACCATGCTTGAAGAACTAGAAAGCTGGGCAAAAATTACTAGATGATTTTGG 4440
Db 4381 TGAAGAACCATGCTTGAAGAACTAGAAAGCTGGGCAAAAATTACTAGATGATTTTGG 4440
Qy 4441 AGCTCATTTAAAGGATGCTCTGAAATGTGGCAAAATCAACCCAGATTAACAAAGAG 4500
Db 4441 AGCTCATTTAAAGGATGCTCTGAAATGTGGCAAAATCAACCCAGATTAACAAAGAG 4500
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Db 4501 CTGATTTGCAAAATAGACAAATTTTGAATCACTGATTAATTAATTAATTAATTAAT 4560
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Db 4561 TAAATTAATTAAGGCTATATATATTTAATTAATTAATTAATTAATTAATTAATTAAT 4620
Qy 4621 TTAATTTGCTGCTGCTTCAAAAAGATTAATTAATTAATTAATTAATTAATTAATTAAT 4680
Db 4621 TTAATTTGCTGCTGCTTCAAAAAGATTAATTAATTAATTAATTAATTAATTAATTAAT 4680
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Db 4681 AAAATATGATGAGAAACCTTTCTTACTTTTACTTTTCACTTTTCTTATG 4740
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Db 4741 TTCAACCCCTGATCAAGCACTAGTAGCACTATCTGCTGATGATTAATTAATTAAT 4800
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Db 4801 ACAGCAAAACAATCTGCTGTGTGGCTCTTTGGGGAAGGAAACAGATAGACGAGGCTC 4860
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Db 4861 AGGCTACCAAGTCTGATCTTGCCCTTAAAGCCAGAGGCAATGGTTGATACAGAAAGTGAG 4920
Qy 4921 GCTCTTGCAAGTGGGTGTGTTAAGTATCAGAAACAGAGGCTCCGGTGTATGAGAT 4980
Db 4921 GCTCTTGCAAGTGGGTGTGTTAAGTATCAGAAACAGAGGCTCCGGTGTATGAGAT 4980
Qy 4981 TATCAGTAAATATCTACCTTATCTCTTATCTATCGAACTTAATCTCTCTTTTCTTGG 5040
Db 4981 TATCAGTAAATATCTACCTTATCTCTTATCTATCGAACTTAATCTCTCTTTTCTTGG 5040
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Db 5041 TGTGTAGGCTGATTAACACACTTTTCTTTTGGAGTTCATGGCTTTGTAGATTTTGA 5100

Db 5041 TGTGTAGGCTGATTAACACACTTTTCTTTTGGAGTTCATGGCTTTGTAGATTTTGA 5100
Qy 5101 GTGCTGCGCAGTCTTGTATAGAGGTTTGTATACCTTGAACACCTGGCTTGAATGTTAGC 5160
Db 5101 GTGCTGCGCAGTCTTGTATAGAGGTTTGTATACCTTGAACACCTGGCTTGAATGTTAGC 5160
Qy 5161 ATGCCAAAGGACACACTTCTGATGCTGTGTGTAAGAAAGGTTATTAATTAATTAATTTGTC 5220
Db 5161 ATGCCAAAGGACACACTTCTGATGCTGTGTGTAAGAAAGGTTATTAATTAATTAATTTGTC 5220
Qy 5221 TTTGGAAGGTGAAGGTTGTGTAAGAAAGAACTCAAGAGATGTTCTCTGTAGGAA 5280
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Qy 5281 ACTTTTCTTCCCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATGCTTAATG 5340
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Qy 5341 ATGCTGTCAATGAAGAGTGTATAGGCGCGCTCTGATGCTGTGGAAGAACCAAT 5400
Db 5341 ATGCTGTCAATGAAGAGTGTATAGGCGCGCTCTGATGCTGTGGAAGAACCAAT 5400
Qy 5401 GGGGAAAGATGTTATGCTGAGAAATCTGACCGGCAAGGAAATGCTGACAGTCCCCG 5460
Db 5401 GGGGAAAGATGTTATGCTGAGAAATCTGACCGGCAAGGAAATGCTGACAGTCCCCG 5460
Qy 5461 AAGACCAACAGGTTTAAGTATAGTAAGCAAGTCCAGGGGTGGGCTCATGTAATAGATGAA 5520
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Db 5521 CAGAGCGAGGAAAGATTAAGTAAAGTTTCAATAGGGTCCGAGTCTTAAAGATACAAA 5580
Qy 5581 TAGCTGCTGGCTTATTAACAAAGAAATCTGGGAAAGCAAGTGAAGTGAAGGAAATG 5640
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Qy 5641 AAAAGGAAAAACAGATGATAGAGACTTGAACAGTACCAATCTCTACCAAGATTT 5700
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Qy 5761 TTGAATCTGGGTTTGTCTCTCCATTTGAGTTGAAAGGCTCACCTTTTACCTCGAA 5820
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Qy 5821 TGGAGGAGGAAAGAGGGGTATGACTGCTACCTGAGGTTTATTAAGTTTACGCAATG 5880
Db 5821 TGGAGGAGGAAAGAGGGGTATGACTGCTACCTGAGGTTTATTAAGTTTACGCAATG 5880
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Qy 6061 CCTGTAGGCGCAGCCCTGCTGCTTGGCACTTAATCATCTCCAGGTCTCAATCACTTC 6120
Db 6061 CCTGTAGGCGCAGCCCTGCTGCTTGGCACTTAATCATCTCCAGGTCTCAATCACTTC 6120
Qy 6121 CTGCTACTTACGACATTTAGAGTTAGCAAACTTTTTCGAAACCCCACTAAATTT 6180
Db 6121 CTGCTACTTACGACATTTAGAGTTAGCAAACTTTTTCGAAACCCCACTAAATTT 6180

QY	6181	AATTGACAAAAGACTGCTGTAATTTGTGGGAATACAGTGTGAATTTGATCTCTATGCTGCAT	6240
Db	6181	AATTGACAAAAGACTGCTGTAATTTGTGGGAATACAGTGTGAATTTGATCTCTATGCTGCAT	6240
QY	6241	TGTGCAGGTCCTCAATTAAGATTAATTAAGCCCATCAACGCTTTATGGGTGTGAANTG	6300
Db	6241	TGTGCAGGTCCTCAATTAAGATTAATTAAGCCCATCAACGCTTTATGGGTGTGAANTG	6300
QY	6301	CAAGTAATATATGATAGATAGCTGTGGGTCTCTTGTGTCAGAAAGGCATGATTTAAGGTC	6360
Db	6301	CAAGTAATATATGATAGATAGCTGTGGGTCTCTTGTGTCAGAAAGGCATGATTTAAGGTC	6360
QY	6361	TTGGGCAAAATCATTTTAACTCATGCTAAAATAATCATATGTTGATATTAATTAATCTTTTAA	6420
Db	6361	TTGGGCAAAATCATTTTAACTCATGCTAAAATAATCATATGTTGATATTAATCTTTTAA	6420
QY	6421	AGAAAGCTGATTACTTGTTGGTTTGGTGTCTACAGACAAATGTCCACAGCTCTTTCTAACTG	6480
Db	6421	AGAAAGCTGATTACTTGTTGGTTTGGTGTCTACAGACAAATGTCCACAGCTCTTTCTAACTG	6480
QY	6481	GTACCACTTTGAAAATATGCTACCTGTGCTCAAAATGGTTGATTCCTAATTTTCAATAGCT	6540
Db	6481	GTACCACTTTGAAAATATGCTACCTGTGCTCAAAATGGTTGATTCCTAATTTTCAATAGCT	6540
QY	6541	TGAGAGAGTGGAGAGATCAAGCGGATTGGGAACTGGACCTGCTGTTATGTCTGAG	6600
Db	6541	TGAGAGAGTGGAGAGATCAAGCGGATTGGGAACTGGACCTGCTGTTATGTCTGAG	6600
QY	6601	AAATGCTTGGCTCTGAGAGGAGAAAGCTAATAAAACGAAGAACTGCTCTCTGCTTC	6660
Db	6601	AAATGCTTGGCTCTGAGAGGAGAAAGCTAATAAAACGAAGAACTGCTCTCTGCTTC	6660
QY	6661	TAAAGAAGACATTAAGATCCCTGAAATGACCTTTTAAAGAAAGTGAGAAAGCTAAC	6720
Db	6661	TAAAGAAGACATTAAGATCCCTGAAATGACCTTTTAAAGAAAGTGAGAAAGCTAAC	6720
QY	6721	GTCCATCATCATTTAGAGATTTCAATGAAACTGGCTCAGTTGAAAAAGAAATAGTGT	6780
Db	6721	GTCCATCATCATTTAGAGATTTCAATGAAACTGGCTCAGTTGAAAAAGAAATAGTGT	6780
QY	6781	CAAGTGTGCCATGAGACAGAGAGTGAATTAATAACGAAGAAATTCATTAACAATATT	6840
Db	6781	CAAGTGTGCCATGAGACAGAGAGTGAATTAATAACGAAGAAATTCATTAACAATATT	6840
QY	6841	TATTTGTCACTGATGATCAACAGAAAAATTAATGTAATTAATAAATGTTTGAAGAGAG	6900
Db	6841	TATTTGTCACTGATGATCAACAGAAAAATTAATGTAATTAATAAATGTTTGAAGAGAG	6900
QY	6901	TTACCTCTCATTTCTTTAGAAAAAAGCTTATGTAACCTTCTTTCCATATCCATATTTT	6960
Db	6901	TTACCTCTCATTTCTTTAGAAAAAAGCTTATGTAACCTTCTTTCCATATCCATATTTT	6960
QY	6961	ATTATATGTAATTTATTTATTAATAGTATTAAGTATTAATTTATTTATGTCAGTTTAAATATG	7020
Db	6961	ATTATATGTAATTTATTTATTAATAGTATTAAGTATTAATTTATTTATGTCAGTTTAAATATG	7020
QY	7021	ATTATATTTATAGAAACATTATCTGTCTATGTAATTTAGTATTAAGGCAATTAATATTATG	7080
Db	7021	ATTATATTTATAGAAACATTATCTGTCTATGTAATTTAGTATTAAGGCAATTAATATTATG	7080
QY	7081	ACAAATTAACATAGGAACAAGATATCTTAGGCTTTAATAAACAATGATATCAATTAACCT	7140
Db	7081	ACAAATTAACATAGGAACAAGATATCTTAGGCTTTAATAAACAATGATATCAATTAACCT	7140
QY	7141	TCTGCTCTGTAAATTTTCTCCCTTTAATATCAACAACTACATCATCATATTAACCA	7200
Db	7141	TCTGCTCTGTAAATTTTCTCCCTTTAATATCAACAACTACATCATCATATTAACCA	7200
QY	7201	ATCATATTCATGATTTTCAATGCTGACCAATATTAACGTTTAAAGTGGTCTCGAGAGC	7260
Db	7201	ATCATATTCATGATTTTCAATGCTGACCAATATTAACGTTTAAAGTGGTCTCGAGAGC	7260

[illegible]

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 Db 61 GCACACAGACGATTTATAGCATGTGTTCTGACCATGACGATGAGTGAATG 120
 QY 121 TAAAGGGGCTTTATACAGATTAACCAATGTTAAATGTTCTTGGGCAAGCAAT 180
 Db 121 TAAAGGGGCTTTATACAGATTAACCAATGTTAAATGTTCTTGGGCAAGCAAT 180
 QY 181 TGAATCTATGTCTTAAACAATCTTCAAGCTCTAATATAGTCTAACAGTGAATG 240
 Db 181 TGAATCTATGTCTTAAACAATCTTCAAGCTCTAATATAGTCTAACAGTGAATG 240
 QY 241 CTGCTGTCCACAGAGCTCTTGAACAAGCTCTCTCTGTTGCAATTTATGTTCTTGA 300
 Db 241 CTGCTGTCCACAGAGCTCTTGAACAAGCTCTCTCTGTTGCAATTTATGTTCTTGA 300
 QY 301 TGAAGTCCCAAGCTCTGACCTTGGGCTCTGATGGGCACTTTCACTTTGCAATTTA 360
 Db 301 TGAAGTCCCAAGCTCTGACCTTGGGCTCTGATGGGCACTTTCACTTTGCAATTTA 360
 QY 361 TGAAGTCCCAAGCTTTTATCTTTTATTAATAATATTACACAATCAGTGTGTCAGT 420
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 QY 421 TGTTCACCCACATGTATGTCTGTGACCAAGTGTCTGTTGTTGGGGGCAAGA 480
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 QY 481 GAGAGAGAGGGTGTCTGTGACCCGAGTCAAGATGTGTGAGCCACATGAGATGCT 540
 Db 481 GAGAGAGAGGGTGTCTGTGACCCGAGTCAAGATGTGTGAGCCACATGAGATGCT 540
 QY 541 GAGAGTGAACCAAGGTCTCTCAAGAGTCAAGCAATGTCTTAAACACAGCAAGCAT 600
 Db 541 GAGAGTGAACCAAGGTCTCTCAAGAGTCAAGCAATGTCTTAAACACAGCAAGCAT 600
 QY 601 TCTCTCTCAGCCCAACATGAGTGTCTTAAATGCTAGATGAGATCTGATGTC 660
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 QY 661 TTTACATCACTGACCTCTCCCTTTGATCTTTCTGCGAAGAAACACCAAGCAAGAT 720
 Db 661 TTTACATCACTGACCTCTCCCTTTGATCTTTCTGCGAAGAAACACCAAGCAAGAT 720
 QY 721 CCCCACTGCTTGGCTCTCAAGTCTGACCTCTCAACAGGTCAAGATCTCCAGTGT 780
 Db 721 CCCCACTGCTTGGCTCTCAAGTCTGACCTCTCAACAGGTCAAGATCTCCAGTGT 780
 QY 781 CCGCTTAACACTTTCCCAAGTGTCTCTTAAACAATTTCTCAAGTGTCTCTTAAACA 840
 Db 781 CCGCTTAACACTTTCCCAAGTGTCTCTTAAACAATTTCTCAAGTGTCTCTTAAACA 840
 QY 841 CTCACATGTCTCTTAAACAATTTGATCTCAATTAAGTGAAGGGAAGAAATCTCAACA 900
 Db 841 CTCACATGTCTCTTAAACAATTTGATCTCAATTAAGTGAAGGGAAGAAATCTCAACA 900
 QY 901 GTGATTTTATGACTTGGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 960
 Db 901 GTGATTTTATGACTTGGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 960
 QY 961 AGGCGTGTCTCTCCGCTGTAGGAAGAACTTTCTAGTCTAGTGTCAAGTGTCTAGT 1020
 Db 961 AGGCGTGTCTCTCCGCTGTAGGAAGAACTTTCTAGTCTAGTGTCAAGTGTCTAGT 1020
 QY 1021 GATTTAGTGAATCAATGCAAAATCCCAAGTATTTTGAATTTCTTTTCAACT 1080
 Db 1021 GATTTAGTGAATCAATGCAAAATCCCAAGTATTTTGAATTTCTTTTCAACT 1080
 QY 1081 ATCCATCTATATAGTATGTTATGTTAGGCTCATTTAAAAATATATTTTGAAGCTTATG 1140
 Db 1081 ATCCATCTATATAGTATGTTATGTTAGGCTCATTTAAAAATATATTTTGAAGCTTATG 1140

QY 1141 TTGCAACAGTAAATGTCAAGAAATTAGCAATGTATGTTATTTTAAATTTTAAATTT 1200
 Db 1141 TTGCAACAGTAAATGTCAAGAAATTAGCAATGTATGTTATTTTAAATTTTAAATTT 1200
 QY 1201 TCTATGCTTAAATGTCTATATAGATTTGCTCACTACCAATTTTCCAACTTACCTGAC 1260
 Db 1201 TCTATGCTTAAATGTCTATATAGATTTGCTCACTACCAATTTTCCAACTTACCTGAC 1260
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 Db 1741 CAAGGTGGGAAGGCTTGGAGGTGTCTGTTGGGCTCTTATGTTAGGATCTCTCTC 1800
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 QY 1861 ACCCTGTGTCTCCGATGCTTATTAAGCAAGCACTTTGCTCTCCATCAAGAGAG 1920
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 QY 1921 ACACCTTAAACAGTATAGCACTAGACCTTCAAGCAATCATCTGTTGGTACATGCTA 1980
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 Db 2161 CAGAGGCAAAATGCGGTGCGCTCAACACCGGTGCAAGCTTGAAGTGTCCAACTTCCAG 2220
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Db 2221 CAGCGTATCATGCTAAACCGACCTTTATGCTGGCCAAAGAGGTACAGCTGATCTCTT 2280
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Db 2521 CATTTCTCTGCTCTCTTCTGAACTCATCTCTTGGCTATCTCTGAGACCCACTGCG 2580
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Qy 7441 TGTAT 7445
Db 7441 TGTAT 7445

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RESULT 3
AAD30628
ID AAD30628 standard; DNA; 7445 BP.

AC AAD30628;
XX 21-MAY-2002 (first entry)
XX Mouse TIF alpha genomic DNA.
DE Mouse TIF alpha genomic DNA.
XX T cell derived inducible factor; TIF; interleukin-21; IL-21; mouse;
KM STAT transcription factor; acute phase protein; inflammation; ds.
XX

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OS Mus musculus.
XX WO200210393-A2.
PN 07-FEB-2002.
XX 27-JUN-2001; 2001WO-US20485.
XX 27-JUL-2000; 2000US-062617.
XX (LUDM-) LUDMIG INST CANCER RES.
PA Dumoutier L, Renaud J;
XX WPI, 2002-195964/25.
DR
XX Stimulating expression of STAT transcription factor and inducing
PT production of acute phase protein in a cell, involves contacting a cell
PT capable of expressing STAT with T cell derived inducible factors -
XX Example 7; Page 49-53; 64pp; English.
PS
XX The invention relates to nucleic acid molecules encoding T cell
CC derived inducible factors (TIFs) also known as interleukin-21 (IL-21).
CC TIF polynucleotides are upregulated by the cytokine, IL-9, IL-TIF or
CC IL-21 molecules are implicated in activation of STAT transcription
CC factors, acute phase proteins and inflammation. The present sequence
CC is mouse TIF alpha genomic DNA.
XX
SQ Sequence 7445 BP; 2059 A; 1568 C; 1597 G; 2221 T; 0 other;
Query Match 100.0%; Score 7441.8; DB 24; Length 7445;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7443; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTCTATACCTGCTTAAAGATTTCTTAAATTTTAAAGAAATCTTAAATGAAAA 60
Db 1 GTCTATACCTGCTTAAAGATTTCTTAAATTTTAAAGAAATCTTAAATGAAAA 60
Qy 61 GCAACAGAGCAGATTTATAGATGCTGACATGAGATGAGATGAGATG 120
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QY 901 GTGATTTTCAAGCTTCCGAGTGTAGCTAGATGTAGGAGATTTGGCGTCAAGTCTAGGT 960
DB 901 GTGATTTTCAAGCTTCCGAGTGTAGCTAGATGTAGGAGATTTGGCGTCAAGTCTAGGT 960
QY 961 AGGCGTCTGCTCCGCTGCTTAGAGAAAGACTTTTCTAGTCTAGTGTGTCAGTCTATCTG 1020
DB 961 AGGCGTCTGCTCCGCTGCTTAGAGAAAGACTTTTCTAGTCTAGTGTGTCAGTCTATCTG 1020
QY 1021 GGAATTCAGTGTACATACATATGCAAAAATCCAGATTTTGTAAATTCCTCTTCAACT 1080
DB 1021 GGAATTCAGTGTACATACATATGCAAAAATCCAGATTTTGTAAATTCCTCTTCAACT 1080
QY 1081 ATCCATCTAT 1140
DB 1081 ATCCATCTAT 1140
QY 1141 TTGCACAAAGTAAATATGTCAGAGAAATAGCAAAATATATATATATATATATATATAT 1200
DB 1141 TTGCACAAAGTAAATATGTCAGAGAAATAGCAAAATATATATATATATATATATATAT 1200
QY 1201 TCTATGCTTAAATATGTCATATATATATATATATATATATATATATATATATATAT 1260
DB 1201 TCTATGCTTAAATATGTCATATATATATATATATATATATATATATATATATATAT 1260
QY 1261 TTGGCTATGATTTCAACCTTGTATTTGATCTACATACATACAGTCTGTGACAGCAACAT 1320
DB 1261 TTGGCTATGATTTCAACCTTGTATTTGATCTACATACATACAGTCTGTGACAGCAACAT 1320
QY 1321 TCTGTGGCAATGGAGGTGTGAAGAAAGCCACATTTCTTATTAATAAAAAAACAGCTA 1380
DB 1321 TCTGTGGCAATGGAGGTGTGAAGAAAGCCACATTTCTTATTAATAAAAAAACAGCTA 1380
QY 1381 GTTATATGTTAGATTTCAAT 1440
DB 1381 GTTATATGTTAGATTTCAAT 1440
QY 1441 AATAATCTCCAGTTTCTAT 1500
DB 1441 AATAATCTCCAGTTTCTAT 1500
QY 1501 TTTATTTCTGTGCTATTTAAAGAGATTAAGATCTATGAAGTTGTGGGAAATATGATGTC 1560
DB 1501 TTTATTTCTGTGCTATTTAAAGAGATTAAGATCTATGAAGTTGTGGGAAATATGATGTC 1560
QY 1561 GTACCAAAAGGCTGATCAAT 1620
DB 1561 GTACCAAAAGGCTGATCAAT 1620
QY 1621 TCTATCAAGGCAAAAGCAATGAGTCTTTTGAATAACCGTGTATAGAAATTTCTGGGATTT 1680
DB 1621 TCTATCAAGGCAAAAGCAATGAGTCTTTTGAATAACCGTGTATAGAAATTTCTGGGATTT 1680
QY 1681 GTGTGAAAAGCACTTGTGTGGCCCTCAACCGTACAGTGTATTAAGAAAGCACTTGTCT 1740
DB 1681 GTGTGAAAAGCACTTGTGTGGCCCTCAACCGTACAGTGTATTAAGAAAGCACTTGTCT 1740
QY 1741 CAAGTGGGAAAGGCTTGAAGTGTGTCTTGTGGCCCTCAATAGTGTATAGTATCTTCTC 1800
DB 1741 CAAGTGGGAAAGGCTTGAAGTGTGTCTTGTGGCCCTCAATAGTGTATAGTATCTTCTC 1800
QY 1801 AGAAGCAGAGCTGGAATTAATATATATATATATATATATATATATATATATATATAT 1860
DB 1801 AGAAGCAGAGCTGGAATTAATATATATATATATATATATATATATATATATATATAT 1860
QY 1861 ACCCTGTGTCCGATGCTATPAAAGCAAGCACTTGTGCTCTCCATCAACAGCAGAG 1920
DB 1861 ACCCTGTGTCCGATGCTATPAAAGCAAGCACTTGTGCTCTCCATCAACAGCAGAG 1920
QY 1921 AACCTPAAACAGTAAAGCACTAGACCTCTACAGAACATCATCTGTGTGTACATGCTA 1980
DB 1921 AACCTPAAACAGTAAAGCACTAGACCTCTACAGAACATCATCTGTGTGTACATGCTA 1980
QY 1981 CCCGAGCAATGCTCCCTGATGTTTGTGCTTGTGCTCTCTCACTAACAGGCTCTCT 2040
DB 1981 CCCGAGCAATGCTCCCTGATGTTTGTGCTTGTGCTCTCTCACTAACAGGCTCTCT 2040
QY 2041 CTCACCTTAACTGTGTGACACTGTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2100
DB 2041 CTCACCTTAACTGTGTGACACTGTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2100
QY 2101 AGTTTTTCCCTATAGGAGACTTGTGGCCGACAGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
DB 2101 AGTTTTTCCCTATAGGAGACTTGTGGCCGACAGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
QY 2161 CAGAGGCAAAATGCGCTGCGCTCAACACCCGCTGCAAGCTTGTGTGTGTGTGTGTGTGT 2220
DB 2161 CAGAGGCAAAATGCGCTGCGCTCAACACCCGCTGCAAGCTTGTGTGTGTGTGTGTGTGT 2220
QY 2221 CAGCGTACATGTCACACGCACTTATATGTCGCAAGAGATGATGATCTCTT 2280
DB 2221 CAGCGTACATGTCACACGCACTTATATGTCGCAAGAGATGATGATCTCTT 2280
QY 2281 CTTCTCATACCGCTTGGCATTTTCTGTGAAGCACTTGAAGCTTTTAGGGGCGCTTTA 2340
DB 2281 CTTCTCATACCGCTTGGCATTTTCTGTGAAGCACTTGAAGCTTTTAGGGGCGCTTTA 2340
QY 2341 TCTCGCAGGCTCTACATACATATATATATATATATATATATATATATATATATATAT 2400
DB 2341 TCTCGCAGGCTCTACATACATATATATATATATATATATATATATATATATATATAT 2400
QY 2401 CTTTTTCTATTTCTATTTCAAGCTCTCAGACCAATTTCTATCTTGTGCTTGAAGCACA 2460
DB 2401 CTTTTTCTATTTCTATTTCAAGCTCTCAGACCAATTTCTATCTTGTGCTTGAAGCACA 2460
QY 2461 TATACGAATTTTATCTACAGAGGCACTTGAAGCAACCAAGCACTGCAATATCTTC 2520
DB 2461 TATACGAATTTTATCTACAGAGGCACTTGAAGCAACCAAGCACTGCAATATCTTC 2520
QY 2521 CATTTCTGTGTCTCTCTCTGAACTCATCTCTTGTGCTCTCTGAGACCACTGCG 2580
DB 2521 CATTTCTGTGTCTCTCTCTGAACTCATCTCTTGTGCTCTCTGAGACCACTGCG 2580
QY 2581 GACATACATCTCTACTTACAGGCTTTTCTCATCTCTCTGACCAAGGCACTTATGCT 2640
DB 2581 GACATACATCTCTACTTACAGGCTTTTCTCATCTCTCTGACCAAGGCACTTATGCT 2640
QY 2641 TTTCTCTCTTACGCGCTTGTGAGATTAACAAGAGCTGCGGCTCATCGGGGAGA 2700
DB 2641 TTTCTCTCTTACGCGCTTGTGAGATTAACAAGAGCTGCGGCTCATCGGGGAGA 2700

Db	2641	TTTTCTCTCTTTCAGAGCCAGCCTTGCAGATACAAACACAGACGTCGCGCTCATGCGGGAGA	2710
Oy	2701	AACGTGTTCCGAGGAGTCAGTGTAAAGTCCTCACTGTGATGAGCAGAGGCTAGCTGCGGAGC	2760
Db	2701	AACGTGTTCCGAGGAGTCAGTGTAAAGTCCTCACTGTGATGAGCAGAGGCTAGCTGCGGAGC	2760
Oy	2761	TGCTGGAACCCCTCTGGGATAGTCTGACGTATACCCCTGCTGCTCTTGTGTCTACCTGAGG	2820
Db	2761	TGCTGGAACCCCTCTGGGATAGTCTGACGTATACCCCTGCTGCTCTTGTGTCTACCTGAGG	2820
Oy	2821	CTAAAGATCACTGCGTACCTGTATGAAGCAGGAGTCTCAACTTCAACCTCGAAAGACGTTGCG	2880
Db	2821	CTAAAGATCACTGCGTACCTGTATGAAGCAGGAGTCTCAACTTCAACCTCGAAAGACGTTGCG	2880
Oy	2881	TCCCCCACTCAGACAGGTTCCAGCCCTACATGACAGAGTGATACCTTCTCTGACCAAC	2940
Db	2881	TCCCCCACTCAGACAGGTTCCAGCCCTACATGACAGAGTGATACCTTCTCTGACCAAC	2940
Oy	2941	TCAGCAATCAGCTCAGCTCTGTGTAAATCTGACTCTGCGTACCTATGCTCTCTCTT	3000
Db	2941	TCAGCAATCAGCTCAGCTCTGTGTAAATCTGACTCTGCGTACCTATGCTCTCTCTCTT	3000
Oy	3001	CCTCTTCAATTCACGTATGAACCCGAGGTCCTGCCCTCTCTCTTCAACAAGTGAAGA	3060
Db	3001	CCTCTTCAATTCACGTATGAACCCGAGGTCCTGCCCTCTCTCTTCAACAAGTGAAGA	3060
Oy	3061	GGGCCTCAGCACACACCATCATATAGCGCATCTTGAATAGGTCACAAGGCTTGGGCTTC	3120
Db	3061	GGGCCTCAGCACACACCATCATATAGCGCATCTTGAATAGGTCACAAGGCTTGGGCTTC	3120
Oy	3121	AATTGAGTAATACCTTTGAGTTGTATGAGTGAAGCTTTATTTGTTTATCCATGGAAGA	3180
Db	3121	AATTGAGTAATACCTTTGAGTTGTATGAGTGAAGCTTTATTTGTTTATCCATGGAAGA	3180
Oy	3181	AATCACTCCAAATTTCTGAGATGAGGAAGATGTTGGGAACGAAAGAAAGGCTGTATGA	3240
Db	3181	AATCACTCCAAATTTCTGAGATGAGGAAGATGTTGGGAACGAAAGAAAGGCTGTATGA	3240
Oy	3241	GAAAAGATCTGCTAGATATAGTACTTATGGGGGAGCAGAGGGGCGATATCCACTGAGTA	3300
Db	3241	GAAAAGATCTGCTAGATATAGTACTTATGGGGGAGCAGAGGGGCGATATCCACTGAGTA	3300
Oy	3301	CAAGTACTTGTGGGGAGAGAAATCCACTGAGTCAAGTACTTGTGGCATGAGATCCAC	3360
Db	3301	CAAGTACTTGTGGGGAGAGAAATCCACTGAGTCAAGTACTTGTGGCATGAGATCCAC	3360
Oy	3361	TGAGTACAAGTACTTGTGGGGGAGAGATGGCACAAGACCAAAAGTTAAAGGAAGAG	3420
Db	3361	TGAGTACAAGTACTTGTGGGGGAGAGATGGCACAAGACCAAAAGTTAAAGGAAGAG	3420
Oy	3421	ATGAGAGAGCCTCATGAGTTGGGGGTGTAAAGGTCACTCTTTTTCATGTATGAGAGT	3480
Db	3421	ATGAGAGAGCCTCATGAGTTGGGGGTGTAAAGGTCACTCTTTTTCATGTATGAGAGT	3480
Oy	3481	TAAAGAAAAACAAGTGTGTGAGTTGTGATGTCTTCAGACACCCCCCACTATGAACATATCC	3540
Db	3481	TAAAGAAAAACAAGTGTGTGAGTTGTGATGTCTTCAGACACCCCCCACTATGAACATATCC	3540
Oy	3541	ACGAGAGAGGGGCAACCTGTGGGAACCTGGCATTTAAGGAAGGGCGGCTTTTTCACACG	3600
Db	3541	ACGAGAGAGGGGCAACCTGTGGGAACCTGGCATTTAAGGAAGGGCGGCTTTTTCACACG	3600
Oy	3601	AGAAACCTTATGCTCATCTTGTGCTACATCCCACTTTGATAGAGTTCAAGTCAAGT	3660
Db	3601	AGAAACCTTATGCTCATCTTGTGCTACATCCCACTTTGATAGAGTTCAAGTCAAGT	3660
Oy	3661	TTTCGTTTCAACGGTTCTTGCTACTGGTGAACCTTCAGTAGATTCCTCCCAAGAGAGAGA	3720
Db	3661	TTTCGTTTCAACGGTTCTTGCTACTGGTGAACCTTCAGTAGATTCCTCCCAAGAGAGAGA	3720
Oy	3721	CAGCTCTTCTGTATAGGAGGAGACCTGAGATTTCAAGTGTCTTAAGAAACGAAATAGTCTAGA	3780
Db	3721	CAGCTCTTCTGTATAGGAGGAGACCTGAGATTTCAAGTGTCTTAAGAAACGAAATAGTCTAGA	3780

QY	3781	GAATCTGAGTCAAGTAAATCTTAGGTCAACGCGGGCAAAAATATCACTGAAGCGCTATT	3840
Db	3781	GAATCTGAGTCAAGTAAATCTTAGGTCAACGCGGGCAAAAATATCACTGAAGCGCTATT	3840
QY	3841	CCAGGTGAACGGTACAGTGCCTCAGATATACTGAGGTATTGGGCTCCACCGGATTAAGT	3900
Db	3841	CCAGGTGAACGGTACAGTGCCTCAGATATACTGAGGTATTGGGCTCCACCGGATTAAGT	3900
QY	3901	TCTGTTAGTGAAGTCTGCTTTTATTTTGGAGACATCAGCGGTGACGACCCAGATCCAG	3960
Db	3901	TCTGTTAGTGAAGTCTGCTTTTATTTTGGAGACATCAGCGGTGACGACCCAGATCCAG	3960
QY	3961	AAGAATGCACAAGGCTGAGGAGACAGTGAAGAAAGGACATATTGGCAAGCAACAATCT	4020
Db	3961	AAGAATGCACAAGGCTGAGGAGACAGTGAAGAAAGGACATATTGGCAAGCAACAATCT	4020
QY	4021	AAGCCATTCAGTAGAGAGCGTGGGAGTTCTTCTCTGCTTCCAGTCCCTTTACTTTG	4080
Db	4021	AAGCCATTCAGTAGAGAGCGTGGGAGTTCTTCTCTGCTTCCAGTCCCTTTACTTTG	4080
QY	4081	TAACTTTTATTTGACTTGCTACTATCTATGCTGCTCACTATGCTTAGTGAACCGTATC	4140
Db	4081	TAACTTTTATTTGACTTGCTACTATCTATGCTGCTCACTATGCTTAGTGAACCGTATC	4140
QY	4141	TAGCTGGCTATATAGATCTTTCATCTGTCTCTAAATTTGTAGTCACAAATTCGAGCT	4200
Db	4140	TAGCTGGCTATATAGATCTTTCATCTGTCTCTAAATTTGTAGTCACAAATTCGAGCT	4199
QY	4201	AGCAGAAAGCTTAGTCTCAGCCAGTCTCATGACACTTCTCTGGAGAGATGGCTTGTGACAG	4260
Db	4200	AGCAGAAAGCTTAGTCTCAGCCAGTCTCATGACACTTCTCTGGAGAGATGGCTTGTGACAG	4259
QY	4261	AGTCAATGCTGAAGAAGACAGCATCCCTGATTCGACACTGCACTTGCGCTAGGCGCATGT	4320
Db	4260	AGTCAATGCTGAAGAAGACAGCATCCCTGATTCGACACTGCACTTGCGCTAGGCGCATGT	4319
QY	4321	GTAATTACTTTGGCTTGAATTAGTATTTTGGAAAGCAGTTCCACGACCTTACATAATC	4380
Db	4320	GTAATTACTTTGGCTTGAATTAGTATTTTGGAAAGCAGTTCCACGACCTTACATAATC	4379
QY	4381	TGAAGAACCAGTCAATGGAAGAACTGAAAGCTGGGGACAACTTACTAGAGATGATTTTG	4440
Db	4380	TGAAGAACCAGTCAATGGAAGAACTGAAAGCTGGGGACAACTTACTAGAGATGATTTTG	4439
QY	4441	AGCTGATTAAACGAGTGTCTGMAATGTGGCAAAATCAACCAGATTAACAACAAGAG	4500
Db	4440	AGCTGATTAAACGAGTGTCTGMAATGTGGCAAAATCAACCAGATTAACAACAAGAG	4499
QY	4501	CTGGATTTTGGCAATGTGACAAAGTATTTGAATCACTGGTATTTAAGCTATCATCTTAT	4560
Db	4500	CTGGATTTTGGCAATGTGACAAAGTATTTGAATCACTGGTATTTAAGCTATCATCTTAT	4559
QY	4561	TAAATATPAGGGCTCATATATATATTTAAGATTTAAACAAGAAGTGAAGTACCTCCAT	4620
Db	4560	TAAATATPAGGGCTCATATATATATTTAAGATTTAAACAAGAAGTGAAGTACCTCCAT	4619
QY	4621	TTACTTGGCTGTGTTCAAAAGAGTAAAAATATCAGTCAAGGATTAATTATGTGCATG	4680
Db	4620	TTACTTGGCTGTGTTCAAAAGAGTAAAAATATCAGTCAAGGATTAATTATGTGCATG	4679
QY	4681	AAAGTATGAGTGAAGAAACCTTCTCTTACTTTTACCTTCACTTCTTGAATTTTTTTTTTC	4740
Db	4680	AAAGTATGAGTGAAGAAACCTTCTCTTACTTTTACCTTCACTTCTTGAATTTTTTTTTTC	4739
QY	4741	TTACAGACCTGTATCAAGCCATAGTAAAGCACTATCTGCTGAGCTATTAATATGACTTT	4800
Db	4740	TTACAGACCTGTATCAAGCCATAGTAAAGCACTATCTGCTGAGCTATTAATATGACTTT	4799
QY	4801	ACAGCAAAACAATTTGCTGTGGGCTCTTTTGGGAGAGGAAACAGATATGACGAGGGCTC	4860
Db	4800	ACAGCAAAACAATTTGCTGTGGGCTCTTTTGGGAGAGGAAACAGATATGACGAGGGCTC	4859

Db 712 AGACATGATCTTTTCTATTTCTATTTCAAGGCTCAGACCATTTCTATCTTGGCC 771
Qy 2451 TCAGACACATATCTAGATTTTATCTACAGAGCCGATTTAGAAAGCCAGCAGACTG 2510
Db 772 TCAGACACATATCTAGATTTTATCTACAGAGCCGATTTAGAAAGCCAGCAGACTG 831
Qy 2511 CAATATCTTTCATTTCTCTGCTCTCTTCTGAACTCATCTCTTGGCTACTCTGAG 2570
Db 832 CAATATCTTTCATTTCTCTGCTCTCTTCTGAACTCATCTCTTGGCTACTCTGAG 891
Qy 2571 ACCCACTGGGAGATATATCTCTACTTACAGGCTTTTCTTCATCTCTTGTACCCAG 2630
Db 892 ACCCACTGGGAGATATATCTCTACTTACAGGCTTTTCTTCATCTCTTGTACCCAG 951
Qy 2631 CACTTGGGTTTCTCTCTTCTTCAAGGAGCTTGCAGATATACAGAGCTCGGCTC 2690
Db 952 CACTTGGGTTTCTCTCTTCTTCAAGGAGCTTGCAGATATACAGAGCTCGGCTC 1011
Qy 2691 ATCGGGAGAACTGTTCCGAGAGTCACTAAGTCTCTCACTGTATGAGCAGGGCTAG 2750
Db 1012 ATCGGGAGAACTGTTCCGAGAGTCACTAAGTCTCTCACTGTATGAGCAGGGCTAG 1071
Qy 2751 CTGCGGAGAGTGTGAGACCTCTGAGATAGTCTGAGCTATGACCCCTGCTCTTCTG 2810
Db 1072 CTGCGGAGAGTGTGAGACCTCTGAGATAGTCTGAGCTATGACCCCTGCTCTTCTG 1131
Qy 2811 TACCTGAGAGCTTAAAGATCTAGTCTACTGATGAGAGGCTGCTCACTTCACTCGAA 2870
Db 1132 TACCTGAGAGCTTAAAGATCTAGTCTACTGATGAGAGGCTGCTCACTTCACTCGAA 1191
Qy 2871 GACGTTCTGCTCCCGAGTGAAGAGTTCCAGCCCTCACTGAGAGAGTGTACCTTTC 2930
Db 1192 GACATCTGCTCCCGAGTGAAGAGTTCCAGCCCTCACTGAGAGAGTGTACCTTTC 1251
Qy 2931 CTGACCAAACTGACGATCTAGCTCTCTGTGTATGATGATCTGCTGCTACTATGCT 2990
Db 1252 CTGACCAAACTGACGATCTAGCTCTCTGTGTATGATGATCTGCTGCTACTATGCT 1311
Qy 2991 CCTCTCTCTCTCTCTTCTATTTCCAGTATGAGAAAGGAGGCTGCTGCTCTCTCTCA 3050
Db 1312 CCTCTCTCTCTCTCTTCTATTTCCAGTATGAGAAAGGAGGCTGCTGCTCTCTCTCA 1371
Qy 3051 AGAGTGAAGAGGCTCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3110
Db 1372 AGAGTGAAGAGGCTCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1431
Qy 3111 CTTTGGCTTCAATTTAGTATTAATCTTTGAGTTTGTATGAGAAAGCTTTATTTGTTATC 3170
Db 1432 CTTTGGCTTCAATTTAGTATTAATCTTTGAGTTTGTATGAGTTATTTATTTGTTATC 1491
Qy 3171 CATGGAAGAAATCAACTCAATTTCTGTAGATGAGAAAGATGTTGGGAACGAAAGAG 3230
Db 1492 CATGGAAGAAATCAACTCAATTTCTGTAGATGAGAAAGATGTTGGGAACGAAAGAG 1551
Qy 3231 CCTAGATAGAGAAAGAGATCTGCTAGATATAGTATCTAT ---GGGGGAGCAGGGGGCG 3286
Db 1552 CCTAGATAGAGAAAGAGATCTGCTAGATATAGTATCTAT ---GGGGGAGCAGGGGGCG 1611
Qy 3287 ATATCCACTGATGATCAAGTCTTTGGGAGAGAAATCCATGATGATCAAGTCTTTG 3346
Db 1612 ATATCCACTGATGATCAAGTCTTTGGGAGAGAAATCCATGATGATCAAGTCTTTG -- 1669
Qy 3347 GCATGAGATCACTGATCAAGTCTTTGGGGGAGAGAGAGAGAGAGAGAGAGAGAG 3406
Db 1670 -----GGGGGAG 1697
Qy 3407 TGAAGGAG---AGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3462
Db 1698 TGAAGGAG 1757
Qy 3463 TTCCATGATGAGAGAGTAAAGAAACAGAGTGTGATGATTTGATGATCTTCAAGACCCC 3522

Db 1758 TTCCATGATGAGAGAGTAAAGAAATCAGTGTGTGATGATGATGATGATGATGATGATGAT 1817
Qy 3523 CAATATGAAACATATCCAGAGAGCGGAGAGCTGTGGAGAGAGAGAGAGAGAGAGAGAGAG 3582
Db 1818 AA-----CTATGAGAGAGCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1855
Qy 3583 GGGCGGCTTTTCAAGAGAAATCTTATGCTCATCTCTTGTCTACACTCCACCTTGTG 3642
Db 1856 GGGCGGCTTTTCAAGAGAAATCTTATGCTCATCTCTTGTCTACACTCCACCTTGTG 1915
Qy 3643 ATGAGGTTAGCTCAGGTTTCTTCTTACCGTTCTTGTCTACTGTGTGAAAGAGAGAGAGAG 3702
Db 1916 ATGAGGTTAGCTCAGGTTTCTTCTTACCGTTCTTGTCTACTGTGTGAAAGAGAGAGAG 1975
Qy 3703 ATTCCCAAG 3762
Db 1976 ATTCCCAAG 2035
Qy 3763 AGAAGAAATAGCTCAGAGAAATCTAGTCAAGCTGAAATCTAGTCAAGCGGAGAGAA 3822
Db 2036 AGAAGAAATAGCTCAGAGAAATCTAGTCAAGCTGAAATCTAGTCAAGCGGAGAGAA 2095
Qy 3823 TGAATGAAAGCTTTATTTCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3882
Db 2096 TGAATGAAAGCTTTATTTCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2155
Qy 3883 GCTCCAGAGAGATTAAGATCTGTAGTGTGCTGCTTTATTTTGCAGAGAGAGAGAGAGAG 3942
Db 2156 GCTCCAGAGAGATTAAGATCTGTAGTGTGCTGCTTTATTTTGCAGAGAGAGAGAGAGAG 2215
Qy 3943 GAGCAGCAGAAATCAGAGAAATCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4002
Db 2216 GAGCAGCAGAAATCAGAGAAATCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2275
Qy 4003 TTGGCAGAGCAGAAATCTAG 4062
Db 2276 TTGGCAGAGCAGAAATCTAG 2335
Qy 4063 CCAGTCCCTTCTACTTTGATGATTTTATTTGAGTCTGCTACTATCTGCTCACTTCTG 4122
Db 2336 CCAGTCTCTTCTACTTTGATGATTTTCTTTGAGTCTGCTACTATCTGCTCACTTCTG 2395
Qy 4123 CTTAGTGACCTGATCTAGTGGGTCTAGAGATCTTCAATCTGTCTTAAATTTGTA 4182
Db 2396 CTTAGTGACCTGATCTAGTGGGTCTAGAGATCTTCAATCTGTCTTAAATTTGTA 2455
Qy 4183 AGTCACAATTTCTGAGCTTGAAGAAAGCTTACTAGCCAGTCTATGAGCACTTGTCTG 4242
Db 2456 AGTCACAATTTCTGAGCTTGAAGAAAGCTTACTAGCCAGTCTATGAGCACTTGTCTG 2515
Qy 4243 GAGAGAGGCTTGTGAGAGAGTCAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4302
Db 2516 GAGAGAGGCTTGTGAGAGAGTCAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2575
Qy 4303 CTTCGCTAGTGGCAATGTTAATTAATCTTGGCTTGAATTAAGTATTTGGAGAGAGAGAG 4362
Db 2576 CTTCGCTAGTGGCAATGTTAATTAATCTTGGCTTGAATTAAGTATTTGGAGAGAGAGAG 2635
Qy 4363 CCAAGGAGCTTATATATCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4422
Db 2636 CCAAGGAGCTTATATATCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2695
Qy 4423 TACTAGAGATGATTTTGGAGCTCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4482
Db 2696 TACTAGAGATGATTTTGGAGCTCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2755
Qy 4483 AGAATTAACAAG 4542
Db 2756 AGAATTAACAAG 2815
Qy 4543 AATAGCTATCATTTAATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4598
Db 2816 AACAGCTGATCATTTAATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2875

QY	4599	CAAGAATGAGATAGCCTCCCAATTTACTTGGCTCGTTTCAAAAGATGTAATAATATCATGTC	4658
Db	2876	CAAAGATGGAATACCTTCCCAATTTTACCTGGGCTGGTTCAATGATGTAATAAATATCATGTC	2935
QY	4659	ATGATTTAATATATAGTGTCAATGAAGATATGATAGGAAACCCCTTCCCTACTTTTACT	4718
Db	2936	ATAGATTATATATAGTGTCAATGAAGATATGATAGGAAACCCCTTCCCTACTTTTACT	2995
QY	4719	TCATTTCCTAGT-----TTTTTTTTTCTTCCACCCCTGATCAAGCCACTAGTAAGCACT	4773
Db	2996	TCATTTCCTAGTATATATTTTTTTTTTCTTCCACCCCTGATCAAGCCACTAGTAAGCACT	3055
QY	4774	ATCTGCTGTAGCTATATATATAGACTTTTACAGCAACAACATTCGTGTGTGGCTCTTTGG	4833
Db	3056	ATCTGCTGTAGCTATATATATAGACTTTTACAGCAACAACATTCGTGTGTGGCTCTTTGG	3115
QY	4834	GGAAGGGAACAGATATAGCAGAGAGCTCAGGCTAGCAAGTCT-GACTTGCCCTTAAGCCAG	4892
Db	3116	GGAAGGGAACAGATATAGCAGAGAGCTCAGGCTAGCAAGTCTGAGACTCAACTTAAGCCAG	3175
QY	4893	AGGCATGTTGATATAGCAGAGAAAGTAGGCTCTTTCCGAAGTGGTGTGCTTAAGTAATCA	4952
Db	3176	AGGCATGTTGATATAGCAGAGAAAGTAGGAGGCTCTTCCGAAGTGGTGTGCTTAAGTAATCA	3235
QY	4953	GAAACAGGAAGGCTCCGGTTATGTAATATACATGTAAGATATCTAACCTTATCTC---CT	5009
Db	3236	GAAACAGGAAGGCTCTGGTTATGTAATATACATGTAAGATATCTAACCTTATCTCCTTCT	3295
QY	5010	TCTATCGAACCCTTAATCGCTCTCTTTTCTTGTGTAGAGCGATATAACAACACTTGTTTC	5069
Db	3296	TCTATGAGGCTTAACCGTCTCTCTTCTTGTGTGTAGAGCGATATAACAACGCTTGTTTC	3355
QY	5070	TTTTGAGTTCATGCTTTGTGTAATTTTTAGTGTCTGCGAGTTCTTGTTAGAGGTTT	5129
Db	3356	TTTTGAGTTCATGCTTTGTGTAATTTTTAGTGTCTGCGAGTTCTTGTTAGAGGTTT	3415
QY	5130	GTTACCTTGAACCTGGGCTTGGANGTGATGCAACCAAGGCAACAACCTTGAAATGCT	5189
Db	3416	GTTACCTTGAACCTGGGCTTGGANGTGATGCAACCAAGGCAACAACCTTGAAATGCT	3475
QY	5190	GTTGTAAGGTTTATTAATTCATTTACTTGTCTTTGAAAAGGTGAAGCGTGTGAGAAAG	5249
Db	3476	GTTGTAAGGTTTATTAATTCATTTACTTGTCTTTGAAAAGGTGAAGCGTGTGAGAAAG	3535
QY	5350	AACCTCAAGAGATGTGTTCTCTGTAGAGAAACCTTTTTTCCCTTAAATGCTATAA	5309
Db	3536	AACCTCAAGAGATGTATCTCTGTAGAGAAAC-TTTTTTTTTCCCTTAAAGCCTATAA	3594
QY	5310	TTCACCTTCACTCAACTTGAACCTTTTANACATGCTGTCAATATAAAGGTTTAAAGCC	5369
Db	3595	TTCACCTTCACTCAACTTGAACCTTTTANACATGCTGTCAATATAAAGGTTTAAAGCC	3654
QY	5370	CGCTCTCATGCTCTGGGAAAGACCAATATGGGGAAGAAATGTTATGCTGAGAAATCTG	5429
Db	3655	CGCTCTGTGTGCTCTGGGAAAGACCAATATGGGGAAGAAATGTTATGCTGAGAAATCTG	3714
QY	5430	ACCGGACGGGAACTGGTCAAGACTCCCCGGAAGCCAACAAGGTGTTAATGTAAGAAACA	5489
Db	3715	ACCGGACGGGAACTGGGTCAAGACTCCCCGGAAGCCAACAAGGTGTTAATGTAAGAAACA	3774
QY	5490	GTCACAGGTGTGGGCTCATGTATATAGAAAGGAACAAGGAGGGAAGATAGCTAACAAAGTT	5549
Db	3775	GTCACAGGTGTGGGTTTCAATATATAGATGGAACAAGGAGGGAAGATAGCTAACAAAGTT	3834
QY	5550	TCATATAGGTCGCGAGTCTTAAAGATATCAAAATAGCTGCTTGCGCTTCAATAAAGGAG	5609
Db	3835	TCATATAGGTCCTTAAGTCTTTTAAAGATACAAAATAGCTGTGTGGGCTTCAATAAAGGAG	3894
QY	5610	TCTGGGAAGGCAAGCAAG--TGAGAGGGAATTGAAAGGGAATAAACAAGATGTAGAGGA	5666
Db	3895	TCTGGGAAGGCAAGCAAGCATTTGAGAGGGAAGTGAATAAGGGAATAAACA--AATGTAGAGGA	3952

QY	5657	CTTGAACGCTACAAATCTCTACCAACGATTTTCTTGGACAATCTAGAA-----GCT	5722
Db	3953	TTTGGAAAAGCTACAAATCTCTCCAGAAAGATTTTTCTTGGAGGAATCTAGAACAAAGGCT	4012
QY	5723	AGTGATTAAGGT-CATTGACAGGGGAGCTGCTTGGCCATTGGAATCTGGGTTTTGTCTC	5781
Db	4013	GGTGATTAGGTGATCGCAGAAAGACTTGGCTTGGCCATTGGAATCTGGGTTTTGTCTC	4072
QY	5782	TCCATTGAGGTTGAAAGGCTCACC-TTTTTACCTCGAATGAGAGGAGAAAGAGGGCT	5840
Db	4073	TCCATTGAGGTTGAGAGGCTCACCTTTTTTACCCTGATAGAGAGGAGAAAGAGGGCT	4132
QY	5841	GTTATGATCTCTACCTGAGATTTTAATAGTTATAGCAATGGAACAGACCTCGGAGACTC	5900
Db	4133	GTTTATGATCTCTACCTGAGATTTTAATAGTTATAGCAATGGAACAGACCTCGGAGACTC	4192
QY	5901	CTCTTTCAC-----AAAAAATAGGAACCTGTTGTTGCTTGTCTTGTCTTGTG	5950
Db	4193	CTCTTTCACAAAAAATAGGAACCTGTTGTTGCTTGTCTTGTCTTGTGCTTGTG	4252
QY	5951	TTAAGAAAGACA-----	5963
Db	4253	TTAAGAAAGACAAGGCAAGCTGGGAGTGGGCAATGGCTTTAATCCAGCAATTGGAG	4312
QY	5964	-----	5963
Db	4313	GCAGAGGAGGTTGACTTTCTAAATTCAGAGCCAGCCTGTCTACAAAGTAGTTCCAGGA	4372
QY	5964	-----	5963
Db	4373	CAGCCAGGGCTATACAGAGAAACCTCTGTCTCGGAAAAAAGAAAAAGAAAAAG	4432
QY	5964	-----	5963
Db	4433	AAAAAAG	4492
QY	5964	-----	5963
Db	4493	GAA	4552
QY	5964	-----	5963
Db	4553	GAA	4612
QY	5964	-----GGCAAGCCCGAACCATGGGT	5985
Db	4613	AAGAGAAAAAGAAAAAGAAAAAGCAAGCAAGACACTGGCAAGACATGCCCAATGGGA	4672
QY	5986	TGAATGTGGGCTCTTGAAGTCAAGGCTTTTGAAGTTAGCACTCATCAATAGTTGATCAGG	6045
Db	4673	CGTATGTGGGCTTTGAGACAAAGCTTTGAATTTGAGGGCTCATCAATAGTTGATCAGG	4732
QY	6046	TCAGGTGAGGCTTACCTGTGAGGCCGAGCCCTGCTGCTTGGCACTTAACATCTCCAGG	6105
Db	4733	TCAGGTGAGGCTTACCTGTGAGGCCGAGCCCTGCTGCTTGGCACTTAACATCTCCAGG	4792
QY	6106	TCTCATGTCACTCTCCGCTACTAGACAGAGTTAGAGAGTTGAGCAAACTTTTTCGAA	6165
Db	4793	TCTCATGTCACTCTCCGCTACTAGACAGAGTTAGAGAGTTGAGCAAACTTTTTCGAA	4852
QY	6166	CCCCCACTAAATTTAATTGACAAAGACTGTGTAAATTTGTGGGATACAGTGTATAAT	6225
Db	4853	CCCCCACTAAATTTAATTGACAAAGCAAGTGTAAATTTGTGGGATACAGTGTATAAT	4912
QY	6226	GATCTATGTGTGATTTGTGCAAGGTTCAATTAAGTATATATATATATATATATATATAT	6285
Db	4913	GATCTATGTGTGATTTGTGCAAGGTTCAATTAAGTATATATATATATATATATATATAT	4972
QY	6286	TATGGGTGTGAAAGTAAATTAATTAAGTATATATATATATATATATATATATATATATAT	6345
Db	4973	TATGGGTGTGAAAGTAAATTAATTAAGTATATATATATATATATATATATATATATATAT	5011
QY	6346	CATGATTTTAAAGTCTTGGGCAAAATCATATTATCTATGCTATAAAATATACATTATGTGA	6405


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Db 5032 CATGATTTAAAGGCTTGAGCAATCATATTAATCTCATGTAATGTAATGCAATTAATGTA 5091
Qy 6406 TTATTAATCTTTTAAAGAGAGGCTGATCTGTTGGTGTCTGACAGCAAGCAATGTCCACC 6465
Db 5092 TTATCAATCTTTTAAAGAGAGGCTGATCTGTTGGTGTCTGACAGCAAGCAATGTCCACC 5151
Qy 6466 AGCTCTTTCTGTAAGGCTGATCTGTTGGTGTCTGACAGCAAGCAATGTCCACC 6525
Db 5152 AGCTCTTTCTGTAAGGCTGATCTGTTGGTGTCTGACAGCAAGCAATGTCCACC 5211
Qy 6526 CTATATTTCTGTAAGGCTGATCTGTTGGTGTCTGACAGCAAGCAATGTCCACC 6585
Db 5212 CTATATTTCTGTAAGGCTGATCTGTTGGTGTCTGACAGCAAGCAATGTCCACC 5271
Qy 6586 GTTATGCTCTGTAAGGCTGATCTGTTGGTGTCTGACAGCAAGCAATGTCCACC 6645
Db 5272 GTTATGCTCTGTAAGGCTGATCTGTTGGTGTCTGACAGCAAGCAATGTCCACC 5331
Qy 6646 CTCTCTCTGCTGTAAGGCTGATCTGTTGGTGTCTGACAGCAAGCAATGTCCACC 6705
Db 5332 CTCTCTCTGCTGTAAGGCTGATCTGTTGGTGTCTGACAGCAAGCAATGTCCACC 5391
Qy 6706 AAGTGAAGAGCTGATCTGATCATATTAATGTAATGTAATGTAATGTAATGTAATGTA 6765
Db 5392 AAGTGAAGAGCTGATCTGATCATATTAATGTAATGTAATGTAATGTAATGTAATGTA 5451
Qy 6766 AAAAGAAATAGTGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 6825
Db 5452 AAGAAATAGTGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5511
Qy 6826 TCATGACAAATATTTTATGTCATGATGATGATGATGATGATGATGATGATGATGATGATG 6885
Db 5512 TCATGACAAATATTTTATGTCATGATGATGATGATGATGATGATGATGATGATGATGATG 5571
Qy 6886 TTGTTGAAAGAGGCTGATCTGATCTGTTGAAAGAGGCTGATCTGATCTGATCTGATCTG 6945
Db 5572 TTGTTGAAAGAGGCTGATCTGATCTGTTGAAAGAGGCTGATCTGATCTGATCTGATCTG 5631
Qy 6946 CATATCAATATTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7005
Db 5632 CATATCAATATTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5691
Qy 7006 AGTTATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7064
Db 5692 AGTTATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5751
Qy 7065 GCAATTAATATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7124
Db 5752 GCAATTAATATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5811
Qy 7125 TGGAATTAATATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7184
Db 5812 TGGAATTAATATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5871
Qy 7185 TCATCATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7244
Db 5872 TCATCATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5931
Qy 7245 GTTG 7248
Db 5932 TTG 5935

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XX Mouse, T cell derived inducible factor; TIFbeta, ds; antiallergic;
KW antiallergic; cytokine; interleukin-9; IL-9; STAT transcription factor;
KW cancer; lymphoma; immune system disorder; allergy; asthma;
KW acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
XX thyroiditis; melanoma; hepatoma.
OS Mus musculus.
PN US2001024652-A1.
XX
XX 27-SEP-2001.
XX
XX 29-DEC-2000; 2000US-0751797.
XX
XX 18-OCT-1999; 99US-0419568.
XX 26-OCT-1998; 98US-0178973.
XX 16-JUL-1999; 99US-0354243.
XX
XX (DUMO/) DUMOUTIER L.
XX (LOUA/) LOUAHED J.
XX (RENA/) RENAULD J.
XX
XX Dumoutier L, Louahed J, Renauld J;
XX
XX WPI; 2001-638496/73.
XX
XX New isolated nucleic acid molecules encoding T cell inducible factors,
XX useful as markers for expression or effect of interleukin (IL)-9 in a
XX subject and diagnosing susceptibility to asthma or allergy
XX
XX Claim 1; Page 21-23; 26p; English.
XX
XX The invention relates to an isolated nucleic acid molecule, which encodes
XX a T cell derived inducible factor (TIF) which are upregulated by the
XX cytokine interleukin-9 (IL-9) and induce STAT transcription factor
XX activation. The TIF proteins (or their mutants) may be used to test IL-9
XX ant/agonists for their potency against lymphomas, immune system
XX disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
XX autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
XX or inhibit differentiation of tissue types in which they are active and
XX therefore be used to develop treatments for melanomas and hepatomas.
XX The present sequence a partial genomic sequence for mouse TIFbeta.
XX
XX Sequence 5935 BP; 1732 A; 1174 C; 1346 G; 1683 T; 0 other;
XX
XX Query Match 57.0%; Score 4245.2; DB 22; Length 5935;
XX Best Local Similarity 88.3%; Pred. No. 0;
XX Matches 5039; Conservative 0; Mismatches 178; Indels 487; Gaps 20;
XX
XX 1971 TACCATGCTACCCGAGCAAGATGCTCCCGATGTTTGGCTTTGGCTCTGACTAC 2030
XX 293 TACCATGCTACCCGAGCAAGATGCTCCCGATGTTTGGCTTTGGCTCTGACTAC 352
XX
XX 2031 AGGCTCTCTCTCACTTATCAACTGTTGACATTTGCGATCTGATGCTGCTGCA 2090
XX 353 AGGCTCTCTCTCACTTATCAACTGTTGACATTTGCGATCTGATGCTGCTGCA 412
XX
XX 2091 GAATCTATGAGTTTTCCTTATGAGGACCTTTGGCCGACGCTGCTTCTCATTCG 2150
XX 413 GAATCTATGAGTTTTCCTTATGAGGACCTTTGGCCGACGCTGCTTCTCATTCG 472
XX
XX 2151 CCTGAGGAGCCAGAGGCAATGCGTCCGCTCAACACCCGCTGCAAGCTTGAAGTCTC 2210
XX 473 CCTGAGGAGCCAGAGGCAATGCGTCCGCTCAACACCCGCTGCAAGCTTGAAGTCTC 532
XX
XX 2211 CAATTCAGAGCCGATACATGTCACACCGACTTATGCTGACCAAGAGGATACAGCT 2270
XX 533 CAATTCAGAGCCGATACATGTCACACCGACTTATGCTGACCAAGAGGATACAGCT 592
XX
XX 2271 GCATCTCTTTCTCTCCATACCGCTTGGCATTTTCTGTAAGCATTTGCAACTCTTAG 2330
XX 593 GCATCTCTTTCTCTCCATACCGCTTGGCA-TTCTCTGTAAGCATTTGCAACTCTTAG 651

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RESULT 6

AA514878 standard; DNA; 5935 BP.

AA514878;

19-DEC-2001 (first entry)

Mouse partial genomic DNA for T cell derived inducible factor, TIFbeta.

QY	2331	GGGGGCTTTAATCTCGGAGGCTCACACCTAATGTTTCTGTCTCTTTAGAGACTCTTTA	2390
Db	652	GGGGGCTTTAATCTCGGAGGCTCACACCTAATGTTTCTGTCTCTTTAGAGACTCTTTA	711
QY	2391	AGGACTGGGCTTTTCTTCTAATTTCTAATTTCAAGGCTCGAGACCAATTTCTATCTTGGCCT	2450
Db	712	AGGACTGGGCTTTTCTTCTAATTTCTAATTTCAAGGCTCGAGACCAATTTCTATCTTGGCCT	771
QY	2451	TCAGGACACATATATCTGAATTTTATCTACAGAGGCGCATTTAGAAAGCCACCAGACTG	2510
Db	772	TCAGGACACATATATCTGAATTTTATCTACAGAGGCGCGTTTAGAAAGCCACCAGACTG	831
QY	2511	CAATACTTTCATTTCTCTGTGCGCTCTGTCTGAACTCACTCTCTTGGGCTACGCTGAG	2570
Db	832	CAATACTTTCATCTGTGTGCTCTTCTGAACTCACTCTCTTGGGCTACGCTGAG	891
QY	2571	ACCCACTGCGGACATACATCTCTAATTACAGAGGCTTTTCTTCATCTCTTGTACCCAGG	2630
Db	892	ACCCACTGCGGACATACATCTCTAATTACAGAGGCTTTTCTTCATCTCTTGTACCCAGG	951
QY	2631	CACTTAAGGTTTCTCTCTTTCAAGCCAGCCTTGCAGATTAACAACAGACGTCGCGCTC	2690
Db	952	CACTTAAGGTTTCTCTCTTTCAAGCCAGCCTTGCAGATTAACAACAGACGTCGCGCTC	1011
QY	2691	ATCGGGGGAACCTGTTCCGAGAGTCACTGTAACTCTCACTGTGATGAGCAGGGCTAG	2750
Db	1012	ATCGGGGGAACCTGTTCCGAGAGTCACTGTAACTCTCACTGTGATGAGCAGGGCTAG	1071
QY	2751	CTGGGGGAGCGTGGGAAACCTCTGSGAATGCTGACGATAGACCCCTGCTCTTCTTC	2810
Db	1072	CTGGGGGAGCGTGGGAAACCTCTGSGAATGCTGACGATAGACCCCTGCTCTTCTTC	1131
QY	2811	TACCTGCAGGCTAAAGATCACTGTCACCTGTATGAAGCAGTGCTCAACCTTGAA	2870
Db	1132	TACCTGCAGGCTAAAGATCACTGTCACCTGTATGAAGCAGTGCTCAACCTTGAA	1191
QY	2871	GACGTTCTGCTCCCCAGTCAAGAGTTTCCAGCCCTTACATGACAGAGGTGATCTTTTC	2930
Db	1192	GACGTTCTGCTCCCCAGTCAAGAGTTTCCAGCCCTTACATGACAGAGGTGATCTTTTC	1251
QY	2931	CTGACCAAACTCAGAAATCAAGCTCAGCTCCGTGTAATCTGACCTCTGGCTACCTAATCT	2990
Db	1252	CTGACCAAACTCAGAAATCAAGCTCAGCTCCGTGTAATCTGACCTCTGGCTACCTAATCT	1311
QY	2991	CCTCTCTCTTCTCTTCTATTTCAAGTAAGAAACCCAGGTCGCGCCTCTCTCTTTACA	3050
Db	1312	CCTCTCTCTTCTCTTCTATTTCAAGTAAGAAACCCAGGTCGCGCCTCTCTCTTTACA	1371
QY	3051	AGAGTGAAGAGGGCTCGACCAACCAACATCATATAGGCACTTGAATATAGTCACAAAGG	3110
Db	1372	AGAGTGAAGAGGGCTCGACCAACCAACATCATATAGGCACTTGAATATAGTCACAAAGG	1431
QY	3111	CTTTGGCTTCAATTGAGTAATACCTTTGAGTTTGTATGAGTGAAGCTTTATTTGTTTATC	3170
Db	1432	CTTTGGCTTCAATTGAGTAATACCTTTGAGTTTGTATGAGTGAAGCTTTATTTGTTTATC	1491
QY	3171	CATGGAAGAATCAACTCAAAATCTGTAGATGAGAAAGATGTTGGGAAACGAAAAAAGG	3230
Db	1492	CATGGAAGAATCAACTCAAAATCTGTAGATGAGAAAGATGTTGGGAAACGAAAAAAGG	1551
QY	3231	CCTAGATAGAGAAACAGATCTGCTGAGTATAGTACTTAT---GGGGGGAGGACAGGGGGG	3288
Db	1552	CCTAGATAGAGAAACAGATCTGCTGAGTATAGTACTTAT---GGGGGGAGGACAGGGGGG	1611
QY	3287	ATATTCACCTGAGTACAAGTACTTGTGGGAGGAATCCACGAGATCAAGTACTTGT--	3344
Db	1612	ATATTCACCTGAGTACAAGTACTTGTGGGAGGAATCCACGAGATCAAGTACTTGT--	1666
QY	3347	GCATGAGATCCACGAGTACAAGTACTTGTGGGGGAGGGAATGGCACAGGCAAAAGT	3400
Db	1670	GCATGAGATCCACGAGTACAAGTACTTGTGGGGGAGGGAATGGCACAGGCAAAAGT	1697

OY		3407	TGAAGGGA---AGAAAGATGAGAAGGGCTCATGTGTGGGGGTGTGAAAAGCTCACTC--TT	3462
Dd		1698	TGAAGGGAAGAGAGAGATGGAAGGCCTTAAGTGTGGGGGTGTGAAAAGCTCACTCCTTT	1757
OY		3463	TTCCATGTGATGAGAGATTAAAGAAAAACAGTGGTGATTTGATGTCTTCAGACACCCC	3522
Dd		1758	TTCCATGTGATGAGAGATTAAAGAAAAACAGTGGTGATTTGATGTCTTCAGACACCCC	1817
OY		3523	CAACTATGAAAACATATCCACGAGAGCGGGCAGACTGTGGGAAGCTTGGCATTTTAGGGAA	3582
Dd		1818	AA-----CTATGGCAGACTGTGGGAAGCTGGGCAATTTAAGGGAA	1855
OY		3583	GGGGGGCTTTTCACAGAGAAACTTAATGCTATCTTGTGTCACTGCCACCTTTG	3642
Dd		1856	GGGGGGCTTTTCACAGAGAAAACCTTAATGCTATCTTGTGTCTAACCTCCACCTTTG	1915
OY		3643	ATGAGTTCAGCTCAGGTTTGGTTTCTACCGTTCTTGCTACTGGTGGAAACTTCAGTAGG	3702
Dd		1916	ATGAGTTCAGCTCAGGTTTGGTTTCTACCGTTCTTGCTACTGGTGGAAACTTCAGTAGG	1975
OY		3703	ATTCCCCAAAAGCAGAGACAGCTCTTCTGTAAAGGAGGAACTGTGATTTCAGTGTCTAG	3762
Dd		1976	ATTCCCCAAAAGCAGAGACAGCTCTTCTGTAAAGGAGGAACTGTGATTTCAGTGTCTAG	2035
OY		3763	AGAAAGAAATNGCTCAGAGAAATCTAGTCAACGTGAAATCTAGSTCAACGGGGCAAAA	3822
Dd		2036	AGAAAGAAATNGCTCAGAGAAATCTAGTCAACGTGAAATCTAGSTCAACGGGGCAAAA	2095
OY		3823	TGACTGAAAGCCTTATTTCCAGGTGAACGGTCACTGCTCAGATAACTGAGGTATTTGG	3882
Dd		2096	TGACTGAAAGCCTTATTTCCAGGTGAACGGTCACTGCTCAGATAACTGAGGTATTTGG	2155
OY		3883	GCTCCCAACGGATNAGATTCTGTTAGTGAAGCTGTGCTTTATTTTGCAGCACATCAGCGGT	3942
Dd		2156	GCTCCCAACGGATNAGATTCTGTTAGTGAAGCTGTGCTTTATTTTGCAGCACATCAGGTGT	2215
OY		3943	GACGACCGAACAATCTCCAGAGAAATGTCTAGAAAGCTGAAGAAGACAGTGAAGAAABAGTACTA	4002
Dd		2216	GACGACCGAACAATCTCCAGAGAAAGTGTCTAGAAAGCTGAAGAAGACAGTGAAGAAABAGTACTA	2275
OY		4003	TTGGCAAGCCACAAATACCTAAGACCATTGACAGTGAAGAGAGTGGGGATTTCTTCTGTGCTTC	4062
Dd		2276	TTGGCAAGCCACAAATACCTAAGACCATTGACAGTGAAGAGAGTGGGGATTTCTTCTGTGCTTC	2335
OY		4063	CCAAGTCCCTTCTACTTTGTAAACATTTTATTTGACTGTCTAATCTGTGTCATTAATCTGTC	4122
Dd		2336	CCAAGTCCCTTCTACTTTGTAAACATTTTATTTGACTGTGTCTAATCTGTGTCATTAATCTGTC	2395
OY		4123	CTTAGCTGACACTGTATCTAGCTGGGTCTAATGATCTTTCAAATCTGTGTCCTAAATTTGTA	4182
Dd		2396	CTTAGCTGACACTGTATCTAGCTGGGTCTAATGATCTTTCAAATCTGTGTCCTAAATTTGTA	2455
OY		4183	AGTACAATTTTGAGCTAGCAGAAAGCTTGAAGTCTTCAATCTGTGTCCTAAATTTGTA	4242
Dd		2456	AGTACAATTTTGAGCTAGCAGAAAGCTTGAAGTCTTCAATCTGTGTCCTAAATTTGTA	2515
OY		4243	GAGAGTGGCTTGTGACAGAGTCAATGCTGAAAGACAGCATCTCTGATTTCCAGCTTGTCA	4302
Dd		2516	GAGAGTGGCTTGTGACAGAGTCAATGCTGAAAGACAGCATCTCTGATTTCCAGCTTGTCA	2575
OY		4303	CTTGCTTAATGTGCGCATGTGTATTAATCTTTGGCTTGATTAAGTATTTGGGAAAGCCACTTC	4366
Dd		2576	CTTGCTTAATGTGCGCATGTGTATTAATCTTTGGCTTGATTAAGTATTTGGGAAAGCCACTTC	2635
OY		4363	CCAGGAGACTGATTAATCTGAAAGAACATGATTTGAAAACCTAGAAAGCTGGGCAAAACT	4422
Dd		2636	CCAGGAGACTGATTAATCTGAAAGAACATGATTTGAAAACCTAGAAAGCTGGGCAAAACT	2695
OY		4423	TACTAGAGATATTTTTAGCTCATTAACCGATGCTCTGAATGTGTGGCAAAATCAACC	4482
Dd		2696	TACTAGAGATATTTTTAGCTCATTAACCGATGCTCTGAATGTGTCAAAATCAACC	2755
OY		4483	AGAAATTAACAAAGAGCTGGATTTGCAAAATAGACAAAGTATTTAGAAATCACTGTGTTT	4542

Db 2756 AATAATTAACAAAGAGCTGATTTGCAAAATAGCAAGATATTAAGATCTAGCTAT 2815
Qy 4543 AATAGTATCATCTTAATTAATAATATAGGCTATATA----TATATTAAGATTAAACA 4598
Db 2816 AACAGTGTCACTTAATTAATAATATAGTGTCTATTTAGCTGCTATTTAATTAACA 2875
Qy 4599 CAAGAGTGATAGCTCCCAATTTAATTGGCTGTGTTCAAAAAGATAAAATATCAGTC 4658
Db 2876 CAAGAGTGATTAATCTCCCAATTTAATTGGCTGTGTTCAATAGATAAAATATCAGTC 2935
Qy 4659 ATGATTAATTAATAGTGTATAGAAATAGAAATGAAACCTTTCTTACTTTTACT 4718
Db 2936 ATAGATTAATTAATAGTGTATAGAAATAGAAATGAAACCTTTCTTACTTTTACT 2995
Qy 4719 TCATTTCTTAGT-----TTTTTTTCTTCAACCTGTATCAAGCAGTATAGACACT 4773
Db 2996 TCATTTCTTAGTATTTATTTTCTTCAACCTGTATCAAGCAGTATAGACACT 3055
Qy 4774 ATCTGTGTAGCTATTAATATAGCTTTACAGCAAAACATTTGCTGTGTGCTTTGG 4833
Db 3056 ATCTGTGTAGCTATTAATATAGCTTTACAGCAAAACATTTGCTGTGTGCTTTGG 3115
Qy 4834 GGAAGGAAACAGATATAGCAAGGCTCAGGCTAGCAAGTCT-GACTTGCTTAAAGCCAG 4892
Db 3116 GGAAGGAAACAGATATAGCAAGGCTCAGGCTAGCAAGTCTGACTTCAACCTTAAAGCCAG 3175
Qy 4893 AGGATGTGTATAGAGAAAGTGAAGGCTCTGCAAGTGGGTGTGTAAATGAATCA 4952
Db 3176 AGGATGTGTATAGAGAAAGTGAAGGCTCTTCAAGTGGGTGTGTAAATGAATCA 3235
Qy 4953 GAAACAGAAAGCTCGGTTGATGGAATATCAGTAAGATATCAACCTTATCTC---CT 5009
Db 3236 GAAACAGAAAGCTCGGTTGATGGAATATCAGTAAGATATCAACCTTATCTCCTCT 3295
Qy 5010 TCTATGAAACCTTAATCGTCTCTTTTCTGTGTGTAGGCTGATTAACACACTTTGTTTC 5069
Db 3296 TCTATGAAAGCTTAACCGTCTCTCTCTGTGTGTAGGCTGATTAACACCGTTGTTTC 3355
Qy 5070 TTTTGAAGTTCATGCTTTGTATGATTTTATAGTGTCTGCAAGTCTTGTATAGAGGTT 5129
Db 3356 TTTTGAAGTTCATGCTTTGTATGATTTTATAGTGTCTGCAAGTCTTGTATAGAGGTT 3415
Qy 5130 GTTACCTTGACACCTGGGCTTGATGATGATGCCAAGGCAACACTTGTGAATGCT 5189
Db 3416 GTTACCTTGACACCTGGGCTTGATGATGATGCCAAGGCAACACTTGTGAATGCT 3475
Qy 5190 GTGTAAAGGTATTTATTTACTTTTCTTTGAAAAGGTGAAGCGTGTGTGAAGA 5249
Db 3476 GTGTAAAGGTATTTATTTACTTTTCTTTGAAAAGGTGAAGCGTGTGTGAAGA 3535
Qy 5250 AACTCAGAGAGTGTCTCTGTAGAAAACCTTTTCTTCCCTTAAATGCCATTA 5309
Db 3536 AACTCAGAGAGTGTATTTCTGTAGAAAAC-TTTTTTTCTTCCCTTAAAGCTTATA 3594
Qy 5310 TCCACTTTGATCACTTTGACTTTTATACATGCTGCAATGAAAGGTATTAAGGCT 5369
Db 3595 TCCACTTTGATCACTTTGACTTTTATACATGCTGCAATGAAAGGTATTAAGGCT 3654
Qy 5370 CGCTCTCATGCTTGTGGAAAAGCAATAGGGGAAGATTTATGCTGAAGAAATCTG 5429
Db 3655 CGCTCTCATGCTTGTGGAAAAGCAATAGGGGAAGATTTATGCTGAAGAAATCTG 3714
Qy 5430 ACCGCGAGGGAATCTGTAGAGCTCCCGAAGAACACACAGAGTGTAAATAGGAACA 5489
Db 3715 ACTGCGAGGGAATCTGTAGAGCTCCCGAAGAACACCTACAGGTGTAAATAGGAACA 3774
Qy 5490 GTTCAGAGTGGGCTCATGTATAGAAATGAAACAGCAGGGAAGATTAAGCTAACAAAGTT 5549
Db 3775 GTTCAGAGTGGGCTCATGTATAGAAATGAAACAGCAGGGAAGATTAAGCTAACAAAGTT 3834
Qy 5550 TCATAGGTCCGAGTCTTAAGATCAAAATAGCTGTGGCTTCAATACAAAGGAAG 5609
Db 5550 TCATAGGTCCGAGTCTTAAGATCAAAATAGCTGTGGCTTCAATACAAAGGAAG 5609

Db 3835 TCATAGGTCTTAAGTCTTTAAGATCAAAATAGCTGTGGCTTCAATACAAAGGAAG 3894
Qy 5610 TCTGGAAAGGAGCAAG---TGAGAGGAATGAAAGGAAAAAAGAAATGTAGAGA 5666
Db 3895 TCTGGAAAGGAGCAAGATTTGAGAGGAGATGAAAGGAAAAAAG---AATGTAGAGA 3952
Qy 5667 CTGGAACGCTAACAAATCTCTTACCAAGCATTTTCTTGAACAATGTAAAG---GGT 5722
Db 3953 TTTGAAAAGCTAACAAATCTCTTACCAAGGATTTTCTTGAAGAAATCTTAACAAGGCT 4012
Qy 5723 AGTGATTAAGT-GATTCAGAGGAGACTGCTTGGCATTTGAATCTGGTATTGTCTC 5781
Db 4013 GGTGATTAAGTGTGATTCAGAAAGACTTCTTGGCATTTGAATCTGGTATTGTCTC 4072
Qy 5782 TCATAGGTGTGAAGGCTCAGCC-TTTTACCTCGAATGAGAGGAAAGAGGCT 5840
Db 4073 TCATAGGTGTGAAGGCTCAGCCCTTTTACCTCGAATGAGAGGAAAGAGGCT 4132
Qy 5841 GTTATGACTCTTACCTGAGTTTATCTATGTTAGCAATGAAACAGACACTCGGACCTC 5900
Db 4133 GTTATGACTCTTACCTGAGTTTATCTATGTTAGCAATGAAACAGACACTCGGACCTC 4192
Qy 5901 CTCTTGAAC-----AAAAAATGAAACCTGTTGTGTGTGTTGTTGTTG 5950
Db 4193 CTCTTGAACAAAAA-----AAAAAAGAAACCTGTTGTGTGTGTTGTTGTTG 4252
Qy 5951 TTAAGAAAGCACA----- 5963
Db 4253 TTAAGAAAGCACAAGGAGCTGGCATGCTGCCATGCTTTAATCCAGCATTTGGAG 4312
Qy 5964 ----- 5963
Db 4313 GCAGAGCAGGTGACTTTCTAATTAAGCCAGCTGTCTACAAAGTGAATTCAGGA 4372
Qy 5964 ----- 5963
Db 4373 CAGCCAGGCTATACAGAAACCTGTCTGGGAAAAA-----AAGAAAGAAAG 4432
Qy 5964 ----- 5963
Db 4433 AAAAGAAAGAAAG 4492
Qy 5964 ----- 5963
Db 4493 GAG 4552
Qy 5964 ----- 5963
Db 4553 GAG 4612
Qy 5964 ----- 5963
Db 4613 AAGAGAAAGAAAGAAAGAAAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAG 4672
Qy 5966 TGAATGTGGCTTTGACTCAAGGCTTTGAGTTGAGCACTCATTAATAGTGTATGAG 6045
Db 4673 CGTATGTGGCTTTGAGCAAGGCTTTGAGTTGAGCAAGGCTCATTAATAGTGTATGAG 4732
Qy 6046 TCAAGTGAAGGCTACCTGTAGGCGAGCCCTGTGCTTGCACCTTAACATCTCCAGG 6105
Db 4733 TCAAGTGAAGGCTACCTGTAGGCGAGCCCTGTGCTTGCACCTTAACATCTCCAGG 4792
Qy 6106 TCTCAGTATCACTTCTGCTACTTATAGCAGTATAGAGTTAGCAAACTTTTTCGA 6165
Db 4793 TCTCAGTATCACTTCTGCTACTTATAGCAGTATAGAGTTAGCAAACTTTTTCGA 4852
Qy 6166 CCCCCACTTAATTAATTAAGCAAAAGCTGTATTTGTGGGATTAAGTGTATAT 6225
Db 4853 CCCCCACTTAATTAATTAATTAAGCAAAAGCTGTATTTGTGGGATTAAGTGTATAT 4912
Qy 6226 GATCTATGTGCAATGTGCAAGGTTCAATATAGATATATATAGCCCATCAAGCTT 6285
Db 4913 GATCTATGTGCAATGTGCAAGGTTCAATATAGATATATATAGCCCATCAAGCTT 4972

QY 6286 TATGGGTGGAATGCAATATATAGTAGATGCTGTGTGCTTATAGTCAGAAAG 6345
 DB 4973 TATGGGTGGAATGCAATATATAGTAGATGCTGTGTGTGCTTATAGTCAGAAAG 5031
 QY 6346 CATGATTTTAAAGTCTTGGGCAAAATCATTTTATACAGTCTTAAATCATTAATGTA 6405
 DB 5032 CATGATTTTAAAGTCTTGGGCAAAATCATTTTATACAGTCTTAAATCATTAATGTA 5091
 QY 6406 TTATTAATCTTTAGAGAGGCTGATCTGTTTGTGTGTGCTCAGAGCAATGTCAAC 6465
 DB 5092 TTATTAATCTTTAGAGAGGCTGATCTGTTTGTGTGTGCTCAGAGCAATGTCAAC 5151
 QY 6466 AGCTCTTTCTAACTGTGACCTTTAGAAAATGCTAAGTGTCTAAATTTGTTGAT 6525
 DB 5152 AGCTCTTTCTAACTGTGACCTTTAGAAAATGCTAAGTGTCTAAATTTGTTGAT 5211
 QY 6526 CTATTTTATAGCTTTGAGAGAGTGAAGATCAAGGATTTGGGAACTGACCTGCT 6585
 DB 5212 CTATTTTATAGCTTTGAGAGAGTGAAGATCAAGGATTTGGGAACTGACCTGCT 5271
 QY 6586 GTTATAGTCTGAGAAATGCTGTGCTGAGCGAGAGAGAGAGAGAGAGAGAGAGAG 6645
 DB 5272 GTTATAGTCTGAGAAATGCTGTGCTGAGCGAGAGAGAGAGAGAGAGAGAGAGAG 5331
 QY 6646 CTCTCTCTGCTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6705
 DB 5332 CTCTCTCTGCTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5391
 QY 6706 AAGTGAGAGCTTACGTCATCATCTTTAGAGAGATTTACATGAACTGTGCTCACTGA 6765
 DB 5392 AAGTGAGAGCTTACGTCATCATCTTTAGAGAGATTTACATGAACTGTGCTCACTGA 5451
 QY 6766 AAAAG 6825
 DB 5452 AAG 5511
 QY 6826 TCATTGACATATTTTATGTCAGTATGATACAGAGAGAGAGAGAGAGAGAGAGAG 6885
 DB 5512 TCATTGACATATTTTATGTCAGTATGATACAGAGAGAGAGAGAGAGAGAGAGAG 5571
 QY 6886 TTGTTTGAAG 6945
 DB 5572 TTGTTTGAAG 5631
 QY 6946 CATATCCATATTTTAT 7005
 DB 5632 CATATCCATATTTTAT 5691
 QY 7006 AGTTTAT 7064
 DB 5692 AGTTTAT 5751
 QY 7065 GCAT 7124
 DB 5752 GCAT 5811
 QY 7125 TGGATTCATTAATCTCTGCTGTGTAATTTTCTCCCTTATATATATATATATATATATAT 7184
 DB 5812 TGGATTCATTAATCTCTGCTGTGTAATTTTCTCCCTTATATATATATATATATATATAT 5871
 QY 7185 TCATCATCTTATCCCATATCTCATGATTTTCACTGAGCCCATATATATATATATATAT 7244
 DB 5872 TCATCATCTTATCCCATATCTCATGATTTTCACTGAGCCCATATATATATATATATATAT 5931
 QY 7245 GTTG 7248
 DB 5932 TTG 5935

RESULT 7
 AAD30660
 ID AAD30660 standard; DNA; 5935 BP.

XX AAD30660;
 AC 21-MAY-2002 (first entry)
 DT XX
 DE Mouse TIF beta genomic DNA.
 XX T cell derived inducible factor; TIF; interleukin-21; IL-21; mouse;
 KW STAT transcription factor; acute phase protein; inflammation; ds.
 OS Mus musculus.
 PN MO200210393-A2.
 XX 07-FEB-2002.
 PD 27-JUN-2001; 2001MO-US20485.
 PF 27-JUL-2000; 2000US-062617.
 PR (LUDW-) LUDWIG INST CANCER RES.
 XX Dumoutier L, Renaud J;
 PI WPI; 2002-195964/25.
 DR
 DX
 XX Stimulating expression of STAT transcription factor and inducing
 PT production of acute phase protein in a cell, involves contacting a cell
 PT capable of expressing STAT with T cell derived inducible factors -
 XX Example 9; Page 61-64; 64pp; English.
 PS
 XX The invention relates to nucleic acid molecules encoding T cell
 CC derived inducible factors (TIFs) also known as interleukin-21 (IL-21).
 CC TIF polynucleotides are upregulated by the cytokine, IL-9, IL-TIF or
 CC IL-21 molecules are implicated in activation of STAT transcription
 CC factors, acute phase proteins and inflammation. The present sequence
 CC is mouse TIF beta genomic DNA.
 XX
 SQ Sequence 5935 BP; 1732 A; 1174 C; 1346 G; 1683 T; 0 other;

Query Match 57.0%; Score 4245.2; DB 24; Length 5935;

Best Local Similarity 88.3%; Pred. No. 0; Mismatches 178; Indels 487; Gaps 20;

Matches 5039; Conservative 0;

QY 1971 TACCATGTCACCGAG 2030
 DB 293 TACCATGTCACCGAG 352
 QY 2031 AGGCTCTCTCTCACTTATCACTGTGACACTGTGCGATCTGATGCTGTCTGTGA 2090
 DB 353 AGGCTCTCTCTCACTTATCACTGTGACACTGTGCGATCTGATGCTGTCTGTGA 412
 QY 2091 GAAATCTATGAGTTTTCCTTATAGGGAGACTTTGGCCGACCTGCTCTCTCATTTG 2150
 DB 413 GAAATCTATGAGTTTTCCTTATAGGGAGACTTTGGCCGACCTGCTCTCTCATTTG 472
 QY 2151 CCGTGGGCGCCAG 2210
 DB 473 CCGTGGGCGCCAG 532
 QY 2211 CAATCTCCAGAGCGGTATCATGTGACACCGACCTTTATGTCGACAGAGAGAGAGAG 2270
 DB 533 CAATCTCCAGAGCGGTATCATGTGACACCGACCTTTATGTCGACAGAGAGAGAGAGAG 592
 QY 2271 GCATCTCTTCTCTCATATCCGCTTGGCATTTTCTCTGAGACACTTGAACCTGTTTG 2330
 DB 593 GCATCTCTTCTCTCATATCCGCTTGGCATTTTCTCTGAGACACTTGAACCTGTTTG 651
 QY 2331 GGGCGCTTATCTCCGAG 2390
 DB 652 GGGCGCTTATCTCCGAG 711

QY	2391	AGAGTGGGCTTTTTCATTTCAATTCATTTCAAGGCTCAGACCAATTCCTATCTTGGCT	2450
Db	712	AGGACTGGAATTTTTCTATTCTATTCTAATTCAGAGCTCAGACCAATTCCTATCTTGGCT	771
QY	2451	TCAGAGCACATATACCTGATATTTTATCTACAGAGCGCATTTAGAAAGCCACCAGACTG	2510
Db	772	TCAGAGCACATATACCTGATATTTTATCTACAGAGCGGCTTTAGAAAGCCACCAGACTG	831
QY	2511	CAATACCTTCCATTTCTCTGTGCTCTCTTCTGAACCTACATCTCTTGGCTACTCTGAG	2570
Db	832	CAATACCTTCCATCTCTGTGCTCTCTTCTGAACCTACATCTCTTGGCTACTCTGAG	891
QY	2571	ACCACATCGGAGACATACATCTCTAATACAGAGCTTTCTTCATCTCTGTGACCCAGG	2630
Db	892	ACCACATCGGAGACATACATCTCTAATACAGAGCTTTCTTCATCTCTGTGACCCAGG	951
QY	2631	CACCTTAGGGTTTTCTCTCTTTCAGAGCCAGCTTCAGATACCAACACAGAGCTCGGCTC	2690
Db	952	CACCTTAGGGTTTTCTCTCTTTCAGAGCCAGCTTCAGATACCAACACAGAGCTCGGCTC	1011
QY	2691	ATCGGGGAGAAACTGTTCCGAGAGTCACTAGTAACTCTCACTGTATGACAGAGGCTAG	2750
Db	1012	ATCGGGGAGAAACTGTTCCGAGAGTCACTAGTAACTCTCACTGTATGACAGAGGCTAG	1071
QY	2751	CTGGGGGAGCTGTGTGAGACCTCTGTGGATAGTCTGACGATACCCCTGTCTCTTGTCT	2810
Db	1072	CTGGGGGAGCTGTGTGAGACCTCTGTGGATAGTCTGACGATACCCCTGTCTCTTGTCT	1131
QY	2811	TACCTGCAGGCTTAAAGATCAGTGTCTACTGTATGAAGCAGGTGCTCAACTCAGCTGGAA	2870
Db	1132	TACCTGCAGGCTTAAAGATCAGTGTCTACTGTATGAAGCAGGTGCTCAACTCAGCTGGAA	1191
QY	2871	GACGTTCTGCTCCCCAGCTCAGACAGGTTCCAGCCCTACATGACAGAGGTGTACTCTTC	2930
Db	1192	GACGTTCTGCTCCCCAGCTCAGACAGGTTCCAGCCCTACATGACAGAGGTGTACTCTTC	1251
QY	2931	CTGACCAAACTCAGCAATCAGCTCAGCTCTGTGTAACTGTGACTCTGGCTACTATGCT	2990
Db	1252	CTGACCAAACTCAGCAATCAGCTCAGCTCTGTGTAACTGTGACTCTGGCTACTATGCT	1311
QY	2991	CCTCTCTCTCTCTCTTATTCAGATGAAGAACCCGAGGTCCTGACCCTCTCTCTTACACA	3050
Db	1312	CCTCTCTCTCTCTCTTATTCAGATGAAGAACCCGAGGTCCTGACCCTCTCTCTTACACA	1371
QY	3051	AGAGTGAAGAGGGCTCAGACACACACATCATAGGCACTTGGAAATAGTGCACAAAG	3110
Db	1372	AGAGTGAAGAGGGCTCAGACACACACATCATAGGCACTTGGAAATAGTGCACAAAG	1431
QY	3111	CTTTGGCTTCAATTGAGTAACTTGTGATTTGTATGTGATGAGTAAAGCTTATTTGTTATC	3170
Db	1432	CTTTGGCTTCAATTGAGTAACTTGTGATTTGTATGTGATGAGTAAAGCTTATTTGTTATC	1491
QY	3171	CATGGAAGAAATCACTCAAAATCTGTAGAGATGAGAAAGATGTGGAAACGAAAAAGG	3230
Db	1492	CATGGAAGAAATCACTCAAAATCTGTAGAGATGAGAAAGATGTGGAAACGAAAAAGG	1551
QY	3231	CCTAGATAGAGAAACAGATCTGCTGAGTATAGTACTTAT---GGGGGGAGCAGGGGCG	3286
Db	1552	CCTAGATAGAGAAACAGATCTGCTGAGTATAGTACTTAT---GGGGGGAGCAGGGGCG	1611
QY	3287	ATATTCACCTAGTACAGTACTTGTGTGGGAGAGAAATCACTGAGTACAGTACTTGTG	3346
Db	1612	ATATTCACCTAGTACAGTACTTGTGTGGGAGAGAAATCACTGAGTACAGTACTTGTG-	1669
QY	3347	GCATGAGAGATCCATGAGTACAAGTACTGTGTGGGGGAGGAAATGCGCACAGCAAAAGT	3406
Db	1670	GCATGAGAGATCCATGAGTACAAGTACTGTGTGGGGGAGGAAATGCGCACAGCAAAAGT	1697
QY	3407	TGAAGGGA---AGGAGATGAGAGAGGCTCATGTGTGGGGGTGTGAAGGTCACTGC-TT	3462
Db	1698	TGAAGGGAAGAGAGAGATGAGAGAGGCTCATATGTGTGGGGGTGTGAAGGTCACTGC-TT	1757
QY	3463	TTCCATGTGATGAGAGATTAAAGAAAACCAAGTGTGTGATTTGATGTCTTCAGACACCCC	3522

D	1758	TTCCATGTGATGAGAGTTAAGAAAATCACTGTGTGAAGTTTGAATGTCTTCAGACACCC	1817
Q	3523	CAACTATGAAACATATCCACGAGGAGCGGCGACGCTGGAGACCTGGCACTTTAGGAA	3582
D	1818	AA-----CTATGGCAGACTGTGGAGACCTGGCACTTTAGGAA	1855
Q	3583	GGCGCGCTTTTCACACGAGAAACTTTATGTCTACTCTGTGTCTAACCTCCACTTTG	3642
D	1856	GGCGCGCTTTTCACACGAGAACTTTATGTCTACTCTGTGTCTAACCTCCACTTTG	1915
Q	3643	ATGAGGTTACAGCTAGGTTTGCTTCTACCGCTTTCTCTACTGGTGGAAACTTCAGTAG	3702
D	1916	ATGAGGTTACAGCTAGGTTTGCTTCTACCGCTTTCTCTACTGGTGGAAACTTCAGTAG	1975
Q	3703	ATTCGCCAAGACGAGGACAGCTCTTCTGTAAAGGAGGACCTGGATTTCACTCTCTAG	3762
D	1976	ATTCGCCAAGACGAGGACAGCTCTTCTGTAAAGGAGGAGACCTGGATTTCACTCTCTAG	2035
Q	3763	AGAAAGAAATGCTCAGAGAACTTAAAGTCAACGTGAATCTAAGTCAACGCGGCAGAA	3822
D	2036	AGAAAGAAATGCTCAGAGAACTTAAAGTCAACGTGAATCTAAGTCAACGCGGCAGAA	2095
Q	3823	TGACGTAAACGCTCTATTTCCAGGTGAACGGTCACTGCGCTCAGATATACAGGATTTGG	3882
D	2096	TGACGTAAACGCTCTATTTCCAGGTGAACGGTCACTGCGCTCAGATATACAGGATTTGG	2155
Q	3883	GCTCCACCGGATTAAGATTCTGTAGTAGAGTCTGCTTTATTTTGCAGCAATCAGCGGT	3942
D	2156	GCTCCACCGGATTAAGATTCTGTAGTAGAGTCTGCTTTATTTTGCAGCAATCAGGTGT	2215
Q	3943	GACGACAGAAACATCCAGAGATGTCAAGAGCTGAAGGAGACAGTGAAGAAAGGTACTA	4002
D	2216	GACGACAGAAACATCCAGAGAAATGTCAAGAGCTGAAGGAGACAGTGAAGAAAGGTACTA	2275
Q	4003	TTGGCAAGCCCAATPACTAAGCCATTAGTAGAGAGCTGGGAAATTTCTTCTCTGCTTC	4062
D	2276	TTGGCAAGCCCAATPACTAAGCCATTAGTAGAGAGCTGGGAAATTTCTTCTCTGCTTC	2335
Q	4063	CCAGTCCCTTCTACTTTGTAACTTTTATTTGACTTGTCTACTATCTGTCATTAACCTG	4122
D	2336	CCAGTCTCTTCTACTTTGTAACTTTTCTTTTGACTTGTCTACTGTCATTAACCTG	2395
Q	4123	CTTAGCTGCACCTGTATCTAGCTGGGTCTATAGATCTTTCATCTGTCTAAATTTGTA	4182
D	2396	CTTAGCTGCACCTGTATCTAGCTGGGTCTATAGATCTTTCATCTGTCTAAATTTGTA	2455
Q	4183	AGTCACAATTTGAGAGCTAGAGAAAGCTTAGCTCAGCCAGTCTCATAAGACACTTTGCTG	4242
D	2456	AGTCACAATTTGAGAGCTAGAGAAAGCTTAGCTCAGCCAGTCTCATAAGACACTTTGCTG	2515
Q	4243	GAGGTGGCTTGTACACAGAGTCAATGTGTAGAAAGACAGATCCCTGATTTCCAGCTGTGA	4302
D	2516	GAGGTGGCTTGTACACAGAGTCAATGTGTAGAAAGACAGATCCCTGATTTCCAGCTGTGA	2575
Q	4303	CTTGCTAGTGGCATGTGTAAATTAATCTTTGGCTTGATTAAGTATTTGGGAAAGCCAGTTC	4362
D	2576	CTTGCTAGTGGCATGTGTAAATTAATCTTTAGCTTGATTAAGTATTTGGGAAAGCCAAATTC	2635
Q	4363	CCAGGAGCTTCAATATTTGAAGAACATGTATTGAAAACCTAGAAAGCTGGGCACTAACT	4422
D	2636	CCAGGAGCTTCAATATTTGAAGAACATGTATTGAAAACCTAGAAAGCTGGGCACTAACT	2695
Q	4423	TACTAGAGATATTTTGAAGCTCAATTAACCGATGCTCTGAAATGTGGCAAAATCAACCC	4482
D	2696	TACTAGAGATATTTTGAAGCTCAATTAACCTGATTAACCTGATTAACCTGATTAACCTG	2755
Q	4483	AGAAATTAACAAGAGCTGAGTTTGGCAATAGACACAAGTATTTAGAACTACTGTATTT	4542
D	2756	AGAAATTAACAAGAGCTGAGTTTGGCAATAGACACAAGTATTTAGAACTACTGTATTT	2815
Q	4543	AATAGCTATCATCTTAATTAATATAGGCGCTATAT---TATATTTAAGATTAACA	4598

Db 2816 AACAGTGCATCTTAATAAATAAGTGTCTTAATTAAGTGCCTTAATAAGTTAAACA 2875
 QY 4599 CAAGATGATAGAGCTCCCAATTTACTTGGCTGTTTCAAAAAGATTAATAATAGTC 4658
 Db 2876 CAAGATGATAGAGCTCCCAATTTACTTGGCTGTTTCAAAAAGATTAATAATAGTC 2935
 QY 4659 AAGGATTAATTAAGTGTCAATGAAGATGAAGAACCTTTCTTAATTTAACT 4718
 Db 2936 AATGATTAATTAAGTGTCAATGAAGATGAAGAACCTTTCTTAATTTAACT 2995
 QY 4719 TCAATTTCTAGT-----TTTTTTTCTCAACCCCTGATCAAGCCACTAGTAAGACCT 4773
 Db 2996 TCAATTTCTAGTATTATTTTCTTCTCAACCCCTGATCAAGCCACTAGTAAGACCT 3055
 QY 4774 ATCTGCTGATGATTAATTAATGAATTTAAGCAAAACAATGCTGTGTGCTCTTTGG 4833
 Db 3056 ATCTGCTGATGATTAATTAATGAATTTAAGCAAAACAATGCTGTGTGCTCTTTGG 3115
 QY 4834 GGAAGGAAACAGATAGCAGAGAGCTCAGGCTAGCAAGTCT-GACTTGCCCTAAAGCCAG 4892
 Db 3116 GGAAGGAAACAGATAGCAGAGAGCTCAGGCTAGCAAGTCTGAGCTCAACCTAAAGCCAG 3175
 QY 4893 AAGCAATGATTAATGAAGAAAGTGAAGGCTCTTCCAGAGTGGTGTAGTATCA 4952
 Db 3176 AAGCAATGATTAATGAAGAAAGTGAAGGCTCTTCCAGAGTGGTGTAGTATCA 3235
 QY 4953 GAAACAGAGAGCTCCGCTGATGATTAATGAATTAATGATTAATGATTAATGATTAATG 5009
 Db 3236 GAAACAGAGAGCTCCGCTGATGATTAATGAATTAATGATTAATGATTAATGATTAATG 3295
 QY 5010 TCTATGAACTTAATAGTCTCTTTTCTTGTGTAGGCTGATTAACACACTGTTTTC 5069
 Db 3296 TCTATGAACTTAATAGTCTCTTTTCTTGTGTAGGCTGATTAACACACTGTTTTC 3355
 QY 5070 TTTTGAAGTGTCAATGCTTGTAGTATTTTAAAGTGTGCTGCAATCTGTTTAAAGGTTT 5129
 Db 3356 TTTTGAAGTGTCAATGCTTGTAGTATTTTAAAGTGTGCTGCAATCTGTTTAAAGGTTT 3415
 QY 5130 GTTACTTGAACACTGAGCTTGTAGTATTTAGCATGCCAAAGCACACTTCTGAATGCT 5189
 Db 3416 GTTACTTGAACACTGAGCTTGTAGTATTTAGCATGCCAAAGCACACTTCTGAATGCT 3475
 QY 5190 GTGTAAAGGTTATTAATCTTACTTGTCTTGTGAAGTGAAGCTGTGTGAAG 5249
 Db 3476 GTGTAAAGGTTATTAATCTTACTTGTCTTGTGAAGTGAAGCTGTGTGAAG 3535
 QY 5250 AACTCAGAGAGATGATCTCTGTGGAAGAACTTTTCCCTTAATGCTTA 5309
 Db 3536 AACTCAGAGAGATGATCTCTGTGGAAGAACTTTTCCCTTAATGCTTA 3594
 QY 5310 TCCACTTTCAGTCACTTGTGATTTTATACATGCTGTCAATGAAGAGTGTTTAGCC 5369
 Db 3595 TCCACTTTCAGTCACTTGTGATTTTATACATGCTGTCAATGAAGAGTGTTTAGCC 3654
 QY 5370 CGCTCTCATAGCTCTGGAAGAAACCAATAGGGAAGATGTTATGCTGAAGAACTG 5429
 Db 3655 CGCTCTCATAGCTCTGGAAGAAACCAATAGGGAAGATGTTATGCTGAAGAACTG 3714
 QY 5430 ACCGGAAGGGAATGCTGTAGAGCTCCCGAAGAACCAACAGAGTGTGAAGAAC 5489
 Db 3715 ACCGGAAGGGAATGCTGTAGAGCTCCCGAAGAACCAACAGAGTGTGAAGAAC 3774
 QY 5490 GTCCAGAGTGGCTCATGATTAATGAATGAACAGAGGAGGAGATTAAGCTTAACAAAGT 5549
 Db 3775 GTCCAGAGTGGCTCATGATTAATGAATGAACAGAGGAGGAGATTAAGCTTAACAAAGT 3834
 QY 5550 TCAATGAGTCCGAGTCTTAAAGATTAACAAATAGCTCTTGGGCTTATTAACAAAGAG 5609
 Db 3835 TCAATGAGTCCGAGTCTTAAAGATTAACAAATAGCTCTTGGGCTTATTAACAAAGAG 3894
 QY 5610 TCTGGGAAGGAGAGAG--TGAGAGGGAATGGAAGGGAAGGGAAGAGAGATGTAGAGAG 5666
 Db 3895 TCTGGGAAGGAGAGAGAGATTTAGAGGGAAGTGAAGGGAAGGGAAGAGAG--AATGTAGAGAG 3952

QY 5667 CTGGAACAGCTCAAAATCTCTCAACAGAGATTTTCTTGAACAATCTAGAA-----GGT 5722
 Db 3953 TTTGAAAGAGCTCAAAATCTCTCAACAGAGATTTTCTTGAAGATCTAGAAAGAGGT 4012
 QY 5722 AGTGAATTAAGT-GATGAGAGGAGACTGCTTTGCAATTAATCTGAGTGTGCTC 5781
 Db 4013 GGTGAATTAAGTGAATTCGCAAGAGACTGCTTTGCAATTAATCTGAGTGTGCTC 4072
 QY 5782 TCCATTAAGTGAAGAGCTCAACC-TTTTTCACCTGATGAGAGAGGAAAGAGGCT 5840
 Db 4073 TCCATTAAGTGAAGAGCTCAACCCTTTTTCACCTGATGAGAGAGGAAAGAGGCT 4132
 QY 5841 GTTATGATCTCTACCTGAGTGTGATTTTAAAGTGAAGAGAGAGAGAGAGAGAGAGAG 5900
 Db 4133 GTTATGATCTCTACCTGAGTGTGATTTTAAAGTGAAGAGAGAGAGAGAGAGAGAGAG 4192
 QY 5901 CTCTTGAC-----AAAAAATGGAACCTGTTGTTGCTGTTGTTGTTGTTGTTG 5950
 Db 4193 CTCTTGACAAAAAATGGAACCTGTTGTTGCTGTTGTTGTTGTTGTTGTTG 4252
 QY 5951 TTAAGAAAGCACA----- 5963
 Db 4253 TTAAGAAAGCACAAGAGAGCTGGGCAATGAGGCCATGCTTTAATCCAGAGATTGGAG 4312
 QY 5964 ----- 5963
 Db 4313 GCAAGAGCAGTGAATTTCAATTCAGGCGAGCTGCTTCAAAAGTGAATTCAGAG 4372
 QY 5964 ----- 5963
 Db 4373 CAGCAGGCTTACAGAGAAACCTGTCTCGGAAAAAAGAGAGAGAGAGAGAGAGAGAG 4432
 QY 5964 ----- 5963
 Db 4433 AAAAG 4492
 QY 5964 ----- 5963
 Db 4493 GAG 4552
 QY 5964 ----- 5963
 Db 4553 GAG 4612
 QY 5964 -----GCAAGGCCGACCATGGT 5985
 Db 4613 AAGAGAAAAAAGAAAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 4672
 QY 5986 TGAATGTGGCTCTTGAATCAAGCTTTTGAATGAGTCAATCAATGATGATGATG 6045
 Db 4673 CGTATGTGGCTCTTGAATCAAGCTTTTGAATGAGTCAATCAATGATGATGATG 4732
 QY 6046 TCAAGTGAAGGCTTACCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6105
 Db 4733 TCAAGTGAAGGCTTACCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4792
 QY 6106 TCTCAGTATCACTTCTGTCTTACAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6165
 Db 4793 TCTCAGTATCACTTCTGTCTTACAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4852
 QY 6166 CCCCCCTAAATTTAATGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6225
 Db 4853 CCCCCCTAAATTTAATGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4912
 QY 6226 GATCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6285
 Db 4913 GATCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4972
 QY 6286 TATGAGTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 6345
 Db 4973 TATGAGTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5031

Qy	6346	CATGATTTTAAAGGCTTGCGCAAAATCAATTAATCTCATGCTAAAAAATACATTAATGTTGA	6405
Dp	5032	CATGATTTTAAAGGCTTGCGCAAAATCAATTAATCTCATGTTAAAATGCAATTAAGTTGA	5091
Qy	6406	TTAATTAATCTTTTAAGAGAAGGCTGATACCTTGTTTTGGTGTCTACGACAAAGCAATGTCAAC	6465
Dp	5092	TTATCAATCTTTTAAGAGAAGGCTGATACCTTGTTTTGGTGTCTACGACAAATGTCAAC	5151
Qy	6466	AGCTCTTTCTAACTGCTACCACTTTAGAAAATGCTACTGTGTCTCAATTTGGTTGTATT	6525
Dp	5152	AGCTCTTTCTAACTGCTACCACTTTAGAAAATGCTACTGTGTCTCAATTTGGTTGTATT	5211
Qy	6526	CTTAATTTTCAATAGCTTGAGAGAGGTGAGAGATCAAGGCGAATTTGGGGAACTGACCTGCT	6585
Dp	5212	CTTAATTTTCAATAGCTTGAGAGAGGTGAGAGATCAAGGCGAATTTGGGGAACTGACCTGCT	5271
Qy	6586	GTTTAATGTCTGTAGAAAATGCTTGCGTGTGCGAGAGAAAGCTTAGAAAACGAAAGACTG	6645
Dp	5272	GTTTAATGTCTGTAGAAAATGCTTGCGTGTGCGAGAGAAAGCTTAGAAAACGAAAGACTG	5331
Qy	6646	CTCCTTCCTGCTCTCTAAAGAACAATCAATCCGTAATGAGACTTTTTAATAAGAA	6705
Dp	5332	CTCCTTCCTGCTCTCTAAAGAACAATCAATCCGTAATGAGACTTTTTAATAAGAA	5391
Qy	6706	AAGTAGAAGCTAAAGTCCATCATCATTTAGAAAGATTTGCATGAAACCTGGCTCAGTTGA	6765
Dp	5392	AAGTAGAAGCTAAAGTCCATCATCATTTAGAAAGATTTGCATGAAACCTGGCTCAGTTGA	5451
Qy	6766	AAAAAATAATGTGTCAAGTGTGCTCATGAGACACAGAGGTAGACTTTGATTAACCAAAAGAT	6825
Dp	5452	AAAAAATAATGTGTCAAGTGTGCTCATGAGACACAGAGGTAGACTTTGATTAACCAAAAGAT	5511
Qy	6826	TCATTGACAAATATTTTATGTCACTGATGATACACAGAAAAATAATGTACTTTAAAAAA	6885
Dp	5512	TCATTGACAAATATTTTATGTCACTGATGATACACAGAAAAATAATGTACTTTAAAAAA	5571
Qy	6886	TTGTTTGAAGAGAGTTACCTCTCATTCCTTTAGAAAAAAAGCTTAGTAACTTCATTTC	6945
Dp	5572	TTGTTTGAAGAGAGTTACCTCTCATTCCTCTAGAAAAAAAGCTTAGTAACTTCATTTC	5631
Qy	6946	CATATCCAAATTTTATATATATGTAAGTTATTTATTAAGATTAACATTTATTTATTTGTC	7005
Dp	5632	CATATCCAAATTTTATATATATGTAAGTTATTTATTAAGATTAACATTTATTTATTTGTC	5691
Qy	7006	AGTTTATTAATATGGAATTTATTTATAGAAACATTAATCTGCAATTTGATATTT-AGTATAG	7064
Dp	5692	AGTTTATTAATATGGAATTTATTTATAGAAACATTAATCTGCAATTTGATATTTGAGATTA	5751
Qy	7065	GCAAAATAATTTTATGACAAATACATGATGGAACAAAGATATCTTAGGCTTTAATAACCA	7124
Dp	5752	GCAAAATAATTTTATGATTAATPACTATGAAACAAAGATATCTTAGGCTTTAATAACCA	5811
Qy	7125	TGGATTAATCAATAAATCTTGTCTGTGTAATTTTCTCCCTTAATAATCAACAAATACCATCA	7184
Dp	5812	TGGATTAATCAATAAATCTTGTCTGTGTAATTTTCTCCCTTTAATAATCAACAAATACCATCA	5871
Qy	7185	TCATCATCATTAACCAATCATCTTCATGATTTTCATGCTTGACCAATTAATACCTGTAA	7244
Dp	5872	TCATCATCATTAACCAATCATCTTCATGATTTTCATGCTTGACCAATTAATACCTGTAA	5931
Qy	7245	GTTG 7248	
Dp	5932	TTTG 5935	
RESULT 8			
AAD27153			
ID	AAD27153 standard; DNA; 5935 BP.		
XX	AAD27153;		
XX	09-APR-2002 (first entry)		
XX			

DE	Mouse T cell derived inducible factor (TIF) beta genomic DNA.
XX	
KW	T cell derived inducible factor; TIF; cytokine; interleukin-9; IL-9;
KW	protein therapy; STAT activation; differentiation; mouse; ds.
XX	
OS	Mus musculus.
XX	
PN	US6331613-B1.
PD	18-DEC-2001.
XX	
PF	18-OCT-1999; 99US-0419568.
XX	
PR	26-OCT-1998; 98US-0178973.
XX	16-JUL-1999; 99US-0354243.
PA	(LUDW-) LUDWIG INST CANCER RES.
PI	Dumoutier L, Louhed J, Renaud J;
DR	WPI; 2002-105277/14.
PT	Nucleic acid encoding T cell derived inducible factors useful for
PT	inducing STAT activation in cells -
XX	
PS	Claim 1; Column 37-44; 24pp; English.
CC	The present invention relates to an isolated nucleic acid molecule, which
CC	encodes a T cell derived inducible factor comprising an amino acid
CC	sequence encoded by 6 defined nucleotide sequences. The nucleic acid
CC	molecules are shown to be up regulated by the cytokine interleukin-9
CC	(IL-9) and are described as T Cell Derived Inducible Factors (TIFs). The
CC	invention is used in protein therapy. The nucleic acid molecules encode
CC	proteins which induce STAT activation in cells. They can be used, for
CC	example, in the stimulation or regeneration of targeted tissues.
CC	Further, their inhibitors or antagonists can be used to retard, prevent
CC	or inhibit differentiation of other tissues. The present sequence is
CC	mouse TIF beta genomic DNA.
SQ	Sequence 5935 BP, 1732 A; 1174 C; 1346 G; 1683 T; 0 other;
	Query Match 57.0%; Score 4245.2; DB 24; Length 5935;
	Best Local Similarity 88.3%; Pred. No. 0;
	Matches 5039; Conservative 0; Mismatches 178; Indels 487; Gaps 20;
OY	1971 TACCATGCTAACCGAGCAATGCTCCCTGGATGTCTTTTGCTTCCTCACTTAAC 2033
DB	293 TACCATGCTAACCGAGCAATGCTCCCTGGATGTCTTTTGCTTCCTCACTTAAC 352
OY	2031 AGGCTTCCTTCATCTAATCAACTGTGAACAATTGGGATCTCGATCGGTGCCGCA 2099
DB	353 AGGCTTCCTTCATCTAATCAACTGTGAACAATTGGGATCTCGATCGGTGCCGCA 412
OY	2091 GAATCTATGAGTTTTTCCCCTTAATGGGAACTTTGGCCGCACGCTGCTTCATTTGC 2156
DB	413 GAATCTATGAGTTTTTCCCCTTAATGGGAACTTTGGCCGCACGCTGCTTCATTTGC 472
OY	2151 CTGTGGGCCCGAGAGCAATGCGCTGCGCTCAACACCCGGTGCAGAGCTTAGAGTGC 2210
DB	473 CCTGTGGGCCCGAGAGCAATGCGCTGCGCTCAACACCCGGTGCAGAGCTTAGAGTGC 532
OY	2211 CAACCTTCAGAGCGCGATACATCGTCAACCCGACCTTATGCTGGCCAAGAGGTACACT 2270
DB	533 CAACCTTCAGAGCGCGATACATCGTCAACCCGACCTTATGCTGGCCAAGAGGTACACT 592
OY	2271 GCATCTCTTTCTCTCAATACCGCCTTGCAATTTCTCTGAAGCACTTGCAACTCTTTAG 2330
DB	593 GCATCTCTTTCTCTCAATACCGCCTTGCAATTTCTCTGAAGCACTTGCAACTCTTTAG 651
OY	2331 GGGGGCTTATCTCCGAGGCTCTACATACCTATGTTTTCTCTCTTTAGAGACTCTTTA 2390
DB	652 GGGGGCTTATCTCCGAGGCTCTACATACCTATGTTTTCTCTCTTTAGAGACTCTTTA 711

QY 2391 AGGACGAGGCTTTTCTATTTCTATTTCAAGGCTCAGGACCAATTTCTATGTCCTT 2450
DB 712 AGGACGAGGCTTTTCTATTTCTATTTCAAGGCTCAGGACCAATTTCTATGTCCTT 771
QY 2451 TCAGGACACATATAGTATTTTATCTACAGAGCGCATTTAGAAAAGCCACGACGACTG 2510
DB 772 TCAGGACACATATAGTATTTTATCTACAGAGCGCGTTTAGAAAAGCCACGACGACTG 831
QY 2511 CAATACCTTTCATTTCTCTGTCCTCTCTCTGTAATCATACCTCTTGGCTACTCTGAG 2570
DB 832 CAATACCTTTCATTTCTCTGTCCTCTCTCTGTAATCATACCTCTTGGCTACTCTGAG 891
QY 2571 ACCCACTGGGGAATATATCTCTACTACAGGCTTTTCTTCCATCTCTCTGTGACCCAGG 2630
DB 892 ACCCACTGGGGAATATATCTCTACTACAGGCTTTTCTTCCATCTCTCTGTGACCCAGG 951
QY 2631 CACTTGAAGGTTTCTCTCTTTCAGGCGAGCTTGCAGATTAACAACAGAGCTCCGAGCTC 2690
DB 952 CACTTGAAGGTTTCTCTCTTTCAGGCGAGCTTGCAGATTAACAACAGAGCTCCGAGCTC 1011
QY 2691 ATCGGGGAGAACTGTTCCGAGAGTCACTGTAAGTCTCACTGTGATGAGCAGGCTAG 2750
DB 1012 ATCGGGGAGAACTGTTCCGAGAGTCACTGTAAGTCTCACTGTGATGAGCAGGCTAG 1071
QY 2751 CTGCGGGAGCTGTGAGACCTCTGCGGATAGTCTGACGTATGACCCCTGCTGCTTCTTGTG 2810
DB 1072 CTGCGGGAGCTGTGAGACCTCTGCGGATAGTCTGACGTATGACCCCTGCTGCTTCTTGTG 1131
QY 2811 TACCTGAGGCTAAAGTCACTGCTACTGATGAAAGAGGCTGCACTTCAACCTGGA 2870
DB 1132 TACCTGAGGCTAAAGTCACTGCTACTGATGAAAGAGGCTGCACTTCAACCTGGA 1191
QY 2871 GAGCTTGTGCTCCCGAGTCAAGAGGTTCCAGGCTTCAACAGCAGAGGCTGCTTTC 2930
DB 1192 GAGCTTGTGCTCCCGAGTCAAGAGGTTCCAGGCTTCAACAGCAGAGGCTGCTTTC 1251
QY 2931 CTGACCAAACTCAGCAATCAGCTCAGCTCCTGTGTAAAGTCTGACTGTGCTACTATGCT 2990
DB 1252 CTGACCAAACTCAGCAATCAGCTCAGCTCCTGTGTAAAGTCTGACTGTGCTACTATGCT 1311
QY 2991 CCTCTCTCTCTCTTCTTCTTATTCAGTAAAGACCGAGGCTCTGCGCTCTCTCTTCA 3050
DB 1312 CCTCTCTCTCTCTTCTTATTCAGTAAAGACCGAGGCTCTGCGCTCTCTCTTCA 1371
QY 3051 AGAGTGAAGGCGCTCAGACCAACCATATAGGCACTTGAATAGGTCACAAAG 3110
DB 1372 AGAGTGAAGGCGCTCAGACCAACCATATAGGCACTTGAATAGGTCACAAAG 1431
QY 3111 CTTTGGCTTCAATTGAGTAACTCTTGAATGATGATGAGGCTTATTTGTTTATC 3170
DB 1432 CTTTGGCTTCAATTGAGTAACTCTTGAATGATGATGAGGCTTATTTGTTTATC 1491
QY 3171 CAGGAAAGAAATCACTCAAAATCTGTAGATGAGAAAGTGTGGAGAGGAAAG 3230
DB 1492 CAGGAAAGAAATCACTCAAAATCTGTAGATGAGAAAGTGTGGAGAGGAAAG 1551
QY 3231 CCTAGATAGAGAAACAGATCTGTAGATAGTACTTAT-----GGGGGGAACAAGGGGCG 3286
DB 1552 CCTAGATAGAGAAACAGATCTGTAGATAGTACTTAT-----GGGGGGAACAAGGGGCG 1611
QY 3287 ATATCACTAGTCAAGTACTTGTGGGAGAGAAATCCACTGATCAATGATCTTGTG 3346
DB 1612 ATATCACTAGTCAAGTACTTGTGGGAGAGAAATCCACTGATCAATGATCTTGTG - 1669
QY 3347 GCATGAGATCACTGAGTACAAGTACTTGTGGGGGAGAGGAAATGGCAACAAGCAAAAGT 3406
DB 1670 -----GGGGGGAAGAAATGGCAACAAGCAAAAGT 1697
QY 3407 TGAAGGGA---AGGAAGATGAGAGAGCTCAATGTTGGGGGTGTGAAGGCTCACTCC-TT 3462
DB 1698 TGAAGGGAAGAGAGATGAGAGGCTCAATGTTGGGGGTGTGAAGGCTCACTCC-TT 1757
QY 3463 TTCAATGTATGAGAGATTAAAGAAAACCAAGTGTGTGATTTGATGCTTTCAGACACCCC 3522

DB 1758 TTCAATGTATGAGAGATTAAAGAAAATCAAGTGTGTGATTTGATGCTTTCAGACACCCC 1817
QY 3523 CAATATGAACATATCCAGAGAGCGGGCAGACTGTGTGGAGACCTGGCACTTTAGGGA 3582
DB 1818 AA-----CTATGCGAGACTGTGTGGAGACCTGGCACTTTAGGGA 1855
QY 3583 GGGCGGCTTTTCAACGAGAAATTTAGGCTATCTGTGTGCTACATCCACCTTG 3642
DB 1856 GGGCGGCTTTTCAACGAGAAATTTAGGCTATCTGTGTGCTACATCCACCTTG 1915
QY 3643 ATGAGGTAGGCTCAGGTTTCTGTTCTACCGTTTCTGTACTAGTGTGAATCTCAGTAG 3702
DB 1916 ATGAGGTAGGCTCAGGTTTCTGTTCTACCGTTTCTGTACTAGTGTGAATCTCAGTAG 1975
QY 3703 ATTTCCCAAGAGAGAGAGAGCTTCTGTAAAGGAGGAGCTGTGATTTCACTGTCTAG 3762
DB 1976 ATTTCCCAAGAGAGAGAGAGCTTCTGTAAAGGAGGAGCTGTGATTTCACTGTCTAG 2035
QY 3763 AGAAGAAATAGCTCAGAGATTTAGTCAAGTGAATCTTAGTCTACAGCGGGCAAAA 3822
DB 2036 AGAAGAAATAGCTCAGAGATTTAGTCAAGTGAATCTTAGTCTACAGCGGGCAAAA 2095
QY 3823 TGACTGAAGGCTCTATTTCCAGGTGAACGCTCACGCTCCAGATATACCTGAGGTATTG 3882
DB 2096 TGACTGAAGGCTCTATTTCCAGGTGAACGCTCACGCTCCAGATATACCTGAGGTATTG 2155
QY 3883 GCTCCACCGGATTAAGTCTGTAGTGAAGTCTGCTTTTATTTTGAGGACATCAGCGGT 3942
DB 2156 GCTCCACCGGATTAAGTCTGTAGTGAAGTCTGCTTTTATTTTGAGGACATCAGTGGT 2215
QY 3943 GACGACGAAATCCAGAGAAATGTCAAGAGCTGAAGAGACACTGAAAAAGTACTA 4002
DB 2216 GACGACGAAATCCAGAGAAATGTCAAGAGCTGAAGAGACACTGAAAAAGTACTA 2275
QY 4003 TTGGCAAGCAATCTAAGGCTTCAAGGAGAGCGTGGGATTTCTTCTCTGCTTTC 4062
DB 2276 TTGGCAAGCAATCTAAGGCTTCAAGGAGAGCGTGGGATTTCTTCTCTGCTTTC 2335
QY 4063 CCACTCCCTTCTACTTTGTAACATTTTATTTGACTGTCTACTAGTGTGCTACTG 4122
DB 2336 CCACTCTTCTTCTACTTTGTAACATTTTATTTGACTGTCTACTAGTGTGCTACTG 2395
QY 4123 CTTAGCTGACCTGTATCTAGCTGGGTCTATAGATCTTTCATCTGTGTAAATTTGA 4182
DB 2396 CTTAGCTGACCTGTATCTAGCTGGGTCTATAGATCTTTCATCTGTGTAAATTTGA 2455
QY 4183 AGTCACAATTTGAGAGCTGACAGAAAGCTTAGTCAAGCAAGTCTCATGAGCACTTGTCTG 4242
DB 2456 AGTCACAATTTGAGAGCTGACAGAAAGCTTAGTCAAGCAAGTCTCATGAGCACTTGTCTG 2515
QY 4243 GAGGATGGCTTGTGACAGAGTCAATGCTGAAGAGACAGCACTCTGATTTCCAGCTGCA 4302
DB 2516 GAGGATGGCTTGTGACAGAGTCAATGCTGAAGAGACAGCACTCTGATTTCCAGCTGCA 2575
QY 4303 CTTGCTAGTGGCAGTGTATTTACTTTGGCTGTATTAAGTATTTGGAAAGCCAGTTT 4362
DB 2576 CTTGCTAGTGGCAGTGTATTTACTTTAGCTGTATTAAGTATTTGGAAAGCCAGTTT 2635
QY 4363 CCAAGGACCTAATCTGAAGAACATGCAATTTGAAAGCTTGAAGAGCTGGGCAAACT 4422
DB 2636 CCAAGGACCTAATCTGAAGAACATGCAATTTGAAAGCTTGAAGAGCTGGGCAAACT 2695
QY 4423 TACTAGAGATATTTTGAAGCTCAATTAAGAGAGTCTGAATTTGTGCAAAATCAACCC 4482
DB 2696 TACTAGAGATATTTTGAAGCTCAATTAAGAGAGTCTGAATTTGTGCAAAATCAACCC 2755
QY 4483 AGAATTAACAACAAAGAGCTGATTTGCAATTAAGAGCAAGTATTTAGATCACTGTATT 4542
DB 2756 AGAATTAACAACAAAGAGCTGATTTGCAATTAAGAGCAAGTATTTAGATCACTGTATT 2815
QY 4543 AATAGCTATCATCTTAATTAATTAAGGCTTATATA-----TATATTTAAAGTTAAACA 4598

Db 2816 AACGCTCATCTTAATTAATAATAGTGTCTTTAGCTGCTTAATTAAGATTAACA 2875
Qy 4599 CAAGAGTGAATAGCTCCCAATTTACTGCTGCTTTCAAAAGAGTAAATATCAGTC 4658
Db 2876 CAAGAGTGAATTAATCTCCCAATTTACTGCTGCTTTCAATAGAGTAAATATCAGTC 2935
Qy 4659 ATGAGTAAATTAATAGTGTCAATGAAGATAGAGTGAACCTTTCTTACTTTTACT 4718
Db 2936 ATAGATTAATTAATAGTGTCAATGAAGATAGAGTGAACCTTTCTTACTTTTACT 2995
Qy 4719 TCATTTCTTACTGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4773
Db 2996 TCATTTCTTACTGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3055
Qy 4774 ATCTGCTGTAGCTAATTAATAGTGTCAATGAAGATAGAGTGAACCTTTCTTACTTT 4833
Db 3056 ATCTGCTGTAGCTAATTAATAGTGTCAATGAAGATAGAGTGAACCTTTCTTACTTT 3115
Qy 4834 GGAAGGAAACAGATAGAGTGAAGCTCAGGCTAGCAAGTCT-GACTTCCCTTAAAGCAG 4892
Db 3116 GGAAGGAAACAGATAGAGTGAAGCTCAGGCTAGCAAGTCTGACTCAACCTTAAAGCAG 3175
Qy 4893 AGGATGTTGATAGAGTGAAGTGAAGCTTCTGAGTGGTGTGCTTAAGTATCA 4952
Db 3176 AGGATGTTGATAGAGTGAAGTGAAGCTTCTGAGTGGTGTGCTTAAGTATCA 3235
Qy 4953 GAAACAGAAAGCTCCGCTGATGAATTAATCAGTAAAGATTAATCCTTATCTC---CT 5009
Db 3236 GAAACAGAAAGCTCCGCTGATGAATTAATCAGTAAAGATTAATCCTTATCTCCTCTCT 3295
Qy 5010 TCTATGAACTTAATGCTCTCTTTTCTTGTGTGATGAGCTGATTAACACACTTTGTTTC 5069
Db 3296 TCTATGAACTTAATGCTCTCTTTTCTTGTGTGATGAGCTGATTAACACACTTTGTTTC 3355
Qy 5070 TTTTGAAGTTCAGTCTTTGATTTTGAATTTTGAAGTCTGCAAGTCTTGTGTAAGGGTTT 5129
Db 3356 TTTTGAAGTTCAGTCTTTGATTTTGAATTTTGAAGTCTGCAAGTCTTGTGTAAGGGTTT 3415
Qy 5130 GTTACCTTGAACCTGCTGCTTGTAGTATGATGATGATGATGATGATGATGATGATGATG 5189
Db 3416 GTTACCTTGAACCTGCTGCTTGTAGTATGATGATGATGATGATGATGATGATGATGATG 3475
Qy 5190 GTGTAAAGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5249
Db 3476 GTGTAAAGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3535
Qy 5250 AACTCAGAGAGATGCTGCTGCTGATGAAACCTTTTCTTCTTCTTCTTCTTCTTCTTCTT 5309
Db 3536 AACTCAGAGAGATGCTGCTGCTGATGAAACCTTTTCTTCTTCTTCTTCTTCTTCTTCTT 3594
Qy 5310 TCCACTTTCAGTCACTTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5369
Db 3595 TCCACTTTCAGTCACTTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3654
Qy 5370 CGCTCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5429
Db 3655 CGCTCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3714
Qy 5430 ACCGCGAGGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5489
Db 3715 ACTGCGAGGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3774
Qy 5490 GTCCAGAGTGGGCTCATGTAATGAATGAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5549
Db 3775 GTCCAGAGTGGGCTCATGTAATGAATGAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3834
Qy 5550 TCATAGAGTCCGAGTCTTAAAGATCAAAATAGCTCTTGGGCTTCAATACAAAGGAG 5609
Db 3835 TCATAGAGTCCGAGTCTTAAAGATCAAAATAGCTCTTGGGCTTCAATACAAAGGAG 3894
Qy 5610 TCTGGAAGGAGAGAG---TGAGAGGAAATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5666
Db 3895 TCTGGAAGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3952
Qy 5667 CTTGAACAGCTCAAAATCTCTTACAGAGATTTTCTTGAACAATTCAGAA---GGT 5722
Db 3953 TTTGAACAGCTCAAAATCTCTTACAGAGATTTTCTTGAAGAATTCAGAAAGAGGT 4012
Qy 5723 AGTGAATTAAGT-GATTGAGAGGAGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 5781
Db 4013 GGTGAATTAAGTGAATGAG 4072
Qy 5782 TCCATGAGGTTGAAGAGCTCAACC-TTTTACCTCGAATGAGAGAGAGAGAGAGAGAGAGAG 5840
Db 4073 TCCATGAGGTTGAAGAGCTCAACCCTTTTACCTCGAATGAGAGAGAGAGAGAGAGAGAGAG 4132
Qy 5841 GTTATAGCTCTAATCTGAGATTTTACTTACTTAAATGGAACAGACACTGCGGACCTC 5900
Db 4133 GTTATAGCTCTAATCTGAGATTTTACTTACTTAAATGGAACAGACACTGCGGACCTC 4192
Qy 5901 CTCTTGAC-----AAAAAATGGAACCTGTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 5950
Db 4193 CTCTTGACAGAAAAAAG 4252
Qy 5951 TTAAGAAAGCACA----- 5963
Db 4253 TTAAGAAAGCACAAGCAGCTGGGCTAGTGGCCATGCTTATCCAGACTTGGGAG 4312
Qy 5964 ----- 5963
Db 4313 GCAGAGGAGGTGACTTTCTTAATTCAGGCCAGCTGCTCTCAAAAGTATTCAGGA 4372
Qy 5964 ----- 5963
Db 4373 CAGCCAGGCTATACAGAGAAACCTGCTCTCGGAAAAAAGAGAGAGAGAGAGAGAGAGAGAG 4432
Qy 5964 ----- 5963
Db 4433 AAAAG 5963
Qy 5964 ----- 5963
Db 4493 GAG 4552
Qy 5964 ----- 5963
Db 4553 GAG 4612
Qy 5964 -----GGCAAGGCCAGCCATGGGT 5985
Db 4613 AAGAGAAAAAAG 4672
Qy 5986 TGAATGAGGCTCTTGAAGTCAAGGCTTTGAGTGAAGCACTCATATAGTATGATGAG 6045
Db 4673 CGTATGAGGCTCTTGAAGTCAAGGCTTTGAGTGAAGCACTCATATAGTATGATGAG 4732
Qy 6046 TCAAGTGAAGGCTACCTGTCAAGCCGAGCCCTGCTGCTTGCACCTTAATCTCAGG 6105
Db 4733 TCAAGTGAAGGCTACCTGTCAAGCCGAGCCCTGCTGCTTGCACCTTAATCTCAGG 4792
Qy 6106 TCTCAGTATCACTCTGCTGCTTACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 6165
Db 4793 TCTCAGTATCACTCTGCTGCTTACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4852
Qy 6166 CCCCACATAAATTAATTAAGCAAAAGCTGTGTAATTTGTGGATACAGTGTGATTAAT 6225
Db 4853 CCCCACATAAATTAATTAAGCAAAAGCTGTGTAATTTGTGGATACAGTGTGATTAAT 4912
Qy 6226 GATCTATGTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6285
Db 4913 GATCTATGTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4972
Qy 6286 TATGGGTGAATATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 6345
Db 4973 TATGGGTGAATATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5031


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QY 6346 CATGATTTTAAAGCTCTTGGGCAAAATATTAATCTCATGCTTAAATATCATTTAGTGA 6405
DB 5032 CATGATTTTAAAGCTCTTGGGCAAAATATTAATCTCATGCTTAAATATCATTTAGTGA 5091
QY 6406 TATATTAATCTTTAGAGAGAGCTGATCTGTTGGTGTCTCAGACAGCAATGTGACC 6465
DB 5092 TATATCAATCTTTAGAGAGAGCTGATCTGTTGGTGTCTCAGACAGCAATGTGACC 5151
QY 6466 AGCTCTTTTAACTGTGTACCTTTAGAAAATGCTACCTGTGCTCAATTTGTTGTAT 6525
DB 5152 AGCTCTTTTAACTGTGTACCTTTAGAAAATGCTACCTGTGCTCAATTTGTTGTAT 5211
QY 6526 CTATTTTATAGCTTGGAGAGAGTGAAGATCAAGGCGATTGGGAACTGACCTGCT 6585
DB 5212 CTATTTTATAGCTTGGAGAGAGTGAAGATCAAGGCGATTGGGAACTGACCTGCT 5271
QY 6586 GTTTATGTCTCTGAGAAATGCTTGGCTGTGAGGAGAGAGAGCTTAAAGAAAGAACTG 6645
DB 5272 GTTTATGTCTCTGAGAAATGCTTGGCTGTGAGGAGAGAGAGCTTAAAGAAAGAACTG 5331
QY 6646 CTCTCTTCTGCTCTTCTTAAAAAGAACATAAGATCCCTGAATGACCTTTTACTTAAAGGA 6705
DB 5332 CTCTCTTCTGCTCTTCTTAAAAAGAACATAAGATCCCTGAATGACCTTTTACTTAAAGGA 5391
QY 6706 AAGTGAAGAGCTTACCTCATCTATCTATGAAGATTTTCAATGAAACCTGGCTCAGTTGA 6765
DB 5392 AAGTGAAGAGCTTACCTCATCTATCTATGAAGATTTTCAATGAAACCTGGCTCAGTTGA 5451
QY 6766 AAAAGAAATAGTGTCAAGTGTGCTGAGAGAGAGAGAGAGCTTGTATGACCAAGAT 6825
DB 5452 AAGAGAAATAGTGTCAAGTGTGCTGAGAGAGAGAGAGAGCTTGTATGACCAAGAT 5511
QY 6826 TCATGACATATTTTATTTATGTCATGATGATGATACAGAGAAATTAATGTAATTAATAA 6885
DB 5512 TCATGACATATTTTATTTATGTCATGATGATGATGACAGAGAAATTAATGTAATTAATAA 5571
QY 6886 TTGTTTGAAGAGAGTGTACCTCTCATCTCTTTTGAAGAAAGAGCTTATGTAATCTTTC 6945
DB 5572 TTGTTTGAAGAGAGTGTACCTCTCATCTCTCTTGAAGAAAGAGCTTATGTAATCTTTC 5631
QY 6946 CATATCCAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 7005
DB 5632 CATATCCAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 5691
QY 7006 AGTTATTAATGATGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 7064
DB 5692 AGTTATTAATGATGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 5751
QY 7065 GCAAAATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 7124
DB 5752 GCAAAATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 5811
QY 7125 TGAATATCAATTAATTTCTGCTGTGTAATTTCTCCCTTAAATATTAACCAATTAATCA 7184
DB 5812 TGAATATCAATTAATTTCTGCTGTGTAATTTCTCCCTTAAATATTAACCAATTAATCA 5871
QY 7185 TCATCATCATTTACCAATCATCTGATGATTTTATTTATTTATTTATTTATTTATTTATTTAT 7244
DB 5872 TCATCATCATTTACCAATCATCTGATGATTTTATTTATTTATTTATTTATTTATTTATTTAT 5931
QY 7245 GTTG 7248
DB 5932 TTGG 5935

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RESULT 9
AAS14876
ID AAS14876 standard; DNA; 4797 BP.
XX
AC AAS14876;
XX
DT 19-DEC-2001 (first entry)
XX

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DE Human partial genomic DNA for T cell derived inducible factor, TIF.
XX
XX Human; T cell derived inducible factor; TIF; ds; anti-allergic;
XX antileukemic; cytokine; interleukin-9; IL-9; STAT transcription factor;
XX cancer; lymphoma; immune system disorder; allergy; asthma;
XX acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
XX chryoiditis; melanoma; hepatoma.
XX
XX Homo sapiens.
XX
XX US2001024652-A1.
XX
XX 27-SEP-2001.
XX
XX 29-DEC-2000; 2000US-0751797.
XX
XX 18-OCT-1999; 99US-0419568.
XX 26-OCT-1998; 98US-0178973.
XX 16-JUL-1999; 99US-0354243.
XX
XX (DUMC/) DUMOUTIER L.
XX (LOUAH/) LOUAHD J.
XX (RENA/) RENAULD J.
XX
XX Dumoutier L, Louahed J, Renauld J;
XX
XX WPI; 2001-638496/73.
XX
XX New isolated nucleic acid molecules encoding T cell inducible factors,
XX useful as markers for expression or effect of interleukin (IL)-9 in a
XX subject and diagnosing susceptibility to asthma or allergy
XX
XX Claim 1; Page 17-19; 26pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule, which encodes
XX a T cell derived inducible factor (TIF) which are upregulated by the
XX cytokine interleukin-9 (IL-9) and induce STAT transcription factor
XX activation. The TIF proteins (or their mutants) may be used to test IL-9
XX ant/agonists for their potency against lymphomas, immune system
XX disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
XX autoimmune diabetes and chryoiditis. TIF molecules promote regeneration
XX or inhibit differentiation of tissue types in which they are active and
XX therefore be used to develop treatments for melanomas and hepatomas.
XX
XX The present sequence a partial genomic sequence for Human TIF.
XX
XX Sequence 4797 BP; 1339 A; 910 C; 1063 G; 1485 T; 0 other;
XX
XX Query Match 9 2%; Score 686; DB 22; Length 4797;
XX Best Local Similarity 53.8%; Pred. No. 2,7e-145; Indels 393; Gaps 44;
XX Matches 2644; Conservative 0; Mismatches 1875;
XX
XX 2034 CTCTCTCTCACTTATCACTGTGACCTGTGACCTGTGATGCTGTGATGCTGTGACGAA 2093
DB 29 CTCTCTCTCACTTATCACTGTGACCTGTGACCTGTGATGCTGTGATGCTGTGACGAA 88
QY 2094 ATCTATGATTTTCTCTTATGAGGACCTTGTGAGGAGCTGTGCTTCTCATTTGCTT 2153
DB 89 ATCTGAGACTCTTCTCTTATGAGGAGCTGTGAGGAGCTGTGCTTCTCATTTGCTT 148
QY 2154 GTGGGCGCCAGAGGAGCAATGCGCTGCGCTCAACACCGGTGCAAGCTTGAAGTGC 2213
DB 149 GTGGTACAGGAGGAGGAGAGCTGCGCGCCATGAGCTTCCATCAGGCTTGAACAAGTCCA 208
QY 2214 CTTCAGAGAGCGGTATCATGTCACACCGACCTTTATGCTGCGCAAGAGAGTACAGCTGA 2273
DB 209 CTTCAGAGAGCGGTATCATGTCACACCGACCTTTATGCTGCGCAAGAGAGTATCATCTC 268
QY 2274 TCTCTTCTCTCCATACCGCTTGCATTTTCTGAGACACTTGCAACTCTTTAGGGG 2333
DB 269 AATCGTCTCTTCTCTGTTGATCTTGAATCAATTAATGTTCTTAATCTTTCTTCA 328
QY 2334 CGCTTATCTCCGAGAGTCTCACTACTTATTTT-----TCTCTCTTTAGAG 2382

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Db 329 GAGCATCTTAAGAGCTTTAGGAAACCACTGTTTACCTGAGGGTAGTAATTTTCG 388
Qy 2383 ACTCTTTAAGAGCTGGGCTTTTCTATTCTATTCAAGGCTCAGACCAATTTCTAT 2442
Db 389 TTTTTCAGAGACTCTTTGGGAATCGGCTTTTTTTTTTTCTTGAACCTCTTCCTCAT 448
Qy 2443 CTGGGCTTCAGAGACATATATCTGAATTTTATCTACAGAGCCGCTT - AGAAGCCA 2500
Db 449 TTTGGCTTTATGATACATATATGTAATTTTCCMAAGAGCGCCATTCAGTAATCCAT 508
Qy 2501 CCCAGACTGCAATACTTCCATTTCTGTGCTCTCTCTGTAACATCACTCTTGGC 2560
Db 509 CTGATGATTTTTTTTCTTTATGCTCTGTGATTTGTTCTAACTCAGACATCTG 568
Qy 2561 TACTC-----CTGAGACCACTGCGACATACATCTTAC 2595
Db 569 AATTCGCTTTTAGTCTTTATGATGTTGCTGAGGAGACGGGATGGGACATGCTAT 628
Qy 2596 TTACAGGCTTTTCTTCATCTCTTGTACCCAGGACCTTAGGGTTTC-TCTCTTACG 2654
Db 629 GATATAATTTTTTTTCTATTGCTCAATGTCAGACCCCTTAGCTTTTCTCTCCAG 688
Qy 2655 GCCAGCTTGCAGATACAAACACAGACGTCGGCTGATGGGGAGAACTGTTCCGAGA 2714
Db 689 GCTAGCTTGCTGATACACACAGACGTTCTCTCATGAGGAGAACTGTTCCAGGA 748
Qy 2715 GTTCAGTGAAGTCTCCTACTGTATGAGCAGGCG-----TAGCTGGGGAGCT 2761
Db 749 GTGAGTGAAGCTAGACGTTGTGACGAACGGGCGGTGCGCCATCGGATCTTGGGT 808
Qy 2762 GGTGACCTCTGGATAG---TCTGACGATAGACCCCTGCTCTTCTTGTACTGCG 2817
Db 809 GGTGGTGAATGATGTTAGTCTTATGCTTATGACCTTGTCTGTTCCCTTCCACTCG 868
Qy 2818 AGGCTAAGATACAGTCTACCTGATGAGAGGTGCTCACTTCACTCCGGAAGCTGC 2877
Db 869 AGATGATGAGCGCTCTATCTGATGAGAGGTGCTGAACCTTCACTTGAAGAGTGC 928
Qy 2878 TGCTCCCCAGTCAGACAGGTTCCAGCCCTACATGAGAGAGGTGACCTTTCTGACCA 2937
Db 929 TGTTCCTCAATCTGATAGGTTCCAGCCTTATATGAGAGAGGTGCGCTTCTGCGCA 988
Qy 2938 AACTGCAATCAGCTCAGCTCTGTGTATGCTGACTTGTGCTACCTTATGCTCTCT 2997
Db 989 GGCTCAGCAACAGGCTTACACATGTGTAATGCTCACTCTCAGCCATGCCACCTAAC 1048
Qy 2998 CTTCCTCTCTATTCAGAGTAAGAACCCGAGTCTGCTCTCTCTCTTCCACAAGTGA 3057
Db 1049 CTCTCTCCCTCTTCCACAGAGACCCCTTACCCCACTCTCTCTCTCCCTTACCCC 1108
Qy 3058 GAGGGCTCAGACACCAACCATCATAGGCCACTTGAATAGTACAAAAGGCTTGGC 3117
Db 1109 TAACTAGCAGAGAAAGTGTCTTGGCAGCAGTGTATACAGAGTGA-----TTTGG 1161
Qy 3118 TTCAATTAAGTAATCTTTGAGTTGTATGAGTGAAGCTTATTTGTTTATTCATGAA 3177
Db 1162 ATCATAGATATTTGCTTTTGTCTTACCTGAGTCAATCTTGAAGTTATAGTGTGATG 1221
Qy 3178 AGAATCACTCAATTTCTGTAGATGAGAAAGATTTGGGAACGAAAGAGCCATGAT 3237
Db 1222 GGGTCTGGAATTTAAGTGTACAGAACCCGATGTTGTTCTTGGAAAAAAGCACTC 1281
Qy 3238 AGAAGAACAGATCTGCTGATATGATTAATGAGGGGAGACAGGGGCGCATATCCACTG 3297
Db 1282 A-----GTTTGCCTAAGATGAGAAAGTGTGG 1309
Qy 3298 GTACAAAGTACTTGTGGGAGAGAAATCCACTAGTACAGTACTTGTGGCATGAGATC 3357
Db 1310 GAAAAATCTAGCTGTGGAAATGATCCATTGATGTTGTTAGGGGAGGGGATGG 1369
Qy 3358 CACTAGTACAACTATGTTGGGGGAGGAGATGAGCAGAGAAAGTTGAAGGGAAGG 3417
Db 1370 CATGAGAGAAATTTAAGAGAAAGTGGAAATGGGAAAGCTTAAA----- 1415

Qy 3418 AAGATGAGAGAGCTCATGTTGGGGGTGTGAAGATCACTCTTTTCCATGTGATGAG 3477
Db 1416 -----GTGGGTGGGTGGCGCAACGTGTGCTCCCTGTGATGTACGGGA 1460
Qy 3478 AGTTAAGAAACCA-GTGTGTAGTGTGATGTCTTCAGACACCCCACTATGAAACAT 3536
Db 1461 AGCCACAAATTCGAGGCGGTGTGAATCTTATGCGCTGAAACATTTGAAACTATGAAAAA 1520
Qy 3537 ATCCAGAGAGAGCGGCGAGACTGTGGAGACCTTGCAATTTAGGAAGCGC--GGCTTT 3594
Db 1521 AGTTGAGTGTGAGTGGCGCCAGTAAAGGCCCTAGACTTACTGAAAGGGCTTATTTT 1580
Qy 3595 CACAGAGAAACTTATGCTATCTCTGTGTACATCTCCACCTTATATAGGTTCAGC 3654
Db 1581 CACATGAGATGTTTATGTATACATTTCTTGTCTTAAGCAATGCAATTTCTTGAGATACAT 1640
Qy 3655 TCAGGTTGTTTTCT-----ACGTTCTTGTACTGTGTGAAC 3693
Db 1641 TGAGGTTTTATCTCTTACAGAAATTTGCATTAACATCTCGCTCTTTCCAAATGCAAAC 1700
Qy 3694 TTCACTAGGATTTCCCAAGACAGAGACAGCTCTTCTGTAAAGGAGGAGCCTGATTTCA 3753
Db 1701 CTCACTAGGATTTCCCAAGATGAGAGAGAGGTCTTGTAAAGGAAAGTGCATTTCTG 1760
Qy 3754 GTTCTAGAGAACGAATTAAGCTAGAGATCTAGTCAACGTGAATCTAGTCAAGC 3813
Db 1761 GCGTCAAGGGAATTCAGAGACTCAGAAATCTAGTCACTGTTGAAATCTAGTCAATG 1820
Qy 3814 GGGCAAAATAGTGAAGGCTCTATTTCCAGTGAACGCTCAGCGCTCAGATATACG 3873
Db 1821 TGGGCAAAATTAAGAGCTTAAATTCAGGTGAATGTACTGACCTCCATGGGCTG 1880
Qy 3874 AGGTATGAGCTCCACCGGATAAGATCTGTATGTA-GTCTGCTTTATTTTCCAGA 3932
Db 1881 GAGGTCATTAAGTTTCAACACATTAATATATATGCTTTATTTATTTATGTA 1940
Qy 3933 CATCAGCGGTGACGACGAACATCAGAAAGATGCAAGAGCTGAAGAGACAGTGA 3992
Db 1941 TATTAAGTGTATGCTGCAATATCCAGAGATGTGCAAAAGCTGAAGSACACAGTGA 2000
Qy 3993 AAAGTACTATTTGGACACACATATCTAAGCCATTCAGTAC--GAGACGTGGGATTT 4050
Db 2001 AAAGTATGAGTGAATCTGTCATGCTAAGTCAATGCAATGAGAGCAAAATGTTGTT 2060
Qy 4051 TTTCTGCTCCAGTCCCTTCTTCTTGTATCAATTTATTTGACTGTCTACTATCTG 4110
Db 2061 TTTCTTCTTCTTCTTCTTCCATCACTTTGTGATTTTCACTTGAATTTCTCCACACAG 2120
Qy 4111 GTCCATTAATCGCTTAGCTGACCTGATCTAGCTGGGTCTATAGATCTTCAATCTGTG 4170
Db 2121 GCGCATTA-----CTTGGGTGTGTATGATGATATATCTATATCTAGATGTCAGT 2176
Qy 4171 TCTAAATTT---GTAAATCAATTTCTGAGCTAGACAAAGCTTATAGCTCAGCTCTC 4227
Db 2177 TCCAAATCTTGGAAATTTGATGATCTGAATCTGAGTGGGATCTTATGCTGTAGTAC 2236
Qy 4228 ATGACACTTGTGCTCGAGATAGCTTGTGACAGATCATGCTAGTAGAAGACATCCCTG 4287
Db 2237 ATMACTTAGATTTCTGGGATGTGTAGTGGCAGAGATAGGCTTAATAGCAGGTCTCTG 2296
Qy 4288 ATTCCAGCTCTGAC-TTGCCTAGTGCATGTGTAAATTAATTTTGCTTGAATAGAT 4346
Db 2297 AATCCCAAGCGACATTTTCCGGGTGGATACAGATTAATTTTGTATCACTTAATTT 2356
Qy 4347 TTGGGAAA--GCAATTTCCAGGACCTAATATCTGAAGAACATGATGAAACATA 4404
Db 2357 TAGGAAATTTTCAATCTTATGACTATGATGAATCTGAAGAGTACTTGTTTAAATA 2416
Qy 4405 GAAAGCTGGGCA-----CAACTTACATGATGATTTTGTAGCTTATTAACGATGCTC 4460
Db 2417 GAAAAATGCTTATGGGCAATTTATTTGAAGTCAATTTTGAAGTCAATTAATGATGCTT 2476

QY 4461 TGAATGTCGCAAAATCAACCAAGATTAACAACAAAGAGCTGGATTGGCAATATAGACA 4520
 DB 2477 TGAACCTTGGAAGAAATTAACAGAACATGAGAAAAGCTGGACTTCATATAGAGCT 2536
 QY 4521 AGTATTGAAATCACTGATTAATATAGTATCATCTTAATTAATAATATAGGCTATATA 4580
 DB 2537 AATTCTGGA-----GTAAATACACTTATTTGAAATTATATATATATATATATATAT 2589
 QY 4581 TATATTTAAGATTAACACACAGAGTGGATAGCCTCCCAATTTACTGGCTGGTTCAAA 4640
 DB 2590 TGAATTAATGTTTAAAGACAG 2648
 QY 4641 AGAGTAAAT 4700
 DB 2649 AGAGTAAAT 2708
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 DB 2709 TTTTCTTCT 2768
 QY 4753 TCAAGCACTAGTAAAGCACTATCTGCTGAGCTATATATATATATATATATATATATATAT 4812
 DB 2769 ACAAATCCCTAGGAGAGATTTATATATATATATATATATATATATATATATATATATAT 2828
 QY 4813 ATTGCTGTGCTCTTTTGGGAG 4872
 DB 2839 ACCATCATGTGCTCTATTTTGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2886
 QY 4873 CTGACTGCTTAAAGCCAG 4932
 DB 2887 GTGACTCACCACCAACCGAG 2945
 QY 4933 TGGGTGTGCTTAAAGTAAAG 4991
 DB 2946 CAGGTAACTAAAT 3005
 QY 4992 -----TATCTACCTTATCTCTCTTATGAACTTAATCTCTCTCTCTCTCTCTCTCT 5042
 DB 3006 GCTTAACCTTAATCT 3065
 QY 5043 TGTAGCTGATTAACACACTTGT--TCTTTTGTAGTTCATGCTTGTATGATTTTA 5100
 DB 3066 CATCATTTATATAGTGTACTGTCTCTCTTGTATATATATATATATATATATATATATAT 3125
 QY 5101 GTGCTGTGCACTTCTGT--TAGAGGTTTGTATCTTACCTGACACTGGCTGTGATTA 5158
 DB 3126 TTGTGAGCCAGTCTCTGTAT 3185
 QY 5159 GCATGCCAAGGACACACTTCTGAATGCTGTGTAAAGTTATATATATATATATATATATAT 5215
 DB 3186 GCATGCCAAGGACACACTTCTGAATGCTGTGTAAAGTTATATATATATATATATATATAT 3245
 QY 5216 -----TGTCTTGAAG 5270
 DB 3246 GCTTGTGTCTTTAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 3296
 QY 5271 CTGTAGAAACTTTTCT 5327
 DB 3297 -----TCTGTGTATTTTCAAGACCTTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3342
 QY 5328 TGACTTTTATACATGCTGTCTACATGAAAGAGTGTATAGAGAGAGAGAGAGAGAGAGAGAG 5387
 DB 3343 TCAATTTTGTCAATGAGTGTCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3402
 QY 5388 AAAAGACCAATATAGGAG 5447
 DB 3403 GAAAGCA--CAG 3461
 QY 5448 CAGAGCTCCCGAAGAGACA-----CCACAGGTGTATTAATAGAG 5485
 DB 3462 CAGAGCTGTCTGAATATAG 3521
 QY 5486 AACAGTCCAGGAG 5545

DB 3522 ACCAAGAGCAGAGTGTGTATTAAT--GCATACAGACAGATAGGAGAGATTAATCTTTAA 3580
 QY 5546 ACTTTCATATAGAGTGC--CGAGTCTTAAAGATACAAATATAGTGC--TTGGCTTCTTAA 5602
 DB 3581 AATTCTTTATATCTTTGAGGCTTTGAGATATATATATATATATATATATATATATATATAT 3640
 QY 5603 AAGAAAGTGTGGAAGGAG 5662
 DB 3641 AAGAAAGTATAGAAAG-----TGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3688
 QY 5663 AGGACTGACAGCTACAAATCTCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5722
 DB 3689 AACCATGTTTATATAG 3748
 QY 5723 ACTGATTAAGTATAGTACAG 5782
 DB 3749 ATAGATTAAGAGAGATTTTCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3805
 QY 5783 CCATTGAGTGAAGAGCTCACCTTTTACCTCGAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 5842
 DB 3806 CGATTAGTGTGAGATCTCATCTGATTTGACT---TGAGAGAGAGAGAGAGAGAGAGAGAG 3861
 QY 5843 TATGACTCTCTACCTGAGAGTTTATAGTTTATAGCAATGGAACAGACACTCGGAGCTCTCT 5902
 DB 3862 TAGACCTATATCTGTGTTTCTTATTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3921
 QY 5903 CTGACAAAG 5962
 DB 3922 TTCCACAG 3981
 QY 5963 AGGCAAGCCGACCAATGAGTGAATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 6022
 DB 3982 CCTATGATATGAGAT 4041
 QY 6023 CACTCAT 6058
 DB 4042 GAGTGTCAAT 4101
 QY 6059 TACTGTGAGGAG 6118
 DB 4102 AAATATCAAGAAAT 4161
 QY 6119 TCTCTCTATTAAGACAGTGTAGAGTGTAGCAAACTTTTCTCTCTCTCTCTCTCTCTCTCT 6163
 DB 4162 TAAAGAAAGTAT 4221
 QY 6164 -----AACCCCACTTAATTTATTTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6205
 DB 4222 CTGTGGGCTGAGAGTGTGACAACTCTTATATAGTAAATCTGTGATATATATATATATAT 4281
 QY 6206 TGGAGTACAGTGTAT 6227
 DB 4282 TGCATAACAGGCAAGCAT 4341
 QY 6228 -----TCTATGTGTGATTTGTGCAAGTTCATATATATATATATATATATATATATAT 6283
 DB 4342 TCAAGTCT 4401
 QY 6284 TTTATGAGTGAATATGCAAT 6343
 DB 4402 TTTATGAGTGAATATGCAAT 4460
 QY 6344 GGCATGATTTTAAAGTCTTGGCAAT 6403
 DB 4461 GGCATGATTTTAAAGTCTTGGCAAT 4508
 QY 6404 GATTATATATCTTTTGAAG 6463
 DB 4509 TACTATGATATTTTACAAATCTTAAACCTGAGTGTCTGATCATCAACTATATCTTG 4568
 QY 6464 CAGCTCTTCTTACAGTGTGAG 6523

Db 4569 CAATTCT--AATTGTCACCTTAGAAAACATGCGATTAATGCTCAAAATCTTTGCA 4625
 Qy 6524 TTTTATTTTTCATAGCTTGGAGAGAGATGAGATCAAGCGATTTGGGAACTGGACCTG 6583
 Db 4626 TTTTATTTTTCACAGCTTGGAGAGATGAGATCAAAAGCAATTTGGAACTGGATTGG 4685
 Qy 6584 CTGTTTATGCTCTGAGAAATGCTGGCTGAGCGAGAAAGCTAGAAAAAGAAAGAAC 6643
 Db 4686 CTGTTTATGCTCTGAGAAATGCTGGCTGAGCGAGAAAGCTAGAAAAAGAAATTAAC 4745
 Qy 6644 TGCCTCTGCTGCTTCTTCAAAAAGCAATTAAGATCCCTGAATGACTTTT 6695
 Db 4746 TAACCCCTTCTGCTGAGAAATACAAATTAAGATGCCCAAGCGATTTTT 4797

RESULT 10

AAD30646
 ID AAD30646 standard; DNA; 4797 BP.

XX AAD30646;
 AC 21-MAY-2002 (first entry)
 DT 21-MAY-2002 (first entry)
 XX Human TIF genomic DNA.
 DE T cell derived inducible factor; TIF; interleukin-21; IL-21; human;
 KW STAT transcription factor; acute phase protein; inflammation;
 KW chromosome 12; ds.
 XX Homo sapiens.
 OS WO200210393-A2.
 PN 07-FEB-2002.
 PD 27-JUN-2001; 2001WO-US20485.
 PF 27-JUL-2000; 2000US-062617.
 PR (LUDM-) LUDMIG INST CANCER RES.
 PA Dumoutier L, Renaud J;
 PI WPI; 2002-195964/25.
 DR Stimulating expression of STAT transcription factor and inducing
 XX production of acute phase protein in a cell, involves contacting a cell
 PT capable of expressing STAT with T cell derived inducible factors -
 PS Claim 6; Page 56-58; 64pp; English.
 XX The invention relates to nucleic acid molecules encoding T cell
 CC derived inducible factors (TIFs) also known as interleukin-21 (IL-21).
 CC TIF polynucleotides are upregulated by the cytokine, IL-9, IL-TIF or
 CC IL-21 molecules are implicated in activation of STAT transcription
 CC factors, acute phase proteins and inflammation. The present sequence
 CC is human TIF genomic DNA located on chromosome 12.
 XX Sequence 4797 BP; 1339 A; 910 C; 1063 G; 1485 T; 0 other;

Query Match 9.2%; Score 686; DB 24; Length 4797;
 Best Local Similarity 53.8%; Pred. No. 2,7e-145;
 Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;

Qy 2034 CTCTCTCTCACTTATTCACACTGTGACATTTGTGCGATCTGATGCGCTGTCTGACAAA 2093
 Db 29 CTCCTTCCCACTCACAGTTCCTGAGTTAGATTGCTGCAATGGCCGCCCTCACAAA 88
 Qy 2094 ATCTATGAGTTTTCCTTATGAGGAGCTTTGGCCGCAAGCTGCTGCTTCTGATGGCCT 2153
 Db 89 ATCTGAGAGCTCTTTCCTTATGAGGAGCTTTGGCCGCAAGCTGCTGCTTCTGATGGCCT 148
 Qy 2154 GTGGGCCCAAGAGGCAATGCGCTGCCCTCAACACCCGCGTCAAGCTTGAAGGTTCACA 2213

Db 149 CTGGTACAGGAGAGAGAGCTGCGCCCATCAGCTCCACATGACAGCTTGACAAATGCCAA 208
 Qy 2214 CTTCAGAGAGCCGTATCTGATACACCGACCTTTATGCTGGCAGAGAGTACAGCTGCA 2273
 Db 209 CTTCAGAGAGCCGTATCTGATACACCGACCTTTATGCTGGCAGAGAGTATTAATCTTC 268
 Qy 2274 TCTCTTTCTCTCCATACAGCCGCTTGGCAATTTCTGGAAGCACTTCAAACTCTTAGGGG 2333
 Db 269 AATCTGCTCTTTCCTGCTGATCTACCTTGGAATCCAAATAGTCTTAACTTTCTTCA 328
 Qy 2334 GCTTTATCTCGCAGGTCTCACTACATGTTT-----TCTGCTCTTGAAG 2382
 Db 329 GAGCATCTCTAAGACCTTAGAACCACCTGTTATCCCTGAGGGTAGATAAATTTCTG 388
 Qy 2383 ACTCTTTAAGAGCTGGGCTTTTGTATTTGATTTCAAGGCTGAGACCATTTCCAT 2442
 Db 389 TTTTTCAGAGACTCTTGGGAATCGCTTTTCTTGAACCTTCTTCCAT 448
 Qy 2443 CTGGCCTTCAAGACACATATACATATTTTATCTACAGAGCGCATTT--AGAAAGCA 2500
 Db 449 TTTGGCCTTTATGATACATATGATGAATTTTCCAAAGAGCGGCATTCAGTATTCAT 508
 Qy 2501 CCCAGACTGCATATCTTCCATTTCTGTGCTCTCTGTAACATACCTCTGTGGC 2560
 Db 509 CTGATGATTTTTCCTTATGCTGCTGTCATGTTCTTAACTCATGACACATCTG 568
 Qy 2561 TACTC-----CTGAAACCCATCGCGGACATATATCTCTAC 2595
 Db 569 AATCTGCTTTTATGCTTATGATGTTGCTCTGGGAGACGGAGTGGGACATGCTAT 628
 Qy 2596 TTACAGGCTTTTCTCCATCTCTTGTACACCAGGACCTTAGAGTTTTC--TCTCTTTCAG 2654
 Db 629 GTATTAATTTTTCCTTATGCTCAATGCTGACAGACCTTATCTTTCTTCTTCCAG 688
 Qy 2655 GCCAGCCTTGCAGATTAACAACAAGACGTCGGCTCATCGGGAGAAAATGTTCCAGGA 2714
 Db 689 GCTAGCTTGGCTGATTAACAACAAGACGTCGGCTCATCGGGAGAAAATGTTCCAGGA 748
 Qy 2715 GTCACTGTAAGTCCCTCACTGATGAGAGAGG-----TAGCTGGGAGCT 2761
 Db 749 GTCACTGTAAGTCCCTCACTGATGAGAGAGGCGCTGCTGCATGAGTACTTGGGT 808
 Qy 2762 GATGACCTCTGGGATAG-----TCTAGCATAGACCCCTGCTCTGCTGCTACCTGC 2817
 Db 809 GGTGATGATGATGTTTATGCTTATCCCTTATAGACCTTTCTGTTCCCTTCCACTGC 868
 Qy 2818 AGGCTAAAGATCAGTCTACTGATGAAGCAGGTGCTCACTTCACTCTGAAAGCTTC 2877
 Db 869 AGATGATGAGCGCTGCTATCTGATGAAGCAGGTGCTCACTTCACTCTGAAAGCTTC 928
 Qy 2878 TGTCTCCCACTGACAGAGTTCAGAGCTTACATGACAGAGAGTGTACTTCTTGACCA 2937
 Db 929 TGTCTCCCACTGATGATGCTTACAGAGCTTATATGACAGAGTGTGCTTCCGCGCA 988
 Qy 2938 AACTGACAACTCAGCTCCTGCTGTAAGTCACTGCTGCTACTATGCTCTCT 2997
 Db 989 GGTCTAGCAACAGCTTAAGCACAATGTGAAGTTCAGCTCTCAGCTTATGCCACTTACC 1048
 Qy 2998 CTTCCTCTTATTCAGTAAGAACCGAGGCTCTGCTCTCTTCAAGAGTGA 3057
 Db 1049 CTCTCTCCCTCTTCAAGAGACCCCTTACCCCACTCTCTCTCCCTTCCCAACCC 1108
 Qy 3058 GAGAGGCTCAGCACACACATCATATGGCCACTGAAATAGCTCACAAAGGCTTGGC 3117
 Db 1109 TAACTTACAGAGAAAGATGCTTGGCAGAGTGTATCAGAGAGCA-----TTTGGG 1161
 Qy 3118 TTCAATGATTAATCTTTGATTTGATGATGAAGCTTATTTATTCATGAA 3177
 Db 1162 ATCATAGATATTTGCTTTGCTTGAATGATGATCACTTGAAGTTATGATGAGATG 1221
 Qy 3178 AGAATCACTCAATTTCTGATGATGAGAAAGATGTTGGAAAGAAAAGGCTTAGAT 3237

Db 1222 GGGCTGGAAGTGTACAGAACCCGCAATGGTTGTCTTGGGAAAAAGGCACTC 1281
Qy 3238 AGAGAAACAGATCTGCTGATATAGTACTTATGGGGGAGACAGGGGGGATATCCATGA 3297
Db 1282 A-----GGTGGCTGAAGATGAGAAAGGTGTGG 1309
Qy 3298 GTACAGATCTTGGGGAGAGAAATCCATGCAATGACAGTACTTGTGGCATGAGATC 3357
Db 1310 GAAAAATCTAGTGTGAAATGATGATCAATGATCTAAGTTGTTAGGGGGAGGAGATGG 1369
Qy 3358 CACTGATGACAGTACTTGTGGGGAGAGAAATGGCAAGACAAAGTTGAAGGAAAG 3417
Db 1370 CATGAGAGAAATTTGAAAGAGAAAGTGGAAATGGAAAGCTTAA----- 1415
Qy 3418 AAGATGAGAGGCTCATGTTGGGGGTGTGAAGGTCACTCTTTTCATGTGATGAG 3477
Db 1416 -----GTGGGTGGTGGGTGGGAGCTGTGGCATGTGTGCTGTGTGATGTGAGGA 1460
Qy 3478 AGTTAAGAAAAACA-GTGTGTGATTTGATGTCTTCAGACACCCCACTATGAAACAT 3536
Db 1461 AGCCCAAAATCGAGGGGTGTGAACCTTGATGCCCTGAACTTTGAACATTTGAAAAA 1520
Qy 3537 ATCCAGAGAGCGGGAGACCTGTGGAGACCTGGCATTTAGGAGAGGCG--GGCTTT 3594
Db 1521 AGTTGAGTGAAGTGGGCCCACTAAAGGCTTAGGACTTACTGAAAGGGCTTAATTT 1580
Qy 3595 CACACGAGAACTTTATGCTCATCTCTGTGTACACATCCACTTGTATGAGTTCAAC 3654
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Qy 3655 TCAGGTTGCTTTCT-----ACCTTCTGTCTACTGTGTGAAC 3693
Db 1641 TGAGGTTTATTTCTTACAGAAATTTGATTAATCTACTCCGCTTTTCCCAATGTGAAC 1700
Qy 3694 TTCATGAGATTTCCCAAGAGAGAGACAGCTCTCTGTAGAGAGAGAGCTGATTTCA 3753
Db 1701 CTCATGAGATTTCCCAAGAGATGAGAGAGGCTCTTGTAGAGAGAGTACTGTGATTCG 1760
Qy 3754 GTGTCTAGAGAACTTAATAGCTCAAGAAATCTAGATCAACGTGAATCTAGATCAAC 3813
Db 1761 GGTGTCAAGGAAATTCAGAGCTCAAGAAATCTAGATCACTGTGAATCTAGATCAATG 1820
Qy 3814 GGGCAAAATGACTGAACCTCTTATTCAGGTGAACGCTCACTGCTCAATATATCTG 3873
Db 1821 TGGGCAAAATTTACTAAGCTTTAATTCAGGTGAATTTGATCTGATCTTCAATGGGTG 1880
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Db 1881 GAGTTTCAATAAGTTTCAAGCAACATTAAGTATGCTTGTATTTATTTATAGCA 1940
Qy 3933 CATCAGCGGTGACGACAGAAATCAGAAATGTCAGAAAGCTGAAAGAGACAGTGA 3992
Db 1941 TATTAAGGTGATGACGTGATATCCAGAGAAATGTCAGAAAGCTGAAAGACAGTGA 2000
Qy 3993 AAAGTACTATTGGCAAGCCACAAATCTAAGCAATTCAGTAC--GAGAGTGGGATTC 4050
Db 2001 AAAGTAGACTGATATCTGATGCTAAGTCAATGCAATGAGAGAGCAAAATGTTGTT 2060
Qy 4051 TTTCTGTGCTCCAGTCCCTCTTACTTGTGAATTTATTTGATTTGATCTTACTATCTG 4110
Db 2061 TTTCTTCTTTCTTTCTTCTTCCATCACTTGTGTGATTTTCACTGTATCTTCAACAG 2120
Qy 4111 GTCCATTAAGCTTATGCTGACCTGTATCTAGCTGGGTCTATAGATCTTTCAATGTG 4170
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Qy 4288 ATTCCCAAGCTGTGAC--TTGCTTAGTGCCATGTGTAAATTAATCTTTGGCTTGAATAGAT 4346
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Qy 4347 TTGGGAAA--GCCAGTTCCACAGACCTTACATTAATCTGAGAACCATGATTTGAAAACTA 4404
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Qy 4461 TGAATGTGGCAAAATCAACCAGATTAACAACAAGAGTGTGATTTGCAATAGGCA 4520
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Qy 4591 TAAATTAAGATTAACAACAAGATGATAGCTTCCCAATTTACTTGGCTGTTCAAA 4640
Db 2590 TTGATTAATGTTAAAGCAAGAGAGCAAC--CCGATCTTTATACAGGTTCAAT 2648
Qy 4641 AGATTAATAATATCATGATGATTAATTAATGTGTCAAGAAATGATAGAGTGAACCC 4700
Db 2649 AGAGTAAATAATTAAGTAAAGATTAATTAATGTAATGAAAGCTGAATGTGAGCT 2708
Qy 4701 TTTCTTACTTTTAACTTCA-----TTTCTAGTTTTTTCTTCAACCTGTA 4752
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Qy 4753 TCAAGCCTAGTAAAGCACTATCTGTGATGATTAATTAATGACTTACAGCAAAAC 4812
Db 2769 ACAAATCCCTAGGAGAGATTAATCAATGTGGGTGTGATCATTTATATGTAATGAT 2828
Qy 4813 ATGTGTGTGGCTCTTTGGGAGAGGAAACAGATAGCAGAGAGCTCAGGCTAGCACT 4872
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Qy 5043 TGTAGGCTGATTAACAACCTGTT--TTCCTTGAAGTCAATGAGCTTGTAGATTTTA 5100
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Db 3126 TGTGAAGCCAGTCTCTTGTATTAAGAACTAATTAAGACATGAGAGGCTGAAATGTA 3185
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Db 3186 GCATCCCAAGGACATGCTTTAACAATTTCTTAAATAATTAATCAATTAATCAAT 3245
Qy 5216 -----TTGCTTGAAGAGTGAAGCTGTGAGAAAGAACTCAAGAGATGTGTTCT 5270
Db 3246 GCTTGTGTCTTTAAGAAAGTGAATGTGAGAGAGAAATCTCAAGTGA----- 3296
Qy 5271 CTGTAGAAACCTTTTCTTCTTAAATGCTTAAATCACTTCACTTCACTTCACTTCA 5327
Db 3297 -----TCTGTGATTTTCAAGACTTTATCAATTTTGAAGAAATCAAT 3342

OY	5328	GCACITTTATATACANAGCTGTCAACATGAAAGAGTGTTTAAAGCCCGCTCANTGGCTCGGG	5387
Db	3343	TCATATTTGCATAGGGGTGCCATGTGGAAAGGTATATATGCTTTTGTCTGTAGCTTCA	3402
OY	5388	AAAAGCACCAATAGGGGAAAGGATATGTATGTGTAGAAATCTGACCGGACAGGAAACTGGT	5447
Db	3403	GAAAGCA-CAGAGGGAGAGCAATGTTGTTTCAAGAAAGATCAACAGGAGGAAACTGT	3461
OY	5448	CAGAGCTCCCCGAAAGCA-----	5485
Db	3462	CAGAGCTGTCAAAATATAGGTGTGTTTGGAGGACATTATTCCTCTGTGTGGGGTTAAA	3521
OY	5486	AACAGTCCAGGGGTGGGCTCATGTATATAGAAACAAAGGAGGAAAGATATAGCTACAA	5545
Db	3522	AGCGAAGACGAGGTTGTAGTAAAT-CCATGACGACAGATGAGGGAGAAATPAACCTTTAA	3580
OY	5546	AGTTTCATAGAGGTC-CGAGAGCTTTPAAGATACAAATATAGTGC--TTGGGCTTCATACA	5602
Db	3581	AATTCCTTATATGTCTGTGAGTCTTTGAAATAGAAAAGAAATATCTTTTGTGGCTTATGCA	3640
OY	5603	AAGGAAGTCTGGGAAGGACGACAGTGAAGGAGAAATGGAAAGGAAAAACAGATGTAG	5662
Db	3641	AAAGAGATAGGAAAG-----TGAAAGGCGGAAAGAAAGCAGGAAAAAGAAAG	3688
OY	5663	AGGACTTGAACAGCTCAAAATCTCTACCAACATTTTCTTGGACATCTAGAAAGT	5722
Db	3689	AACCATGTATATATATAGAGCAAAATGTGACAAAGGTTTTTCTTGAAATATAGCAATATG	3748
OY	5723	AGTGGATTAAGTGAATGACAGGGGGACCTTGCTTGGCATTTGAATCTGGGTTTTGTCTCT	5782
Db	3749	ATAGATTAGAGGAATTCAGTAGGGGAATGCTTTTCACTGAATTTGGGTTCTCT--T	3805
OY	5783	CCATTGAGGTGAAAGCCGTCAACCCTTTTACCCTCGAATGGAAGAGAGAAAGGGGTGT	5842
Db	3806	CGATTAAATTTGGGATCTCTCATCTGCAATTGACT---TGAGAGAGAAAGAAATGAATGT	3861
OY	5843	TATGATCTCTTACCTGGAGTTTACTAGTTTACGATGGAACAGACTCGGACCTCTCT	5902
Db	3862	TAGGACCTATATCTGGTTTCTATTAATCAAGCAAGTGGAAAGACTTATTTGGTATTT	3921
OY	5903	CTTGACAAAAAATGGAACCTGTGTGTTGTTCTGTGTTGTTCTTTGTTTAAGAAAGAC	5962
Db	3922	TTCCACAAAAGTGAAACTTTTCTTTTACTGTGTGTCAAAAAGGTGAAATGAAAAAG	3981
OY	5963	AGGCAAAAGCCGACACATAGGTTGGAATGTGGGCTTTGAGTCAAGCTTTTGAATTAG	6022
Db	3982	CCTTAATGTATTTGGGATACATGTTCAAAAGTCATTTGAATAGAGATCTTTTAATCAG	4041
OY	6023	CATCTATCATATAGTT-----GATCATGTGACGTGGAGGGC	6058
Db	4042	GAGGTGTCAATCATTTGGCTTCCCTGACACACTGAAAGAAATGTCTTGTAACACAT	4101
OY	6059	TACCTGTAGGCCAGACCCCTGTGGCTTCGCACTTAATATCTCAGGCTCAGATACAT	6118
Db	4102	AAATATACAGAAACAATAGCTATGAGCTAAAAAAGTCCATGCAATPAATCTCATCTGTTT	4161
OY	6119	TCCTGCTACTTAGCACAGTATGAGAGTTGAGCAAACTTTTTTTC-----	6163
Db	4162	TAAAGAAATTTATGAATTTCTGTTAAGGTGCAATCAAGCGTCTCTGGGCCATGTGGCGC	4221
OY	6164	-----AACCCCACTPAAAATTTATATGACAAAGACGTGTGAATTTG	6205
Db	4222	CTGTGGGCTGAGGTTGGACAAGCTCTTATTAAGTAATCTGTCAATAGATTGTTTGGAGC	4281
OY	6206	TGGGATTAAGTGTGATATATGA-----	6227
Db	4282	TGCAAAACAGGCAAGGCATATATGGGTGGCACTCGGGAATCCCCAGATCCAGCCTCACT	4341
OY	6228	---TCTATGTGTGATTTGTGCAAGGTTCAATTAAGATATGATTTAATAGGCCCATCAACGC	6283
Db	4342	TCAGTCTCTTGTCTCTGTGTAAAGAGGGGTGTCAACTCTGCCACACTTTTAACACGC	4401
OY	6284	TTTATGGGTGTCAAAATGCAGATATATATAGTATGATGCTGTGTGTCTTATAGCTACAAA	6343

Db	4402	TTCAATTAGTGTGAGAGTGCACCTGAAATTGATGCTGCTGGTGGGCTT-CTCAGTCCAGAGA	4460
Oy	6344	GGCATTGATTTTAAAGCTCTTGGGCAATCATATTACTCATGTCTAAAAATACATTATGTT	6403
Db	4461	GCCGTGATTTTAAAGCTCTTGGGCAAAATCATTCATACTAAAGGGATA-----T	4508
Oy	6404	GATTATTAATCTTTTAAAGAGAGCGTGATACTGTGTTTGGCGCTCAGCAAGCAATGTCA	6463
Db	4509	TACATAGAAATGTTTACAAATGCTTAAACCTGGTTCGTCTCCATCAACCTAATCTTG	4568
Oy	6464	CCAGCTCTTGTCTAAGTGGTACCACTTTAGAAAATGCTACCTGCTCAAAATGGTTGTA	6523
Db	4569	CAATTTCT--AAATTGTCACCTTAGAAAAATGCGATAATGCTCAAAATCTTTGCA	4625
Oy	6524	TTCTTAATTTTCATAGCTTGGAGAGAGTGGAGAGATCAAGGCAATGGGGAATGAGCTG	6583
Db	4626	TTCTTAATTTTCACAGCTTGGAGAGAGTGGAGAGATCAAGCAATGGGGAATGAGCTG	4685
Oy	6584	CTGTTTATGCTCTTCGAGAAATGCTTGGCTCTGACGAGAGAAAGACTAGAAAACGAGAC	6643
Db	4686	CTGTTTATGCTCTTCGAGAAATGCTTGGCTCTGACGAGAGAAAGCTGAAAATGATTAAC	4745
Oy	6644	TGCTCTTCCGCTTCTTCTTAAAGAACAAATAGATCCCTGAAATGAGACTTTT	6695
Db	4746	TACCCCTTCTCCCTCTGAGAAATACATTAAGATGCCCCAAAGCATTTTT	4797
RESULT 11			
ADD27151	1D	ADD27151 standard; DNA; 4797 BP.	
XX	AC	ADD27151;	
XX	DT	09-APR-2002 (first entry)	
XX	XX	Human T cell derived inducible factor (TIF) beta genomic DNA.	
XX	KM	T cell derived inducible factor; TIF; cytokine; interleukin-9; IL-9;	
XX	KM	protein therapy; STAT activation; differentiation; human; de.	
XX	XX	Homo sapiens.	
OS	XX	US6331613-B1.	
PN	XX	18-DEC-2001.	
PD	XX	18-OCT-1999; 99US-0419568.	
PF	XX	26-OCT-1998; 98US-0178973.	
PR	XX	16-JUL-1999; 99US-0354243.	
PA	XX	(LUDM-) LUDWIG INST CANCER RES.	
PI	XX	Dumoutier L, Louhed J, Renaud J;	
PT	XX	WPI; 2002-105277/14.	
PT	XX	Nucleic acids encoding T cell derived inducible factors useful for	
PT	XX	inducing STAT activation in cells -	
PS	XX	Claim 1; Column 31-36; 24pp; English.	
CC	XX	The present invention relates to an isolated nucleic acid molecule, which	
CC	XX	encodes a T cell derived inducible factor comprising an amino acid	
CC	XX	sequence encoded by 6 defined nucleotide sequences. The nucleic acid	
CC	XX	molecules are shown to be up regulated by the cytokine interleukin-9	
CC	XX	(IL-9) and are described as T Cell Derived Inducible Factors (TIFs). The	
CC	XX	invention is used in protein therapy. The nucleic acid molecules encode	
CC	XX	proteins which induce STAT activation in cells. They can be used, for	
CC	XX	example, in the stimulation of regeneration of targeted tissues.	
CC	XX	Further, their inhibitors or antagonists can be used to retard, prevent	
CC	XX	or inhibit differentiation of other tissues. The present sequence is	

CC human T1F beta genomic DNA.

XX Sequence 4797 BP; 1339 A; 910 C; 1063 G; 1485 T; 0 other;

Query Match 9.2%; Score 686; DB 24; Length 4797;

Best Local Similarity 53.8%; Pred. No. 2.7e-145;

Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;

2034 CTCCTCTCTCACTTATCACTGTGACACTGTGCGATCTGTGATGCTGTCTTGACAA 2093
29 CTCCTCCCACTCAACAGTGTCTGAGTAAATGTCTGCATATGGCCGCTTGACAA 88
2094 ATCTATGAGTTTTCCTTATAGGGAATTGGCCGACAGTGTCTGTCTTCAATGCCCT 2153
89 ATCTGTAGCTCTTTCCTTATAGGGAACCTTGCCACACAGTGTCTCTTCTTGAGCCCT 148
2154 GTGGGCCCCAGAGGGAATAGCGCTGCGGTCAACCCGGTGCAAGCTTGAGGTGCAA 2213
149 CTGTGTACAGGAGAGGACAGTGCAGCCATCAGCTTCCAGTGAAGCTTGACAAATCCAA 208
2214 CTTCCAGAGCCGTCATCTGATCAACCGACCTTATAGTGTGCGCAAGAGTACAGTGA 2273
209 CTTCCAGAGCCGTCATCTGATCAACCGACCTTCAATGCTGTGATAGAGATATACATCTC 268
2274 TCTCTTTCTCTCCATACCGCTTGCCATTTCTCTGAAAGCACTTGCAAACTCTTTAGGG 2333
269 AATCTGTCTTCTCTGTTGATCTACTTGAAATCCAAATAGTCTTAAACTTTTCTCA 328
2334 CGCTTATATCCGAGAGTCTCACTACTATGTTT-----TCTGTCTTTTAGAG 2382
339 GAGCATCTCTAAGAGCTTAGAACCACCTGTTATCCCTGAGGAGATAAATTTTCTG 388
2383 ACTCTTAAAGAGCTGGGCTTTTCTATTTCTAATTTCAAGGTCTAGACCAATTTCCAT 2442
389 TTTTTCAGAGACTCTTTGGGAATCTGGCTTTTCTTTTCTTGAACCTTCTCTCCAT 448
2443 CTTGAGCTTCAGAGACATATATCTGAATTTTATCTACAGAGGGCAATTT--AGAAAGCA 2500
449 TTTGGCTTTATGATATGATATGATGATTTTCCCAAGAGGGCCATTCAGTAAATCAT 508
2501 CCGAGAGCTCAATATCTTCCATTTCTGTGTCTCTTCTGAACTCAATCTCTTGGC 2560
509 CTGATGATTTTCTTATGCTTATGCTGTGATGTTCTTAACTCAAGCAACATCTG 568
2561 TACTC-----CTGAGACCACTGCGGACATACATCTCTAC 2595
569 AATTCCTTTTATGCTTATGATGTTGCTCTGGGAGACGGGATGGGCAATGCTCAT 628
2596 TTACAGGCTTTTCTTCATCTCTTGTCAACCGAGCACTTAGGGTTTC-TCTTTTCAG 2654
629 GATATAATTTTCTTATTTGCTCAATGTCAGACCTTAGCTTTTCTTCTCTCCAG 688
2655 GCGAGCTTCGAGATTAACAACAACAGCTGCGCTCATGGGAGAAACTGTTCGAGGA 2714
689 GGTAGGTTGCTGATTAACAACAACAGCTGCTCATTTGGGAGAAACTGTTCACGGA 748
2715 GTCAAGTAAAGTCTCACTGTATGAGCAAGGC-----TAGTGTGGGAGAGCT 2761
749 GTCAAGTAAAGTCTCACTGTATGAGCAACAGGCTGCTGTGCTCAATGGGATCTTGGGT 808
2762 GGTGAGCCCTCTGGAGTAG---TCTGAGGTATGACCCCTGCTTCTTGTGTACCTGC 2817
809 GGTGGATGATGATGATTTAGGCTTTATCCCTATGACCTTCTGTTTCCCTTCACTGC 868
2818 AGGCTTAAAGTCAAGTCTATCTGATGAAGAGTGTCTCAACTTCACTTGGAGAGAGTTT 2877
869 AGATGAGTGAAGCGCTCTATCTGATGAAGAGTGTCTGAACCTTCACTTGAAGAGTGC 928
2878 TGTCTCCCAAGTCAAGAGTTCAGCCCTTACATGACAGAGAGTGTGATACCTTTCTGACA 2937
929 TGTCTCCCAATGTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 988
2938 AACTGACATATGCTCAAGCTCTGTGTAAAGTCTGACTGTGGCTACCTATGCTCTCTT 2997

989 GGTTCAGACACAGCTAAGACATGTGTAATTTCACTCTAGGCTATGCCACTTACC 1048
2998 CTTCTCTTCTATTTCCAGTAAAGAACCGAGGTCTGCTCTCTCTTCTTCAAGAGTGA 3057
1049 CTCCTTCCCTCTTCCACAGAGACCCCTTACCCCAATCTCTCTCTCTCTCTCTCTCC 1108
3058 GAGGAGCTCAGACACACACATCATATAGGCACTTGAATAGTCAAAAGGCTTTGGC 3117
1109 TAACTGACAGAGAAAGATGTCTTGACAGAGTGTATCAGAGTCA-----TTTGGG 1161
3118 TTCAATGATTAATCTTATGATTTGATGATGATGATGATGATGATGATGATGATGAT 3177
1162 ATCATAGATATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1221
3178 AGAAATCAATCAATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3237
1222 GGTCTGGAATTTAGTGTACAGAAAGCGCATGTTGTTGTTGTTGTTGTTGTTGTTGTT 1281
3238 AGAGAAACAGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3297
1282 A-----GGTTCGTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1309
3298 GTACAGTACTTGTGGGAGAGAAATTCAGTGAATCAAGTACTTGTGGCATGAGATG 3357
1310 GAAACATCTAGCTGTGAAATGATTCATGATGATGATGATGATGATGATGATGATGAT 1369
3358 CACTGATGATCAAGTACTTGTGGGAGAGAGAAATGACACAGACAAAGATTGAAGGAA 3417
1370 CATGAGAGAAATTTGAAGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAG 1415
3418 AAGATGAGAGAGCTCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 3477
1416 -----GTGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1460
3478 AGTTAAGAAAAACA-GTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3536
1461 AGCCCAAAATGAGAGGAGTGTGAACTGATGATGATGATGATGATGATGATGATGAT 1520
3537 ATCCAGAGAGAGGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGGAGGCT 3594
1521 AGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1580
3595 CACAGAGAACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3654
1581 CACATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1640
3655 TTAGGTTTCTTCT-----ACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3693
1641 TTAGGTTTATTTCTTACAGATTTGATTAATTAATTAATTAATTAATTAATTAATTA 1700
3694 TTCAAGTAAATTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3753
1701 CTCAAGTAAATTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1760
3754 GTGTCTTGAAG 3813
1761 GGTTCAG 1820
3814 GGGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3873
1821 TGGGCAAAATTTCTAAG 1880
3874 AGTATGAG 3932
1881 GAGGTTCAATTAAGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1940
3933 CATCAGCGTGAAG 3992
1941 TATTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2000
3993 AAGGATCAATTTGAG 4050


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QY 6119 TCCTGCTAGTACAGATTAGAGTTGAGCAACCTTTTTC----- 6163
DB 4162 TAAGAAAGTTATGAAATTTCTGTTAGGGTGCATTCAGAGCTGTCGGGCCATGTGGCGC 4221
QY 6164 -----AACCCCACTAAATTTATTTAGACAAAAGACTGTGTAATTTG 6205
DB 4222 CTGTGGGCTGCAGAGTTGGAACAACCTCTTATAGTATCTGTATAGATAGTTTGGAGC 4281
QY 6206 TGGGATACAGTGTGATTAATTGA----- 6227
DB 4282 TGCATAAAGAGGCAATGAGGTGCGACTCGGGATCCCGAGTCCACGCTCACT 4341
QY 6228 -----TCTATGTGTGCAATTGTGCAAGTTCAATAAGATTAAAGGCCCATCAACAGC 6283
DB 4342 TCAGTCTCCTGCTGTGGTTAAGAGAGGGGTGTCACCTCTCTGCCAGCTTTTAAAGAGC 4401
QY 6284 TTATAGGCTGTGAATGCAAGTATATAGTAGATGCTGTGTCCTTAGGTCAGAA 6343
DB 4402 TTCTATTAGTGTGAGTGCACCTGAATTAATGATGCTGTGTCCT-CTCAGTCCAGAGA 4460
QY 6344 GGCATGATTTTAAAGTCTTGGGCAATCATATTATCTCATGTCTAAATAATCATTTATGTT 6403
DB 4461 GCCGTCACTTTAAGCTCTTTGGCAATCATCAATCACTAAAGGATA-----T 4508
QY 6404 GATTATTAATCTTTTGAAGAGGCTGATATTGCTTTGCTGCTCAGCAAGCAATGTCA 6463
DB 4509 TACTATGAATGTTTCAATATGCTTAAACTCGGTTTCTCTCCATCAACCTTAATCTTG 4568
QY 6464 CCAGCTCTTCTACAGTGTACCACTTTAGAAAATGCTACTGTCCTCAATTTGTTGTA 6523
DB 4569 CAATTTCT--AATTTGTCACCTTTAGAAAACATGGCATTAATGCTCAATTTTGCA 4625
QY 6524 TTCTATTATTCATAGCTTGGAGAGAGTGAAGATCAAGGCGATTGGGGAATGGAACCTG 6583
DB 4626 TTCTATTATTCACAGCTTGGAGAGAGTGAAGATCAAGCAATTTGGAGAGTGGATTG 4685
QY 6584 CTGTTATGCTCTTGAAGAAATGCTTGGCTGTGACGAGAAAGAACTAGAAAAGAGAAC 6643
DB 4686 CTGTTATGCTCTGAGAAATGCTGCTGATTTGACAGAGCAAGCTGAAAAATGAATTAAC 4745
QY 6644 TGTCTCTCTGCTCTTAAAGAAACAATTAAGATCCCTTAATGAGACTTTT 6695
DB 4746 TAACCCCTTTCCCTCTAGAAATTAACAATTAGATGCCCAAGCGATTTT 4797

RESULT 12
AAA28840
ID AAA28840 standard; DNA; 4796 BP.
XX
AC AAA28840;
XX
DT 04-SEP-2000 (first entry)
XX
DE Human T cell inducible factor genomic DNA.
XX
KW TIF; T cell derived inducible factor; interleukin 9; STAT; IL-9;
KW Anti-asthmatic; anti-allergic; cytosolic; inhibitor; antagonist;
KW probe; chromosome 12q15; ss.
XX
OS Homo sapiens.
XX
XX
Key Location/Qualifiers
FH 108..4717
FT /+tag= a
FT 1..257
FT exon
FT /+tag= b
FT 258..688
FT intron
FT /+tag= c
FT 689..754
FT exon
FT /+tag= d
FT 755..870
FT intron
FT /+tag= e
FT 871..1014
FT exon

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FT FT /+tag= f
FT intron 1015..1938
FT /+tag= g
FT exon 1939..2004
FT /+tag= h
FT intron 2005..3837
FT /+tag= i
FT exon 3838..4796
FT /+tag= j
XX
XX WO200024758-A1.
XX
XX 04-MAY-2000.
XX
XX 18-OCT-1999; 99WO-US24424.
XX
XX 26-OCT-1998; 98US-0178973.
XX 16-JUL-1999; 99US-0354243.
XX
XX (LUDM-) LUDMIG INST CANCER RES.
XX
XX Dumoutier L, Louhed J, Renaud J;
XX
XX WPI: 2000-422495/36.
XX P-PSDB; AAY2879.
XX
XX New nucleic acid molecule encoding a T cell derived inducible factor
XX for treating asthma, an allergy or lymphoma
XX
XX Claim 1; Page 39-40; 46pp; English.
XX
XX This DNA encodes a human T cell derived inducible factor (TIF). The gene
XX was mapped to chromosome 12q15. The human TIF was identified based on
XX homology to a murine TIF, which was identified by subtraction cloning
XX from a murine lymphoma cell line BM5147 in the presence or absence of
XX interleukin 9 (IL-9). BM5147, can be grown in vitro, without the need to
XX add any cytokines to its culture medium. Many IL-9 activities are
XX mediated by activation of STAT transcription factors. The novel TIFs were
XX expressed in the presence of IL-9, but not in its absence. TIFs induce
XX STAT activation in cells. They can be used, e.g. in the stimulation of
XX regeneration of targeted tissues. Their inhibitors or antagonists can be
XX used to retard, prevent or inhibit differentiation of other tissues. The
XX TIFs and their coding sequences are useful in the treatment of asthma,
XX allergies and lymphoma (claimed). They are also useful for identifying
XX compounds that inhibit or activate T cell induced factor activity in a
XX cell (claimed).
XX
XX Sequence 4796 BP; 1339 A; 912 C; 1063 G; 1482 T; 0 other;
XX
XX
XX Query Match 9.2%; Score 682.4; DB 21; Length 4796;
XX Best Local Similarity 53.8%; Pred. No. 1.8e-144;
XX Matches 2642; Conservative 0; Mismatches 1876; Indels 394; Gaps 44;
XX
QY 2034 CTCTCTCTCACTTATCAACTGTGACACTTGTGCATCTCTGATGGCTGCTGCAGAA 2093
DB 29 CTCTCTCCCAAGTACACAGATGCTCGAGTAGAATGTCTGCAATGCGCGCTGAGAA 88
QY 2094 ATCTAGAGTTTTCCTTATGAGGACCTTGGCGCCAGCTGCTCTCTCAATGGCCCT 2153
DB 89 ATCTGAGAGCTCTTCTTATGAGGACCTTGGCGCCAGCTGCTCTCTCTCTTGGCCCT 148
QY 2154 GTGGGCCAGAGGCAATGCGTGGCCGCTCAACCCCGATGACCTTGAAGTGTCCA 2213
DB 149 CTGTGTAACAGGAGAGGAGCTGCGCCATGAGCTCCACTGAGGCTTGAACAAGTCCA 208
QY 2214 CTTCAGACAGCCGTATCATGTCAACCGACCTTATGCTGGCCAGAGAGTACAGTCA 2273
DB 209 CTTCAGACAGCCGTATATCAACCAACCGACCTTATGCTGGCCAGAGAGTATACATTC 268
QY 2274 TCTCTTCTCTCATACCGCTTGCATTTTCTGGAAGCACTGCAAACTCTTGAAGG 2333
DB 269 AATCTGCTCTTCTGTTGATCTACTGGAATCAAAAGCTTTTAAACTTTTCTTCA 328

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QY 2334 CGCTTATCTCCGAGGTCTCACTACATATGTT-----TCTGTCTCTTAGAG 2382
 DB 329 GAGCATCTCTAAGACCTTTAGAACCCACTGTTATCCCTGAGGGTAAGTAATTTCTG 388
 QY 2383 ACTCTTTAGAGACTGGTCTTTTCTATTTCTATTTCAAGGTCAGAGACCATTTCTAT 2442
 DB 389 TTTTTCAGAGACTCTTTGGGAACTGTGGCTTTTCTTTTCTTGAACCTTCTCCAT 448
 QY 2443 CTGGCTTCAGAGACATATCTGAATTTATCTACAGAGCGCATTT--AGAAAGCCA 2500
 DB 449 TTTGGCTTTATGATACATATGATGAATTTTCCAAAGAGCGGCATTCACTATTCAT 508
 QY 2501 CCCAGACTGCATCTTCTCTGTCCTCTCTTCTCAATCTCTCTTGGC 2560
 DB 509 CTGATGATTTTCTTTCTTATGCTCTGTGCACTGTCTTAACTCATGACACATCTG 568
 QY 2561 TACTC-----CTGAGACCACTGCGGACATACATCTAC 2595
 DB 569 AATTCTGCTTTTAGCTTTATGATGTGCTCTGGGAGACGGGATGGGGACATGTCTAT 628
 QY 2596 TTACAGGCTTTTCTTCATCTCTCTGTCACCCGAGCACTTAGGGTTTC-TCTCTTTCAG 2654
 DB 629 GATATAATTTTCTTCTATTTGCTCAATGTCCAGACCTTAGTCTTTCTCTCTCCAG 688
 QY 2655 GCCACCTTCAGATTAACAACAAGCGTCCGCTCATCGGGAGAAATCTTCCGAGA 2714
 DB 689 GCTACCTTGGCTGATTAACAACAAGCGTCTCATTTGGGGAAATCTGTCCACGA 748
 QY 2715 GTCACTGTATGCTCCACTGTGATGAGAGGCG-----TAGCTGGGGAGCT 2761
 DB 749 GTCACTGTATGCTCACTGTGATGAGAGAGGCGCGTCCATGAGGATCTTGGGT 808
 QY 2762 GGTGAGACCTCTGGGATAG---TCTGACGTATGACCCCTGCTCTTCTGTCTACTGC 2817
 DB 809 GGTGTGATGATGTTTATGCTTATCCCTTATGACCTTCTGTCTTCCCTCCACTGC 868
 QY 2818 AGGCTAAAGATGATGCTACTGATGAGACAGGCTCTCACTTCACTCTGAGAGCTTC 2877
 DB 869 AGATAGTGTAGCGCTGCTATCTGATGAGAGAGGCTGTAACCTTCACTCTGAGAGCTGC 928
 QY 2878 TGCTCCCCAGTCACAGACAGGTCACAGCTCTACATCAGAGAGGTGATCTTCCGACA 2937
 DB 929 TGTCTCTCAATCTATAGTGTCCAGCTTATATCAGAGAGGTGTGCTTCCGACA 988
 QY 2938 AACTCAGCAATCAGCTCAGCTCTGTATGCTGATCTGTGCTACTTACTTCTCTCT 2997
 DB 989 GGTCTAGCAACAGGCTTAGCAATGTGTAGTTCACTCTAGCCCTATGCCACCTTACC 1048
 QY 2998 CTTCCTCTTATTCAGTACAGACCCGAGGCTGCTCTCTCTTACAGAGTGA 3057
 DB 1049 CTCTCTCCCTCTTCCACAGAGACCCCTTACCCCACTCTCCCTTCCCTTACC 1108
 QY 3058 GAGAGGCTCAGACACACACATCATAGGCACTTGAATAGTTCACAAAGCTTGGC 3117
 DB 1109 TAAAGTACAGAGAAAGTGTCTGGCAGCAGTGTATCAGAGTCA-----TTTGGG 1161
 QY 3118 TTCAATTGATATCTTTGAGTTGTATGATGAGCTTATTTGTTTATCATGNA 3177
 DB 1162 ATCATAGAGTATTTGCTTTTGTGCTTGAAGTCACTCATCTTATAGTTTATGCTGAATG 1221
 QY 3178 AGAAATCAACTCAAAATCTGATGATGAGAAAGATGTTGGAGCAAGAAAGGCTTAT 3237
 DB 1222 GGGTCTGGAACCTTAAAGTATGAGAAAGCCGATTTGTTGTCTTGGAAAGGCAATCC 1281
 QY 3238 AGAGAAACGATCTCTGTAGTATGATCTTATGGGGGAGCAGAGGGGCGATTCACATGA 3297
 DB 1282 A-----GGTTGCTAAGATGAGAAAGGTGTGG 1309
 QY 3298 GTACAGATCTTGTGGGAGAGAAATCCACTGATACAGTACTTGTGGCTGAGATC 3357
 DB 1310 GAAACATCTAGCTGTGGAATGATCCATTGAGTAAAGTTGTGGAGGAGGGGATGG 1369
 QY 3358 CACTGATACAAAGTACTTGTGGGGGAGGGAATGGCAGAGCAAAAAGTTGAAGGAGAG 3417

DB 1370 CATGAGAGAAATTAAGAGAAAGTGGAAATGGGAAGCTTAA----- 1415
 QY 3418 AAGATGAGAGAGCTCATGTTGGGGGTGTAAGAGTCACTCTTTTCATGTGATGAG 3477
 DB 1416 -----GTGGTGTGGGTGGGCGAGACTGTGCTCCCTGTGATGTATGGGA 1460
 QY 3478 AGTTAAGAAACCA-GTGTGTAGTTGATGTCTTGACAGACACCCCACTATGAACT 3536
 DB 1461 AGCCACAAATCGAGGGGTGTGAATGTGATGCGCTGAAATTTGAAACTATGAAAAA 1520
 QY 3537 ATCCACGAGAGCGGGCAGACTGTGGGAGCTGGCATTTTGGGAAGCGCGGC--TTT 3594
 DB 1521 AGTTGATGATGTGGGCCCACTAAGAGCCCTTAGACTTACTGAAGAGGCTTATTT 1580
 QY 3595 CACACGAGAACTTATGCTCATCTTGTGCTACACTCCACCTTATGATGAGTTCAGC 3654
 DB 1581 CACATGAGATTTTATGTATCTTCTTCTTAAAGCATGCAATTTCTGGAGATACAT 1640
 QY 3655 TCAGGTTTCTTTCT-----ACGTTCTTGTACTGTGGAAC 3693
 DB 1641 TGAGGTTTATTTCTTACAGAAATTTGCAATAACTCTCCGCTTTCCACAAATCAAC 1700
 QY 3694 TTCAATGATTTCCCAAGAGAGAGAGAGAGCTCTTCTGTAAGGAGGAGACCTGATTC 3753
 DB 1701 CTCACTAGATTTTCCCAAGAGAGAGAGAGCTCTTCTGTAAGGAGAGAGCTGATTTCTG 1760
 QY 3754 GTGTCTAGAGAGCAATTAAGTCTGAGATCTAGGTCAGAGTGAATCTAGGTCAGAC 3813
 DB 1761 GCGTCAAGAGAAATTAAGAGACTCAGAGAAATCTAGGTCAGCTTGAATCTAGGTCAT 1820
 QY 3814 GGGCAAAATGACTGAAGAGCTTATTCAGGTCAGAGAGTCACTGCTCAGATATCTG 3873
 DB 1821 TGGGCAAAATTAAGAGAGCTTATTCAGGTCAGAGATGTACTGATCTCCATGAGGTG 1880
 QY 3874 AGATTTGGGCTCCACCGGATTAAGATCTGTATGTA-GTCTGCTTTATTTTCAGCA 3932
 DB 1881 GAGGTCATTAAGTTTCAGCAACCATTAAGATTAATGCTGTATTTGTTTATGTA 1940
 QY 3933 CATCAGCGGTGACGACAGACATCCAGAAATGTCAAGAGCTGAAGAGACAGTGA 3992
 DB 1941 TATTGAAGTATGACCTGTCAATTCAGAGAAATGTCAAGAGCTGAAGAGACAGTGA 2000
 QY 3993 AAAAGTACTATGGCAACCAATTAAGTCAATTCAGTACAGTACAGTACAGTACAGT 4050
 DB 2001 AAAGTATGACTGATTAAGTCAATTCAGTACAGTACAGTACAGTACAGTACAGT 2060
 QY 4051 TTTCTGCTTCCAGTCTCTTCTTATCTTGTATCAATTTATTTGATCTGTCTACTATCTG 4110
 DB 2061 TTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2120
 QY 4111 GTCACTTACGCTTGTAGTACCGTATCTAGTGGCTATAGATCTTCAATCTGTG 4170
 DB 2121 GCGCATTA-----CTTGGTGTGTGTATGTATATCTTATATCTTATGTCAAGT 2176
 QY 4171 TCTAATTT---GTATGACAAATTCAGTACAGAAAGCTTACAGTACAGTACAGT 4227
 DB 2177 TCCAAATCTTCAAAATTTAGATTTCTAGAACTGTGGATCTTACGTTGTCTGTGTC 2236
 QY 4228 ATGAGCACTTGTGGAGAGTGTGTGTGACAGAGTCAATGTATAGACAGATCTCTG 4287
 DB 2237 ATAACTTCAGATTTCTGGGATGTGTGAGGAGATGTGGCTTAAGAGAGTCTCTG 2296
 QY 4288 ATTCACAGCTGTGAC-TTGCTAGTGTGCTATATTAATCTTGGCTGTATTAAGTAT 4346
 DB 2297 AATCCAGAGCAAGCTTTTCCGCTGTGTATCAGATTAATTTTGTGTATCAATTAATCT 2356
 QY 4347 TTGGAAA--GCCATTCACAGACCTTACATATCTGAGAAACCATCATTTGAAACTA 4404
 DB 2357 TAGGAAATTTCAATCTCTATGATCATGTAACTGAAGATGTTGTTTAAACAA 2416
 QY 4405 GAAAGCTGGGCA---CAACTTACTAGATGATTTTGGAGCTCATTAACAGATGTCTC 4460

Db 2417 GAAAAATGCTATGGGCAATTTATTTGAAGTCATTTTGAAGTCATTAATGATGCTT 2476
QY 4461 TGAATATGTGCAAAATCAACCAGAAATTAACAACAAAGAGCTGATTTGCAATAGACA 4520
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QY 4521 AGATTATTAAGATCACTGATTAATTAATAGTATCATCTTAATTAATTAATTAAGGCTTAATA 4580
Db 2537 AATTCTCGA-----GTAATTAACACTTAATTTTGAATTAATCAATTAATCTATAGATA 2589
QY 4581 TATATTAAGATTAACAAGAGAGTAGAGTCCCAATTAATTAATTAATTAATTAATTAATTA 4640
Db 2590 TGAATTAATAGTTTAAAGCAAGAGAGACAACCC-CCGATCTCTTTTAATACAGGTTCAAT 2648
QY 4641 AGAGTAAATATATCAGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4700
Db 2649 AGAGTAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2708
QY 4701 TTCTCTTAATTTTAATCTTCA-----TTTCTTAATTTTCTTCTTCACTCTGA 4752
Db 2709 TTTTCA 2768
QY 4753 TCAAGCCATAGTATAGCACTATGCTGATGAGCTATTAATTAATTAATTAATTAATTAATTA 4812
Db 2769 ACAAATCCCTAAGGAGCAATTAATCAATGAGGCTGCTGATCAATTTCTATAGTATGAT 2828
QY 4813 ATTGCTGTGAGCTCTTTGGGAAAGGAGACAGATAGCAGAGGCTCAGGCTTACAGT 4872
Db 2829 ACCATCATATGAGCTATTTGGTGAAGAAAGAAC--ACAATGAGAGCTTATGACTATCAATA 2886
QY 4873 CTGATCCCTTAAGCCAGAGAGCATGCTGATAGCAGAGAAAGTGAAGCTCTTCCAG 4932
Db 2887 GTGATCTACCCCAAAACCGAGAGAAATGATTAAGAGCAGTGAAGAGAGCTCTT--GCAAG 2945
QY 4933 TGGGTGTCTTAAGTATCAAGAAACAGAGAGCTCCGCTGATGGAATTAATTAATTAATTAAG 4991
Db 2946 CAGGTACAACATAAATCAAGAAACATAGAGCTCAGTGAATTAATTAATTAATTAATTAAG 3005
QY 4992 -----TATCTACCTTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5042
Db 3006 GCTTAACCTTAATCTAG 3065
QY 5043 TGTAGGCTGATTAACACACTGTT--TTCTTTTGAAGTTCATGAGCTTTTGAATTTTA 5100
Db 3066 CATCATTAATTAAGAGTACGCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3125
QY 5101 GTGCTCTGCAAGTCTTGT--TAGAGGTTGTATCTTGAACCTGAGGCTTGAATTTTA 5158
Db 3126 TTGTGAAGCCCAAGTCTTA 3185
QY 5159 GCATGCCAAGGACACACTCTGTAATGCTGTGTAAGAAAGTTATTAATTAATTAATTAATTAAT 5215
Db 3186 GCATGCCAAGGACACACTCTTACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3245
QY 5216 -----TTGCTCTTGAAGAGTGAAGCTGTGTGAAGAAAGTCAAGAGATGTGCT 5270
Db 3246 GCTTGTCTCTTTAAGAAAGTGAAGTGAAGAGAGAACTCATGTGA----- 3296
QY 5271 CTGTAGAAAACTTTTCT 5327
Db 3297 -----TCTGTGATTTTCAAGACCTTTTATCTATCTTTTGAAGAAATCAAT 3342
QY 5328 TGACTTTATATCATGCTGTCAATGAAGAGTGTGAGGCGCGCTCATAGGCTGTGG 5387
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QY 5388 AAAACACCAATAGGAGAGAGATGTATGCTGAAGAAATCTGACCGGACAGGAAATGTGT 5447
Db 3403 GAAAGCA--CAGGAGGAGAGCATGTGTTCAGAGAAAGATCAACAGAGAGAGAAATCTGT 3461
QY 5448 CAGAGCTCCCGAAGACA-----CCACAGGTGTTAAGTAG 5485
Db 3462 CAGAGCTGTCTGAAATAGGAGTGTGAGAGGCAATTAATCTCTCTCTCTCTCTCTCTCTCT 3521

QY 5486 AACGCTCAGGCTGGCTCATGTATTAATGAATGGAACAGAGAGAGAGATTAAGTACAA 5545
Db 3522 AGCAGAAACGAGGTGTGTAGTAAAT--GCATGACAGCAGTGAAGGAGCAGTAACTTTAA 3580
QY 5546 AGTTCAATAGGCTC--CGAGATCTTAAGATTAATTAATTAATTAATTAATTAATTAATTA 5602
Db 3581 AATCTTTATATGTCTTGAAGCTTTGAGATTAAGAAAGAAATATCTTTTGGCTTATGTCA 3640
QY 5603 AAGNAGCTGGAGAGCAGCAAGTGAAGAGAAATGAAAGGAGAAACAGATATGAG 5662
Db 3641 AAAGAGATTAAGAG-----TGAAGGCGAGAGAAAGAGAGAGAGAGAG 3688
QY 5663 AGAATTAAGACAGTCAATATCTCTACAGAGATTTTCTTGAACATCTGAAGT 5722
Db 3689 AACCATGATTAATTAAGAGCAATGTGACAAAGTCTTCTTGAATTAAGCAATATG 3748
QY 5723 AGTGATTAAGTGAATGAGAGGAGACTGCTTGCATTTGAATCTGGGTTTGTCTCT 5782
Db 3749 ATGATTAAGAGAAATTCAGAGAGAAATGCTTTCACTGAATTTGGGTTCTCT--T 3805
QY 5783 CCATTGAGGTTGAAGGCTCACTCTTTTACCTCGAATGAGAGAGAGAGAGAGAGGCTGT 5842
Db 3806 CGATTAAGTGGATCTCTATCTGCAATTAAGT--TGAAGAGAGAGAGAGAGATGT 3861
QY 5843 TATGATCTCTAAGTCTGAGTTTACTAGTTTACGAATGGAACAGACACTCGGACCTCT 5902
Db 3862 TAGGACCTATATCTGTTTCTATTAATTAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 3921
QY 5903 CTGACAAAAAATGAAACCTGTTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5962
Db 3922 TTCCACAAAAAGTAAACCTTTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3981
QY 5963 AGGCAAGCCCGACCAACATGAGGTTGAATGTGGCTCTTGAAGTCAAGGCTTGAAGTGAAG 6022
Db 3982 CTTATATGATTTGAGAAATCATGTTCAAGTCAATTTGAGTAAAGATTTTAAATAG 4041
QY 6023 CACTCATCAATAGT-----GATCATGTGAGTGAAGGCT 6058
Db 4042 GAGTGTCAATCATTTGGCTTCCCTGACCACTTGAAGAAAGATTTGCTGTATACACAT 4101
QY 6059 TACCTGTAGGCGGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6118
Db 4102 AAAATACAGAAACATATGCTATGAGCTAAAGAAAGTCCATGCAATTAATCTATCTGTT 4161
QY 6119 TCTGCTACTTGAACAGTGAAGTGAAGGAGAACTTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 6163
Db 4162 TAAGAAATTAATGATTTCTGTTAAGGCTGATTAAGAGCTCTCTGAGGCTATGTGGGC 4221
QY 6164 -----AACCCCACTAAATTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 6205
Db 4222 CTGTGGCTGAGGTTGAGCAAGCTCTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4281
QY 6206 TGGATACAGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 6233
Db 4282 TGCAAAACAGGCAAGGATATGAGTGAAGCTGAGGATCCCGAGATCCAGCTCACT 4341
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QY 6464 CCAGCTCTTCTAAGTGGACACTTGAAGAAATGCTACTGCTCAATTTGTTGTA 6523
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QY 6524 TTCTTAATTTTCAATGCTTGGAGAGAGTGGAGATCAAGCGATTGGGAACTGGACCTG 6583
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QY 6584 CTGTTATGTCCTGAGAAATGCTTGGCTTGGAGGAGAAAGCTAGAAAAAGAAAC 6643
DB 4685 CTGTTATGTCCTGAGAAATGCTTGGCAATTTGACCAAGCAAGCTGAAAAATGATTAAC 4744
QY 6644 TGCTCTCTCTGCTCTTAAAAAGAACATAAGATCCCTGAATGACTTTT 6695
DB 4745 TAACCCCTTTCCCTGCTAGAAATTAAGATGCCCAAGCAATTTT 4796

RESULT 13
ID AAA28815 standard; cDNA, 1119 BP.
AC AAA28815;
XX 04-SEP-2000 (first entry)
DE Murine T cell inducible factor alpha cDNA.
XX TIF-alpha; T cell derived inducible factor; interleukin 9; STAT; IL-9;
KW Anti-asthmatic; anti-allergic; cyostatic; inhibitor; antagonist; ss.
XX Mus sp.
FH Key Location/Qualifiers
FT CDS 52..591
FT /*tag= a

WO200024758-A1.
XX PD 04-MAY-2000.
XX PF 18-OCT-1999; 99WO-US24424.
XX FR 26-OCT-1998; 98US-0178973.
XX PR 16-JUL-1999; 99US-0354243.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Dumoutier L, Lohued J, Renaud J;
XX WPI; 2000-422495/36.
XX P-PSDB; AAY92877.
XX PT New nucleic acid molecule encoding a T cell derived inducible factor
XX for treating asthma, an allergy or lymphoma
XX Claim 1; Page 33; 46p; English.
XX This cDNA encodes T cell derived inducible factor (TIF) alpha identified
XX by subtraction cloning from a murine lymphoma cell line BW5147 in the
XX presence or absence of interleukin 9 (IL-9). BW5147, can be grown in
XX vitro, without the need to add any cytokines to its culture medium. Many
XX IL-9 activities are mediated by activation of STAT transcription
XX factors. The novel TIFs were expressed in the presence of IL-9, but not
XX in its absence. TIFs induce STAT activation in cells. They can be used,
XX e.g. in the stimulation of regeneration of targeted tissues. Their
XX inhibitors or antagonists can be used to retard, prevent or inhibit
XX differentiation of other tissues. The TIFs and their coding sequences are
XX useful in the treatment of asthma, allergies and lymphoma (claimed). They
XX are also useful for identifying compounds that inhibit or activate T cell
XX induced factor activity in a cell (claimed).

Sequence 1119 BP; 352 A; 233 C; 232 G; 302 T; 0 other;

Query Match 8.1%; Score 601.4; DB 21; Length 1119;
Best Local Similarity 99.8%; Pred. No. 2.3e-126;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6535 ATACCTGGAGAGAGTGGAGATGATCAAGCGATTGGGAACTGGACCTGTTTATGTC 6594
DB 510 AAACCTGGAGAGAGTGGAGATGATCAAGCGATTGGGAACTGGACCTGTTTATGTC 569
QY 6595 TCTGAGAAATGCTTCCCTTGGAGGAGAAAGCTAGAAAAAGAAAGCTGCTCTTCT 6654
DB 570 TCTGAGAAATGCTTCCCTTGGAGGAGAAAGCTAGAAAAAGAAAGCTGCTCTTCT 629
QY 6655 GCCTTCTAAAAAGAACATAAGATCCCTGAATGACTTTTACTTAAAGAAAGTGAGAA 6714
DB 630 GCCTTCTAAAAAGAACATAAGATCCCTGAATGACTTTTACTTAAAGAAAGTGAGAA 689
QY 6715 GCTAAGTCCATCATCTATTAGAAATTCATGAAACCTGGCTCAGTTGAAAAAGAAA 6774
DB 690 GCTAAGTCCATCATCTATTAGAAATTCATGAAACCTGGCTCAGTTGAAAAAGAAA 749
QY 6775 TAGTGTCAAGTGTGTCATGAGACCAAGGTTAGCTGTATTAACCAAGATTCTTACA 6834
DB 750 TAGTGTCAAGTGTGTCATGAGACCAAGGTTAGCTGTATTAACCAAGATTCTTACA 809
QY 6835 ATATTTTATGTCATGATGATACAGAAAAATTAATGATCTTAAAAATGTTGAA 6894
DB 810 ATATTTTATGTCATGATGATACAGAAAAATTAATGATCTTAAAAATGTTGAA 869
QY 6895 AGAGAGTTACTCTCATCTCTTTAGAAAAAGTTATGTAATTCATTTCCATATCCA 6954
DB 870 AGAGAGTTACTCTCATCTCTTTAGAAAAAGTTATGTAATTCATTTCCATATCCA 929
QY 6955 TATTTTATATGTAAGTTATTTATTAAGTATTAATTTATTTATGTCAGTTATTA 7014
DB 930 TATTTTATATGTAAGTTATTTATTAAGTATTAATTTATTTATGTCAGTTATTA 989
QY 7015 ATATGATTTTATTAAGAAACATTAATCTGATATGTAATTTATTAAGGCAATATA 7074
DB 990 ATATGATTTTATTAAGAAACATTAATCTGATATGTAATTTATTAAGGCAATATA 1049
QY 7075 TTTATGACATTAATTAAGAAACAGATTTTGGCTTTATTAATTAACCATGATATCAT 7134
DB 1050 TTTATGACATTAATTAAGAAACAGATTTTGGCTTTATTAATTAACCATGATATCAT 1109
QY 7135 AAA 7137
DB 1110 AAA 1112

RESULT 14
ID AAS14858 standard; cDNA, 1119 BP.
AC AAS14858;
XX 19-DEC-2001 (first entry)
XX Mouse cDNA encodingT cell derived inducible factor, TIFalpha.
XX Mouse; T cell derived inducible factor; TIFalpha; ss; antiallergic;
XX antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;
XX cancer; lymphoma; immune system disorder; allergy; asthma;
XX acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
XX thyroiditis; melanoma; hepatoma.
XX Mus musculus.
FH Key Location/Qualifiers
FT CDS 52..591
FT /*tag= a
FT /product= "TIFalpha"
FT primer_bind 106..126
FT /*tag= b


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FT /note= "PCR primer appearing as AAS14861"
FT primer_bind Complement (764..784)
FT C /tag= "C"
FT /note= "PCR primer appearing as AAS14862"
PN US2001024652-A1.
XX
XX 27-SEP-2001.
XX
XX 29-DEC-2000, 2000US-0751797.
XX
XX 18-OCT-1999, 99US-0419568.
XX 26-OCT-1998, 98US-0178973.
XX 16-JUL-1999, 99US-0354243.
XX
XX (DUMO/) DUMOUTIER L.
XX (LOUA/) LOUAHED J.
XX (RENA/) RENAULD J.
XX
XX Dumoutier L, Louahed J, Renauld J;
XX
XX WPI, 2001-638496/73.
XX P-PSDB; AAU09090.
XX
XX New isolated nucleic acid molecules encoding T cell inducible factors,
XX useful as markers for expression or effect of interleukin (IL)-9 in a
XX subject and diagnosing susceptibility to asthma or allergy
XX
XX Claim 1; Page 10; 26pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule, which encodes
XX a T cell derived inducible factor (TIF) which are upregulated by the
XX cytokine interleukin-9 (IL-9) and induce STAT transcription factor
XX activation. The TIF proteins (or their muteins) may be used to test IL-9
XX and/or agonists for their potency against lymphomas, immune system
XX disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
XX autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
XX or inhibit differentiation of tissue types in which they are active and
XX therefore be used to develop treatments for melanomas and hepatomas.
XX The present sequence encodes mouse TIFalpha.
XX
XX Sequence 1119 BP; 352 A; 233 C; 232 G; 302 T; 0 other;
XX
XX Query Match 8.1%; Score 601.4; DB 22; Length 1119;
XX Best Local Similarity 99.8%; Pred. No. 2.3e-126;
XX Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6535 ATAGCTTGAGAGAGTGAAGATCAAGCGATTGGGAACTGGACTGCTTTATGTC 6594
DB 510 AAAGCTTGAGAGAGTGAAGATCAAGCGATTGGGAACTGGACTGCTTTATGTC 569
QY 6595 TCTGAGAAATGCTTGGCTTGAGCGGAAAGAAAGCTAGAAAACGAAAGACTGCTCTTCC 6654
DB 570 TCTGAGAAATGCTTGGCTTGAGCGGAAAGAAAGCTAGAAAACGAAAGACTGCTCTTCC 629
QY 6655 GCCCTCTAAAAGAAACAATTAAGTCCCTGAATGCACTTTTACTAAGGAAGTGAAGAA 6714
DB 630 GCCCTCTAAAAGAAACAATTAAGTCCCTGAATGCACTTTTACTAAGGAAGTGAAGAA 689
QY 6715 GCTAAGCTCATCATCATTAAGAAAGATTTCATGAAAGCTGGCTAGTGAAGAAAGAA 6774
DB 690 GCTAAGCTCATCATCATTAAGAAAGATTTCATGAAAGCTGGCTAGTGAAGAAAGAA 749
QY 6775 TAGTGCAAGTTGTCATGAGACGAGAGGTAGACTTGATPACCAAGAAATTCATTGACA 6834
DB 750 TAGTGCAAGTTGTCATGAGACGAGAGGTAGACTTGATPACCAAGAAATTCATTGACA 809
QY 6835 AATATTTATGTCATGAGATGATACACAGAAATAATGACTTTAAATTTGTTGAA 6894
DB 810 AATATTTATGTCATGAGATGATACACAGAAATAATGACTTTAAATTTGTTGAA 869
QY 6895 AGAGAGTACCTCTCATTCCTTTAGAAAAAAGCTTATGTAATCTTCAATATCCAA 6954

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DB 870 AGAGAGTACCTCTCATTCCTTTAGAAAAAAGCTTATGTAATCTTCAATATCCAA 929
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DB 930 TATTTATATATGATTAAGTTATTTATTAAGATACATTTTATTTATGTCAGTTATTA 989
QY 7015 ATATGATTTATTTATAGAAACATTTATCTGCTATTTGATTTTATGATTAAGCAATPATA 7074
DB 990 ATATGATTTATTTATAGAAACATTTATCTGCTATTTGATTTTATGATTAAGCAATPATA 1049
QY 7075 TTATGACATATACATATGGAAGAAAGATATCTTAGGCTTTAATAAACAATGATATCAT 7134
DB 1050 TTATGACATATACATATGGAAGAAAGATATCTTAGGCTTTAATAAACAATGATATCAT 1109
QY 7135 AAA 7137
DB 1110 AAA 1112
XX
XX RESULT 15
XX AAD30627
XX ID AAD30627 standard; cDNA; 1119 BP.
XX
XX AAD30627;
XX
XX AC AAD30627;
XX
XX DT 21-MAY-2002 (first entry)
XX
XX DE Mouse TIF alpha cDNA.
XX
XX KW T cell derived inducible factor; TIF; interleukin-21; IL-21; mouse;
XX KW STAT transcription factor; acute phase protein; inflammation; ss.
XX
XX OS Mus musculus.
XX
XX FH Key Location/Qualifiers
XX FT CDS 52..591
XX FT /tag= a
XX FT /product= "Mouse TIF alpha protein"
XX
XX PN W0200210393-A2.
XX
XX PD 07-FEB-2002.
XX
XX PF 27-JUN-2001; 2001WO-US20485.
XX
XX PR 27-JUL-2000; 2000US-062617.
XX
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX PI Dumoutier L, Renauld J;
XX
XX DR WPI; 2002-195964/25.
XX
XX P-PSDB; AAE19235.
XX
XX PT Stimulating expression of STAT transcription factor and inducing
XX PT production of acute phase protein in a cell, involves contacting a cell
XX PT capable of expressing STAT with T cell derived inducible factors -
XX
XX PS Example 6; Page 49; 64pp; English.
XX
XX CC The invention relates to nucleic acid molecules encoding T cell
XX CC derived inducible factors (TIFs) also known as interleukin-21 (IL-21).
XX CC TIF polynucleotides are upregulated by the cytokine, IL-9. IL-TIF or
XX CC IL-21 molecules are implicated in activation of STAT transcription
XX CC factors, acute phase proteins and inflammation. The present sequence
XX CC is mouse TIF alpha cDNA.
XX
XX SQ Sequence 1119 BP; 352 A; 233 C; 232 G; 302 T; 0 other;
XX
XX Query Match 8.1%; Score 601.4; DB 24; Length 1119;
XX Best Local Similarity 99.8%; Pred. No. 2.3e-126;
XX Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```


QY 6535 ATAGCTTGAGAGAGTGAAGATCAAGCCATTGGGAACTGGACCTGCTGTTTANGTC 6594
| | | | |
Db 510 AAAGCTTGAGAGAGTGAAGATCAAGCCATTGGGAACTGGACCTGCTGTTTANGTC 569
| | | | |
QY 6595 TCTGAGAAATGCTGCGCTCTGAGCGAGAGAAAGCTAGAAAACGAAGAACTGCTCTTCT 6654
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Db 570 TCTGAGAAATGCTGCGCTCTGAGCGAGAGAAAGCTAGAAAACGAAGAACTGCTCTTCT 629
| | | | |
QY 6655 GCCTTCCTAAGAAACATTAAGATCCCTGAATGACCTTTTACTAAGAAAGTGAGAA 6714
| | | | |
Db 630 GCCTTCCTAAGAAACATTAAGATCCCTGAATGACCTTTTACTAAGAAAGTGAGAA 689
| | | | |
QY 6715 GCTAAGCTCCATCATCATTAAGAAATTTCAATGAAACCTGGCTCAGTTGAAAAAGAAA 6774
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Db 810 ATATTATTTGTCACCTGATGATACACAGAAAAATPATGTACTTTAAAAAATGTTGAA 869
| | | | |
QY 6895 AGGAGGTACCTCTCATTCCTTTAGAAAAAAAGCTTATGTAACTTCATTCATATCCAA 6954
| | | | |
Db 870 AGGAGGTACCTCTCATTCCTTTAGAAAAAAAGCTTATGTAACTTCATTCATATCCAA 929
| | | | |
QY 6955 TATTTTATATATGATGATTTATTTATTTATAGTATACATTTTATTTATGTCAGTTTATTA 7014
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Db 930 TATTTTATATATGATGATTTATTTATTTATAGTATACATTTTATTTATGTCAGTTTATTA 989
| | | | |
QY 7015 ATATGATTTTATTTATAGAAACATATATCTGATGATATTTATAGTATAGGCAATAATA 7074
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Db 990 ATATGATTTTATTTATAGAAACATATATCTGATGATATTTATAGTATAGGCAATAATA 1049
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QY 7075 TTTATGACAAATTAACATATGAGAAACAAAGATATCTTAGGCTTTAATAAACAATGATATCAT 7134
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QY 7135 AAA 7137
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Db 1110 AAA 1112
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	601.4	8.1	1119	10	US-09-751-797-7
5	598.2	8.0	1166	15	US-10-084-298-3
6	555.2	7.5	1111	10	US-09-751-797-9
7	499	6.7	1050	15	US-10-090-365-40
8	489	6.7	1050	15	US-10-104-919-42
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13	214.2	2.9	1152	11	US-09-870-574-1
14	214.2	2.9	1152	14	US-10-063-588-153
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16	214.2	2.9	1152	15	US-10-066-500-125

17	214.2	2.9	1152	15	US-10-063-547-153	Sequence 153, App
18	214.2	2.9	1152	15	US-10-063-616-153	Sequence 153, App
19	214.2	2.9	1152	15	US-10-063-502-153	Sequence 153, App
20	214.2	2.9	1152	15	US-10-227-884-243	Sequence 243, App
21	214.2	2.9	1152	15	US-10-002-796-125	Sequence 125, App
22	214.2	2.9	1152	15	US-10-066-273-125	Sequence 125, App
23	214.2	2.9	1152	15	US-10-066-494-125	Sequence 125, App
24	214.2	2.9	1152	15	US-10-230-163-243	Sequence 243, App
25	214.2	2.9	1152	15	US-10-066-269-125	Sequence 125, App
26	214.2	2.9	1152	15	US-10-066-211-125	Sequence 125, App
27	214.2	2.9	1152	15	US-10-066-193-125	Sequence 125, App
28	214.2	2.9	1152	15	US-10-230-338-243	Sequence 243, App
29	214.2	2.9	1152	15	US-10-218-631-243	Sequence 243, App
30	214.2	2.9	1152	15	US-10-063-518-153	Sequence 153, App
31	214.2	2.9	1152	15	US-10-230-414-243	Sequence 243, App
32	214.2	2.9	1152	15	US-10-063-598-153	Sequence 153, App
33	214.2	2.9	1152	15	US-10-227-693-153	Sequence 153, App
34	214.2	2.9	1152	15	US-10-063-567-153	Sequence 153, App
35	214.2	2.9	1152	15	US-10-216-159A-243	Sequence 243, App
36	214.2	2.9	1152	15	US-10-218-849-243	Sequence 243, App
37	214.2	2.9	1152	15	US-10-227-873-243	Sequence 243, App
38	214.2	2.9	1152	15	US-10-227-883-243	Sequence 243, App
39	214.2	2.9	1152	15	US-10-219-076-243	Sequence 243, App
40	214.2	2.9	1152	15	US-10-230-434-243	Sequence 243, App
41	214.2	2.9	1152	15	US-10-063-599-153	Sequence 153, App
42	214.2	2.9	1152	15	US-10-063-595-153	Sequence 153, App
43	214.2	2.9	1152	15	US-10-219-003-243	Sequence 243, App
44	214.2	2.9	1152	15	US-10-219-075-243	Sequence 243, App
45	214.2	2.9	1152	15	US-10-219-464-243	Sequence 243, App

ALIGNMENTS

RESULT 1
US-09-751-797-8
Sequence 8, Application US/09751797
Patent No. US20010024652A1
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louned, Jamila
TITLE OF INVENTION: Renalud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/751,797
CURRENT FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 09/419,568
PRIOR FILING DATE: 1998-10-18
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 8
LENGTH: 7445
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-751-797-8
Query Match 100.0%; Score 7445; DB 10; Length 7445;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

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RESULT 2
US-09-751-797-29
: Sequence 29, Application US/09751797
: Patent No US20010024652A1
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: GENERAL INFORMATION:
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: APPLICANT: Dumoutier, Laure
: APPLICANT: Louheud, Jamila
: TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factors
: TITLE OF INVENTION: (Tifs) The Proteins Encoded, and Uses Thereof
: FILE REFERENCE: LUD 5543.2
: CURRENT APPLICATION NUMBER: US/09/751,797
: CURRENT FILING DATE: 2000-12-29
: PRIOR APPLICATION NUMBER: 09/419,568
: PRIOR FILING DATE: 1999-10-18
: PRIOR APPLICATION NUMBER: US09/178,973
: PRIOR FILING DATE: 1998-10-26
: NUMBER OF SEQ ID NOS: 29
:
: SEQ ID NO 29
:
: LENGTH: 5935

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Query Match	Similarity	Score	DB	Length
Beat Local	88.3%	Pred. No. 0;		
Matches 5039;	Conservative	0;	Mismatches 178;	Indels 487; Gaps 20;

TYPE: DNA	ORGANISM: Homo sapiens
FEATURE:	US-09-751-797-29
1971	TACCATGCTACCCGACGAACTGCTCCCTGATGTTTGGCTTTGCTCTCTCACTAC
293	TACCATGCTACCCGACGAACTGCTCCCTGATGTTTGGCTTTGCTCTCTCACTAC
2031	AGGCTTCCTCCTCACTTATCACTGTTGACCTGTGGGATCTCGATGAGTGCCTGCA
353	AGGCTTCCTCCTCACTTATCACTGTTGACCTGTGGGATCTCGATGAGTGCCTGCA
2091	GAATATCTATGAGTTTTCCTTATGAGGACCTTTGAGCGCCAGCTGCTCTTCATTC
413	GAATATCTATGAGTTTTCCTTATGAGGACCTTTGAGCGCCAGCTGCTCTTCATTC
2151	CCTGTGAGCCAGAGGCAAAATGCGTCCCTGACACCCGCTGCAAGCTTGAAGTGC
473	CCTGTGAGCCAGAGGCAAAATGCGTCCCTGACACCCGCTGCAAGCTTGAAGTGC
2211	CAACTTCAGAGGCGTACATGCTACACCGACCTTATGCTGGCCAGAGGATACAGCT
533	CAACTTCAGAGGCGTACATGCTACACCGACCTTATGCTGGCCAGAGGATACAGCT
2271	GCATCTCTTCTCTCATACCGCTGCTGCTTTCTGAAAGCATTTGCAAACTTTTAA
533	GCATCTCTTCTCTCATACCGCTGCTGCTTTCTGAAAGCATTTGCAAACTTTTAA
2331	GAGGCGCTTATCTCGCAGGCTCTCACTATGTTTCTGCTTTTGAAGCTCTTAA
652	GAGGCGCTTATCTCGCAGGCTCTCACTATGTTTCTGCTTTTGAAGCTCTTAA
2331	AGGACTGGGCTCTTTTTCATTTCAATTTCAAGGCTCTGAGCAATTCCTATCTGAGCT
712	AGGACTGGGCTCTTTTTCATTTCAATTTCAAGGCTCTGAGCAATTCCTATCTGAGCT
2451	TCAGGACATATATGATGATTTTATCTACAGAGGCGATTTTGAAGGCAACCCAGCTG
772	TCAGGACATATATGATGATTTTATCTACAGAGGCGATTTTGAAGGCAACCCAGCTG
2511	CAATATCTTCAATTTCTGTGCTCTCTTGAATCAATCTCTTGGCTACTCTCTAG
832	CAATATCTTCAATTTCTGTGCTCTCTTGAATCAATCTCTTGGCTACTCTCTAG
2571	ACCCATCTGGGACATACATCTCTACTTACAGGCTTTTTCATCTCTGTCACCCAGG
892	ACCCATCTGGGACATACATCTCTACTTACAGGCTTTTTCATCTCTGTCACCCAGG
2631	CACCTAGAGGTTTCTCTCTTTCAGGCGACCTTGCAGATTAACAACAGAGCTCGAGCTC
952	CACCTAGAGGTTTCTCTCTTTCAGGCGACCTTGCAGATTAACAACAGAGCTCGAGCTC
2691	ATCGGGGAGAAATCTTTCGAGAGGATCACTGTAAGTCTCTCACTGATGAGCAGGGCTAG
1012	ATCGGGGAGAAATCTTTCGAGAGGATCACTGTAAGTCTCTCACTGATGAGCAGGGCTAG
2751	CTGCGGAGAGCTGTGAGACCTCTTGGGATAGTCTGAGATGATGACCCCTGCTTCTTGTG
1072	CTGCGGAGAGCTGTGAGACCTCTTGGGATAGTCTGAGATGATGACCCCTGCTTCTTGTG
2811	TACCTGAGGCTTAAATCACTGCTACCTGATGAGAGAGGCTCACTTCAACCTGAA
1132	TACCTGAGGCTTAAATCACTGCTACCTGATGAGAGAGGCTCACTTCAACCTGAA
2871	GACGTTTCTGCTCCCCAGTCAAGAGGTTTCAAGCCCTTCAATGAGAGAGTGTGACCTTTC
1192	GACGTTTCTGCTCCCCAGTCAAGAGGTTTCAAGCCCTTCAATGAGAGAGTGTGACCTTTC

Db 3356 TTTGAGTGTGATGGCTTTGAGATTTTCAGTGTCTGCGACGTTCTTGTAAGGCTT 3415
Qy 5130 GTTACCTTGACACCTGGGCTTGATGTTAGCATGCCAAAGGCAACACACTTCTGAATGCT 5189
Db 3416 GTTACCTTGACACCTGGGCTTGATGTTAGCATGCCAAAGGCAACACACTTCTGAATGCT 3475
Qy 5190 GGTGTAAGGTTATTTATTTACTTTACTTTGTAAGGTTGTAAGGTTGTAAGG 5249
Db 3476 GGTGTAAGGTTATTTATTTACTTTACTTTGTAAGGTTGTAAGGTTGTAAGG 3535
Qy 5250 AACTCAGAGAGATGTTCTCTGTAGAGAAAATTTTTTTTCCCTTAATGCTTATA 5309
Db 3536 AACTCAGAGAGATGTTCTCTGTAGAGAAAATTTTTTTTCCCTTAATGCTTATA 3594
Qy 5310 TCCACTTTGATGCACTTTGACTTTTATTAACATGCTGTCAATGAAAGTGTGAGCC 5369
Db 3595 TCCACTTTGATGCACTTTGACTTTTATTAACATGCTGTCAATGAAAGTGTGAGCC 3654
Qy 5370 CGCTCTCAATGCTCTGGGAAAAGCAATAGGGGAAAGAAATGTTATGCTGAGAAATCTG 5429
Db 3655 CGCTCTCTGCTCTGGGAAAAGCAATAGGGGAAAGAAATGTTATGCTGAGAAATCTG 3714
Qy 5430 ACCGCGAGGAAACTGTGACAGAGCTCCCGGAAAGCAACACAGGTGTTAAGTAGAGACA 5489
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Qy 5490 GTCCAGGGTGGCTCATGTATAGAAATGAAACAGACGAGGAGAAATGAACTTCAAAAGTT 5549
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Qy 5610 TCTGGGAGGCAAGCAAG--TGAGAGGAAATGAAAGGAAAGAAACAGATGTAGAGA 5666
Db 3895 TCTGGGAGGCAAGCAAGCTTGAAGGAGATGAAAGGAAAGAAAC--ATGTAGAGA 3952
Qy 5667 CTGGAACAGCTACAAATCTCTACACAGAGATTTTCTTGGAACAACTTAGAA--GGT 5722
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Qy 5723 AGTGATTAAGT- GATTCAGAGGGGACTGCTTGGCATTTGAATCTGGGTTTGTCTC 5781
Db 4013 GGTGATTAAGTGAATGCAAGAGGACTGCTTGGCATTTGAATCTGGGTTTGTCTC 4072
Qy 5782 TCCATTGAGGTGAAAGGCTCACCC--TTTTTACCCTGCAATGAGAGGAAAGAGGGT 5840
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Qy 5901 CTCTTAC-------AAAAAATGGAACCTGTTGTTGTTCTGTTGTTCTTTG 5950
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Qy 5951 TTAAGAAAGCACA------- 5963
Db 4253 TTAAGAAAGCAGCAGAGCTGGGCTAGTGGCCCATGCTTAAATCCAGCAATTTGGAG 4312
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Qy 5964 ----- 5963
Db 4433 AAAAGAAAG 4492

Qy 5964 ----- 5963
Db 4493 GAG 4552
Qy 5964 ----- 5963
Db 4553 GAG 4612
Qy 5964 ----- 5963
Db 4613 AAGAGAAAAAAGAAAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 4672
Qy 5986 TGAATGAGGCTTTGAGTCAAGGCTTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 6045
Db 4673 GGTATGAGGCTTTGAGTCAAGGCTTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4732
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Db 4733 TCAGGTGAGGCTCTGTCAGGCGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4792
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Db 4793 TCTCAGTATCACTTCTCTGCTACTTACGACAGTTAGAGTTGAGCAAACTTTTCCAA 4852
Qy 6166 CCCCCCACTAAATTTATTTGACAAAGAGTGTGTAATTTGTTGTTGTTGTTGTTGTTG 6225
Db 4853 CCCCCCACTAAATTTATTTGACAAAGAGTGTGTAATTTGTTGTTGTTGTTGTTGTTG 4912
Qy 6226 GATCTATGTGCTATTTGCAAGTTCAATAAGATAGATTAATAGGCCCATCAAGCTT 6285
Db 4913 GATCTATGTGCTATTTGCAAGTTCAATAAGATAGATTAATAGGCCCATCAAGCTT 4972
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Db 5092 TTATTAATCTTTAGAGAGGCTGATACCTGTTTGGTCTCAGCAAGCAATGCTCAC 5151
Qy 6466 AGCTCTTTCTAACTGATACCACTTTAGAAAATGCTAACCTGCTCAAAATGTTGTAT 6525
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Db 5212 CTATTTTATATGCTTGAAGAGGCTGATACCTGTTTGGTCTCAGCAAGCAATGCTCAC 5271
Qy 6586 GTTATGCTCTGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6645
Db 5272 GTTATGCTCTGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5331
Qy 6646 CTCTCTCTGCTCTTCAAAAAGCAATTAAGATCCCTGAATGGAATTTTCTAAGA 6705
Db 5332 CTCTCTCTGCTCTTCAAAAAGCAATTAAGATCCCTGAATGGAATTTTCTAAGA 5391
Qy 6706 AAGTGAAGCTAACGTCACATCTTGAAGATTTTCAATGAATCCGCTCAGTTGA 5451
Db 5392 AAGTGAAGCTAACGTCACATCTTGAAGATTTTCAATGAATCCGCTCAGTTGA 5451
Qy 6766 AAAAGAAATAGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6825
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Qy 6826 TCATAGCAATATTTATTTGCTGATGATGATCAACAGAAAAATATATGATTTAAAAA 6885
Db 5512 TCATAGCAATATTTATTTGCTGATGATGATGATCAACAGAAAAATATATGATTTAAAAA 5571

QY 3298 GTACAACTACTTGTGGGAGAGAAATCCAGTAGTACAGTACTTGTGGATGAGATC 3357
DB 1310 GAAACATCTAGCTGTGGAATGATCCATTGATCTTAAGTGTGTGGGAGAGGATGG 1369
QY 3358 CACTGAGTACAGTACTTGTGGGAGAGAAATGACACAGCAAAAGTTGAAAGGAGG 3417
DB 1370 CATGAGAGAAATTTAGAAAGAAAGTGGAAATGGGAAGGCTTAA----- 1415
QY 3418 AAGATGAGAGGCTCATGTGGGGGTGTGAAAGGTCACTCTTTTCCATGTGATGAG 3477
DB 1416 -----GTGGGTGGGTGGGCTGGCAGACGTGGCCCTGTGTGATGTATGAGGA 1460
QY 3478 AGTTAAGAAACCA-GTGTGTGAGTTTGAATGTCTTCAAGACACCCCAATGAAACAT 3536
DB 1461 AGCCACAAATCGAGAGCGGTGTGAATCTTGATCCGCTGAACATTTGAACTATAAAAA 1520
QY 3537 ATCCAGAGAGGCGGAGACAGTGTGGAGACCTGGCATTATTTAGGAGAGCGC--GGCTTTT 3594
DB 1521 AGTTTGTGAGAGTGGGCGCCAGTAAAGCCCTAGACCTTACTGAAGAGGCTTAATTTT 1580
QY 3595 CACACGAGAACTTTATGCTCATCTGTGTGCTACCTCCACCTTTGATGAGGTTACG 3654
DB 1581 CAAATGAGATGTTTATGTACATTTCTGTCTTGAAGATGCAATTTCTGGAGATACAT 1640
QY 3655 TCAAGTTTGGTTT-----ACGTTCTTGTCTACTGTGTGAAC 3693
DB 1641 TGAAGTTTATCTCTTACAGAAATTTGCAATAACTCTCCGCTCTTCCACAAAGTCAAC 1700
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DB 1821 TGGCAAAATTAATAAGTCTTATTTCAAGTGAATGTACTGAACCTTCATGAGGTG 1880
QY 3874 AGATTTGGGCTCCACCGGTAAGATCTGTAGTGA-GTGTGTTTATTTTGCACGA 3932
DB 1881 GAGGTTATTAAGTTTCAAGCAACATTAAGATGATGCTGTGTATTTATTTATACCA 1940
QY 3933 CATAGCGGTGACGACCAAGACATTCAGAGAAATGTCAGAAAGCTGAAGAGACAGTGA 3992
DB 1941 TATGAAAGTATGATCTGCATATCCAGAGAAATGCAAAAGCTGAAGAGACAGTGA 2000
QY 3993 AAAGTACTATTTGCAAGCACAATCTAAGCATTCACTGAG--GAGACGTGGGATTC 4050
DB 2001 AAAGTAGGACGATTAATCTCAATGCTAAGTCAATGAGCAATGAGAGACAATGTGTTT 2060
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QY 4111 GTCCATTACTGCTAGCTGACCTGTATCTAGTGGGTCTATAGATCTTTCAATCTGTG 4170
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DB 2477 TGAATCTGAGAAATTAATCTCAGAAATTAAGAAAGAGCTGATCTGATATAGGCT 2536
QY 4521 AGTATTTAGATCACTGTATTAATAGCTATCATCTTAATTAATATAGGCTATATA 4580
DB 2537 AATTTCTGA-----GTATTAACACTAATTTGATGATATATATATATATATATAT 2589
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DB 2590 TTGATTTATGTTTAAAGCAAGAGCAGACAAAC--CCGATCTCTTTATACAGGTTCAAT 2648
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DB 2829 ACAAATCAGGCTTATTTGGTGAAGAAACA--ACAATGAGGCTTATGCTAACATA 2886
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QY 4933 TGGGTGTCTTAATTAACAAGAAACAGAAAGCTCCGCTGATGAAATTAATCAATGA 4991
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DB 3006 GCTTAACCTTAATTCCTCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTGAG 3065
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DB 3066 CATCAATTAATGAGTGTGACTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3125
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QY 5328 TCACTTTATATCATGCTGTCAATGAAAGTGTGAGGCGCTCATGAGGCTGTGG 5387
DB 3343 TCAATTTTGCATGAGGTTCCATGTGAAGGTGATTAATGCTTTTGTCTGTGACTTCA 3402
QY 5388 AAAAGCACCAATAGGGAAGAAATGTTATGCTGAAGAACTGACCGGAGGAACTGAT 5447


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Db      3403 GAAGCA-CAGGAGGAGCAATGTTGTTAGAGAAAGATCAACAGAGAGAACTGT 3461
QY      5448 CAGAGCTCCCGAAGCA-----CCACAGGTGTTAAGTAGG 5485
Db      3462 CAGAGCTGTGAAATAGGGGTGTTTGGAGGCAATTAATTCCTCTGTTGGGGTAAA 3521
QY      5486 AACAGTCCAGGGGTGGCTCATGTAAATAGAAACAGAGGAGGAAATAGCTCAA 5545
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QY      5546 AGTTCAAGAGGTC-CGAGCTTAAAGATACAAATAGAGTC--TTGGGCTTCATACA 5602
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QY      5603 AAGGAAGTGGGAGGAGCAGACAGTAGAGAGGAAATGAAAAGGAAAAACAGATGTAG 5662
Db      3641 AAGGAAGTATGAAAAG-----TGAAAGGGCGGAGAAACAGAAAAGAGAG 3688
QY      5663 AGGACTGGAACAGCTACAAATCCTTACACAGCATTTTCTTGGAAACATTAAGAGT 5722
Db      3689 AACCATGTATTAATATAGAGCAATGGTGCACAGGTTTCTTGAAATTAATGCAAAATATG 3748
QY      5723 AGTGGATTAGGTGATGACAGGGGAGCTTGCTTGCATTTGAATCTGGGTTTTGTCTCT 5782
Db      3749 ATGATTAAGAGAAATTTCAAGTAGGAAATGCTTTTCACTTGAATTTGGGTTTCTCT--T 3805
QY      5783 CCATTGAGGTGAAAGCGTCACTTTTAACTCCCTGATGAGAGGAGAAAGAGGGGTGT 5842
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QY      5843 TAGGACTCCTACTCGAGTTTACTAGTTTAACGATAGAAACAGACACTGGGACCTCT 5902
Db      3862 TAGAGCTTAATCTGTTTCTTCTTAATAAGCAAGTGAAGAAAGACTTATTTGGTATTT 3921
QY      5903 CTGACAAAAAATGAAACCTGTTGTCTGTGTTGTCTTTTGTATTAAGAAAGCAC 5962
Db      3922 TTCCCAAAAGGAAAGAACTTTCTTTTACTGTTTGCAAAAAGGTGAAATAGAAAAG 3981
QY      5963 AGGCAAAAGCCGACACATGGGTGAAATGGGTCTTTGAGTCAAGCTTTTGAATGAG 6022
Db      3982 CTTAATGTATGGTGAATACATGGTCAAAAGTCAATTTGATGAGATGTTTAAATCAG 4041
QY      6023 CACTCATCATAGTT-----GATCATGCTCAGGTGAGGGC 6058
Db      4042 GAGTGTCAATCAATTTGGCTTCCCTGACCACTTGAAGAAATGTTGTGTACACAT 4101
QY      6059 TACCTGCAGCGAGCCCTGCTGGCTTGCACTTAACATCTCAGGCTCAGATCACT 6118
Db      4102 AAATATCAAGAAATATGCTGATGAGCTAATAAAAGTCCATGATTAATCTCATACCTGTT 4161
QY      6119 TCCTGCTACTTACACAGTTAGAGAGTTGACAAACCTTTTTTCC-----6163
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QY      6164 -----AACCCCAATAAATTTAATTGACAAAGACTGTGTAATTTG 6205
Db      4222 CTGTGGCTGAGAGTTGACAAAGCTCCTTAATGATATCTCATATAGATGTTTGGAGC 4281
QY      6206 TGGATTCAGTGTGATTAATGA-----6227
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QY      6228 -----TCTATGTGATCTTGTGCAAGTTCAATAGATAGATTAATAGGCCATCAACAGC 6283
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QY      6284 TTTATGGGTGTGAAATGCAATATATAGTGAATGCTGTGTTGTTCTTAAGTCAAAA 6343
Db      4402 TTATATAGTGTAGGTGACACTGAAATGATGCTGTGTGGCT-CTAGTGCAGAGA 4460
QY      6344 GGCATGATTTTAAGGTCTTGGGCAATCATATTTACTCATGCTTAAAAAATACATTAATGTT 6403
Db      4461 GCGGTATTTTAAGCTCTTTGGCAATCATCAATACTTAAGGAT-----T 4508

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QY      6404 GATTATTAATCTTTTAGAGAGGCTGATACCTTGTTTGGTGTCTAGCAAGAAATGTCA 6463
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QY      6464 CCAGCTTTTCTTACTGTAACCTTTAGAAAATGCTACTGTGCTCAAAATGGTTTGA 6523
Db      4569 CAATTTCT--AATTTGTTCACTTTAGAAAACATGCGCATTAATAGCTCAAAATCTTTTGA 4625
QY      6524 TTCTATTTTCAATAGCTGAGAGAGTGGAGATCAAGGCGATTTGGGGAACTGGACCTG 6583
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QY      6644 TGCTCTCTCTGCTCTTCTTAAAGAACATTAATCCCTGATGACCTTTT 6695
Db      4746 TAACCCCTTTCCTCTGTAATAATCAATTAATGATGCCCAAGCGATTTT 4797

RESULT 4
US-09-751-797-7
; Sequence 7, Application US/09751797
; Patent No. US20010024652A1
; GENERAL INFORMATION:
; APPLICANT: Dumoulier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
; FILE REFERENCE: LUD 5543.2
; CURRENT APPLICATION NUMBER: US/09/751, 797
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 09/419, 568
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US09/178, 973
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 7
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; US-09-751-797-7

Query Match      8.1%; Score 601.4; DB 10; Length 1119;
Best Local Similarity 99.8%; Pred. No. 6.2e-126;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6535 ATAGCTTGAAGAGAGTGAAGATCAAGGCAATGGGGAACTGGACCTGCTTATGTC 6594
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QY      6595 TCTGAGAAATGCTTGGCTGAGCGAGAAAGCTTGAAGAAAGAACTGCTCTTCT 6654
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QY      6655 GCGTTTAAAGAAAGAAATGAATCCCTGAATGAGATTTTTTACTAAGAAAGTAGAA 6714
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QY      6715 GCTAAGCTCATCATCATTAAGAAATTTTCAATGAAACCTGGCTCAGTTGAAAAGAAA 6774
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QY      6775 TAGTGTCAAGTTGTCCATGAGACAGAGGTAGACTTGAATACACAAAGATTCATTGACA 6834
Db      750 TAGTGTCAAGTTGTCCATGAGACAGAGGTAGACTTGAATACACAAAGATTCATTGACA 809
QY      6835 AATTTTATTTGTCACGATGATCAACAGAAAATTAATGATCTTTTAAAAATTTGTTGA 6894

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Db 810 ATATTATTGTGCTAGTATGATACACAGAAAAAATATGTAATTAATTTGTTGAA 869
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Db 870 AGAGGTTACCTGCTCATTCCTTTAGAAAAAAGCTTATGTAATTCATTTCCATATCCAA 929
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QY 7015 ATATGATTTTATTTATAGAAACATATATCTGCTATGATATTTAGTATAGGCAATATATA 7074
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QY 7135 AAA 7137
Db 1110 AAA 1112

RESULT 5

US-10-084-298-3
Sequence 3, Application US/10084298
Publication No. US2003009649A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: Pitman, Debora
APPLICANT: Fouser, Lynette
APPLICANT: Spaulding, Vikki
APPLICANT: Xuan, Dejun
TITLE OF INVENTION: Composition and Method for Treating Inflammatory
TITLE OF INVENTION: Disorders
FILE REFERENCE: G15358 CIP
CURRENT APPLICATION NUMBER: US/10/084,298
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/270,823
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/281,353
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/131,473
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/561,811
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 1166
TYPE: DNA
ORGANISM: Murine
US-10-084-298-3

Query Match 8.0%; Score 598.2; DB 15; Length 1166;
Best Local Similarity 99.5%; Pred. No. 3.4e-125;
Matches 600; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6535 ATAGCTTGAGAGAGTGGAGAGATCAAGCGATTTGGGGAACCTGGACCTGCTTTATGTC 6594
Db 533 AAAGCTTGAGAGAGTGGAGAGATCAAGCGATTTGGGGAACCTGGACCTGCTTTATGTC 592
QY 6595 TCTGAGAAATGCTTGCGTCTGAGCGAGAGAAAGCTAGAAAACGAAAGCTGCTTCCCT 6654
Db 593 TCTGAGAAATGCTTGCGTCTGAGCGAGAGAAAGCTAGAAAACGAAAGCTGCTTCCCT 652
QY 6655 GCCTTCTAAAAAACAATPAAGATCCCTGAATGAGACTTTTATCTAAGAGAAAGTAGAA 6714
Db 653 GCCTTCTAAAAAACAATPAAGATCCCTGAATGAGACTTTTATCTAAGAGAAAGTAGAA 712
QY 6715 GCTAAGTCCATCATATTAGAAAGATTTCACATGAACCTGCTGAGTTGAAGAAAGAAA 6774
Db 713 GCTAAGTCCATCATATTAGAAAGATTTCACATGAACCTGCTGAGTTGAAGAAAGAAA 772

QY 6775 TAGTTCAGTTCCTGCTAGAGACGAGAGTAGACTTGATTAACCAACAAGATTCATGACA 6834
Db 773 TAGTTCAGTTCCTGCTAGAGACGAGAGTAGACTTGATTAACCAACAAGATTCATGACA 832
QY 6835 ATATTTTATGTCACGCTGATGATACACAGAAAAAATATGTAATTTTAAAAAATTTGGA 6894
Db 833 ATATTTTATGTCACGCTGATGATACACAGAAAAAATATGTAATTTTAAAAAATTTGGA 892
QY 6895 AGAGGTTACCTGCTCATTCCTTTAGAAAAAAGCTTATGTAATTCATTTCCATATCCAA 6954
Db 893 AGAGGTTACCTGCTCATTCCTTTAGAAAAAAGCTTATGTAATTCATTTCCATATCCAA 952
QY 6955 TATTTTATATATGTAAGTTTATTTATATATAGTATACATTTTATATGTCAGTTTATTA 7014
Db 953 TATTTTATATATGTAAGTTTATTTATATATAGTATACATTTTATATGTCAGTTTATTA 1012
QY 7015 ATATGATTTTATTTATAGAAACATATATCTGCTATGATATTTAGTATAGGCAATATATA 7074
Db 1013 ATATGATTTTATTTATAGAAACATATATCTGCTATGATATTTAGTATAGGCAATATATA 1072
QY 7075 TTTATGACATATACATGTAAGAAACAAGATATCTTAGGCTTTAATAACAACATGATATCAT 7134
Db 1073 TTTATGACATATACATGTAAGAAACAAGATATCTTAGGCTTTAATAACAACATGATATCAT 1132
QY 7135 AAA 7137
Db 1133 AAA 1135

RESULT 6

US-09-751-797-9
Sequence 9, Application US/09751797
Patent No. US20010024652A1
GENERAL INFORMATION:
APPLICANT: Dumoulier, Laure
APPLICANT: Renauld, Jamille
APPLICANT: Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
TITLE OF INVENTION: (TfR) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/751,797
CURRENT FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 09/419,568
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-751-797-9

Query Match 7.5%; Score 555.2; DB 10; Length 1111;
Best Local Similarity 96.0%; Pred. No. 1.9e-115;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

QY 6535 ATAGCTTGAGAGAGTGGAGAGATCAAGCGATTTGGGGAACCTGGACCTGCTTTATGTC 6594
Db 508 AAAGCTTGAGAGAGTGGAGAGATCAAGCGATTTGGGGAACCTGGACCTGCTTTATGTC 567
QY 6595 TCTGAGAAATGCTTGCGTCTGAGCGAGAGAAAGCTAGAAAACGAAAGCTGCTTCCCT 6654
Db 568 TCTGAGAAATGCTTGCGTCTGAGCGAGAGAAAGCTAGAAAACGAAAGCTGCTTCCCT 627
QY 6655 GCCTTCTAAAAAACAATPAAGATCCCTGAATGAGACTTTTATCTAAGAGAAAGTAGAA 6714
Db 628 GCCTTCTAAAAAACAATPAAGATCCCTGAATGAGACTTTTATCTAAGAGAAAGTAGAA 687
QY 6715 GCTAAGTCCATCATATTAGAAAGATTTCACATGAACCTGCTGAGTTGAAGAAAGAAA 6774

Db 688 GCTAACGCCACCATCATTTAGAGATTTTCACATGAAACCTGCTCAGTTGAAAGAGAAA 747
Qy 6775 TAGTGTCAAGTTGTCCATGAGACCAAGGTAGACTTGATTAACCAAAAGTTGATTGACA 6834
Db 748 TAGTGTCAAGTTGTCCATGAGACCAAGGTAGACTTGATTAACCAAAAGTTGATTGACA 807
Qy 6835 ATATTTTATTTGTGACGATGATACACAGAAAAAATATGACTTTAAAAAATGTTTGA 6894
Db 808 ATATTTTATTTGTGATGATATACACAGAAAAAATATGACTTTAAAAAATGTTTGA 867
Qy 6895 AGAGAGTTACCTCTCATCTTCTTAGAAAAAAAGCTTATGTAATCTTATTCATCCAA 6954
Db 868 AGAGAGTTACCTCTCATCTTCTTAGAAAAAAAGCTTATGTAATCTTATTCATCCAA 927
Qy 6955 TATTTTATATGTAAGTTTATTTATTAAGTATACATTTTATTTATGTCAGTTTATTA 7014
Db 928 TACTTTATATGTAAGTTTATTTATTAAGTATACATTTTATTTATGTCAGTTTATTA 987
Qy 7015 ATATGATTTATTTATAGAAACATTTCTGCTATGATATTT -AGTATAGGCAATAT 7073
Db 988 ATATGATTTATTTATAGAAACATTTCTGCTATGATATTTAGTATTAAGCAATATAT 1047
Qy 7074 ATATGATTTATTTATAGAAACATTTCTGCTTATTAATTAACATGATATCA 7133
Db 1048 ATATGATTTATTTATAGAAACATTTCTTATGCTTTATTAACATGATATCA 1107
Qy 7134 TAAA 7137
Db 1108 TAAA 1111

RESULT 7
US-10-090-365-40
; Sequence 40, Application US/10090365
; Publication No. US2003007706A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindvogel, Wayne
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: Mouse Cytokine Receptor
; FILE REFERENCE: 01-08
; CURRENT APPLICATION NUMBER: US/10/090,365
; PRIOR FILING DATE: 2002-03-04
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/279,232
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)...(589)
US-10-090-365-40

Query Match 6.7%; Score 499; DB 15; Length 1050;
Best Local Similarity 96.1%; Pred. No. 1e-102;
Matches 522; Conservative 0; Mismatches 20; Indels 1; Gaps 1;
Qy 6535 ATAGCTTGAGAGAGTGAAGATCAAGCGATTGGGGAAGTGAAGCTGCTGTTATGTC 6594
Db 508 AAAGCTTGAGAGAGCGGAGAGATCAAGCGATCGGGAAGTGAAGCTGCTGTTATGTC 567
Qy 6595 TCTGAGAAATGCTTGGCTGTGAGCGGAGAAAGCTTGAAAGCAAGAACTGCTCTTCT 6654
Db 568 TCTGAGAAATGCTTGGCTGTGAGCGGAGAAAGCTTGAAAGCAAGAACTGCTCTTCT 627
Qy 6655 GCCTTTAAAAAGAACATTAAGATCCCTGAATGCACTTTTACTTAAAGAAAGTGAGA 6714

Db 628 GCCTTTAAAAAGAACATTAAGATCCCTGAATGCACTTTTACTTAAAGAAAGTGAGA 687
Qy 6715 GCTAACGCCACCATCATTTAGAGATTTTCACATGAAACCTGCTCAGTTGAAAGAGAAA 6774
Db 688 GCTAACGCCACCATCATTTAGAGATTTTCACATGAAACCTGCTCAGTTGAAAGAGAAA 747
Qy 6775 TAGTGTCAAGTTGTCCATGAGACCAAGGTAGACTTGATTAACCAAAAGTTGATTGACA 6834
Db 748 TAGTGTCAAGTTGTCCATGAGACCAAGGTAGACTTGATTAACCAAAAGTTGATTGACA 807
Qy 6835 ATATTTTATTTGTGACGATGATACACAGAAAAAATATGACTTTAAAAAATGTTTGA 6894
Db 808 ATATTTTATTTGTGATGATATACACAGAAAAAATATGACTTTAAAAAATGTTTGA 867
Qy 6895 AGAGAGTTACCTCTCATCTTCTTAGAAAAAAAGCTTATGTAATCTTATTCATCCAA 6954
Db 868 AGAGAGTTACCTCTCATCTTCTTAGAAAAAAAGCTTATGTAATCTTATTCATCCAA 927
Qy 6955 TATTTTATATGTAAGTTTATTTATTAAGTATACATTTTATTTATGTCAGTTTATTA 7014
Db 928 TACTTTATATGTAAGTTTATTTATTAAGTATACATTTTATTTATGTCAGTTTATTA 987
Qy 7015 ATATGATTTATTTATAGAAACATTTCTGCTATGATATTT -AGTATAGGCAATAT 7073
Db 988 ATATGATTTATTTATAGAAACATTTCTGCTATGATATTTAGTATTAAGCAATATAT 1047
Qy 7074 ATT 7076
Db 1048 ATT 1050

RESULT 8
US-10-104-919-42
; Sequence 42, Application US/10104919
; Publication No. US20030099608A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindvogel, Wayne
; APPLICANT: Chen, Zhi
; APPLICANT: Hughes, Steven D.
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 01-12
; CURRENT APPLICATION NUMBER: US/10/104,919
; PRIOR FILING DATE: 2002-03-23
; PRIOR APPLICATION NUMBER: US 60/279,222
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5)...(589)
US-10-104-919-42

Query Match 6.7%; Score 499; DB 15; Length 1050;
Best Local Similarity 96.1%; Pred. No. 1e-102;
Matches 522; Conservative 0; Mismatches 20; Indels 1; Gaps 1;
Qy 6535 ATAGCTTGAGAGAGTGAAGATCAAGCGATTGGGGAAGTGAAGCTGCTGTTATGTC 6594
Db 508 AAAGCTTGAGAGAGCGGAGAGATCAAGCGATCGGGAAGTGAAGCTGCTGTTATGTC 567
Qy 6595 TCTGAGAAATGCTTGGCTGTGAGCGGAGAAAGCTTGAAAGCAAGAACTGCTCTTCT 6654
Db 568 TCTGAGAAATGCTTGGCTGTGAGCGGAGAAAGCTTGAAAGCAAGAACTGCTCTTCT 627
Qy 6655 GCCTTTAAAAAGAACATTAAGATCCCTGAATGCACTTTTACTTAAAGAAAGTGAGA 6714
Db 628 GCCTTTAAAAAGAACATTAAGATCCCTGAATGCACTTTTACTTAAAGAAAGTGAGA 687

QY 6715 GCTAACGTCATCATATTGAGAAATTTCACATGAAACCTGCTCAGTTGAAAAAGAA 6774
DB 688 GCTAACGTCACCATCATATTGAGAAATTTCACATGAAACCTGCTCAGTTGAAAAAGAA 747
QY 6775 TAGTGCAGGTTGTCATGAGACCAAGGAGAGCTTGATACCAAGAAAGTTGATGAC 6834
DB 748 TAGTGCAGGTTGTCATGAGACCAAGGAGAGCTTGATACCAAGAAAGTTGATGAC 807
QY 6835 AATATTTATTTGTCATGATGATCAACAGAAAAATATGATCTTAAAAAATTGTTGAA 6894
DB 808 AATATTTATTTGTCATGATGATCAACAGAAAAATATGATCTTAAAAAATTGTTGAA 867
QY 6895 AGAGAGTAACTCTCATCTCTCTTTAGAAAAAGCTTATGTAATCTTCAATTCACAA 6954
DB 868 AGAGAGTAACTCTCATCTCTCTTTAGAAAAAGCTTATGTAATCTTCAATTCACAA 927
QY 6955 TATTTATATATGATGATGATTTATTTATATGATGATGATTTATTTATGATGATTA 7014
DB 928 TATTTATATATGATGATGATTTATTTATATGATGATGATTTATTTATGATGATTA 987
QY 7015 AATATGATTTATTTATGAAAAACATATCTGCTATGATATTT-AGTATAAGCAAAATAT 7073
DB 988 AATATGATTTATTTATGAAAAATATCTGATGATGATTTATTTATGATTAAGCAAAATAT 1047
QY 7074 ATT 7076
DB 1048 ATT 1050

RESULT 9

US-10-084-298-1
; Sequence 1, Application US/10084298
; Publication No. US2003009649A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Piltman, Debra
; APPLICANT: Fouser, Lynette
; APPLICANT: Spaulding, Vikki
; APPLICANT: Xuan, Dejun
; TITLE OF INVENTION: Composition and Method for Treating Inflammatory
; FILE REFERENCE: Disorders
; CURRENT APPLICATION NUMBER: US/10/084,298
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/270,823
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/281,353
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/111,473
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/561,811
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-084-298-1

Query Match 2.9%; Score 217.6; DB 15; Length 1191;
Best Local Similarity 70.9%; Pred. No. 8.3e-39;
Matches 454; Conservative 0; Mismatches 149; Indels 37; Gaps 11;
QY 6535 ATAGCTTGGAGAGATGAGAGATCAAGCGATTGGGAACTGGACCTGCTTTATGTC 6594
DB 529 AAGGCTTGGAGAGATGAGAGATCAAGCAATGGAGAACTGGATTGCTTTATGTC 588
QY 6595 TCTGAGAAATGCTTGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6654
DB 589 TCTGAGAAATGCTTGGCTGAG 648

QY 6655 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGACCTTTT-----ACTAAGAAAGTG 6710
DB 649 CCTGTCTAATAATAACATTAAGATGCCCAAGCAATTTTTTTAAACCAAGAAAGATG 708
QY 6711 AGAAGCTAACGTCATCATCATTTAGAAATTTACATGAAACCTGCTCAGTTGAAAAAG 6770
DB 709 GGAAGCAAACTCATCATGATGAGGATGATCCAAATGAAACCTGCTGATTTACAAAG 768
QY 6771 AAAATATGTCAA--GTTGTCATGAGACAG--AGTATGATGATTAACCAAGATTC 6827
DB 769 GGAACCAATGCCATTTGTTTATTAAGACCAAGATGATGATTTTAAAGCATATATTT 828
QY 6828 ATTAGCAATTTTATTTGTCATGATG--ATACAGAAAAATATGATCTTAA 6883
DB 829 ATTAGCAATTTTATTTGTCATGATGATGATGATGATGATGATGATGATGATGATGAT 888
QY 6884 AATGTTT-----AAAGAGTTACCTCTCATCTCTTTA---GAAAAAGCTTATG 6933
DB 889 AATGCTCTTTTCCATTAATAAGATTAATCTTCCATTTCTTTAGGGGAAAAACCTTAA 948
QY 6934 TAACCTCA--TTTCATATCCAAATTTATATATGTAAGTTATTTATTTATATAGTAT- 6990
DB 949 TAGCTTCATGTTTCCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1008
QY 6991 -----CATTTTATTTATGTCATTTATTAATGATGATTTATTTATGAAACATTAATGTC 7045
DB 1009 GACTGATTTTATTTATATCATTTATTAATGATGATTTATTTATGAAACATCATTTCA 1068
QY 7046 TATTTGATA--TTAGTATAAGCAATA--ATATTTATGACATTAATGATG--AAAC 7097
DB 1069 TATTTGCTACTGAGTATAGGCTAATATTTATTTATTTATTTATTTATTTATTTATTTAT 1128
QY 7098 AAGATATCTTAGGCTTTATTAATAACATGATATCATTA 7137
DB 1129 CATGTTTATTTGACCTCATTAACATTTGATATCTTAA 1168

RESULT 10

US-09-728-911-14
; Sequence 14, Application US/09728911
; Patent No. US20020012669A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenteng
; APPLICANT: Kindesvogel, Wayne
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 99-93
; CURRENT APPLICATION NUMBER: US/09/728,911
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/169,049
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 60/232,219
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/244,610
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (21)...(557)
US-09-728-911-14

Query Match 2.9%; Score 215.6; DB 10; Length 1116;
Best Local Similarity 70.8%; Pred. No. 2.3e-38;
Matches 452; Conservative 0; Mismatches 149; Indels 37; Gaps 11;
QY 6535 ATAGCTTGGAGAGATGAGAGATCAAGCGATTGGGAACTGGACCTGCTTTATGTC 6594


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Db      479 AAAGCTTGAGAGAGTGGAGAGATCAAGCAATTGGAGAACTGGATTGCTGTTATGTC 538
Qy      6595 TCTGAGAAATGCTTGGCGTGTGACCGAGAAAGAGTGAAGAAACAGAACTGCTCTTCCT 6654
Db      539 TCTGAGAAATGCTGATTTGACAGAGCAAGAGCTGAAATGATTAATCAACCCCTT 598
Qy      6655 GCCTTTTAAAGAAACAATAAGATCCCTGAATGACTTTT---ACTAAGAAAGT 6710
Db      599 CCTGCTAGAAATTAAGATAGATGCCCAAGCCGATTTTAAACCAAGAGAAAGT 658
Qy      6711 AGAAGTAAAGTCCATCATCATTAAGAAATTCACATGAACCTGGCTCAGTTGAAG 6770
Db      659 GGAAGCAAACTCCATCATGATGAGGATGCCAAATGAACCCCTGGTGTAGTACAAAG 718
Qy      6771 AAAATAGTCA--GTGTCCATGAGACGAG--AGGTAGACTTGATTAACACAAAGTTC 6827
Db      719 GAAACCAATGCCACTTTGTTTATAGACCAAGAGTGAAGCTTTAGCATAGATATT 778
Qy      6828 ATTGAACAATTTTATTTGTCAGTGAAG---ATACACAGAAATAATAGTACTTTAAA 6883
Db      779 ATTGAACAATTTTATTTGTAAGTGTGTCTATACAGAAACAAATTAATTTTAAAT 838
Qy      6884 AATTGTTT-----GAAAGAGGTACCTCTCATTCCTTTA---GAAAAAAGCTTATG 6933
Db      839 AATTGCTTTTCCATTAAGAAATTAATTTTCCATTCCTTTAGGGGAAAAACCCCTAAA 898
Qy      6934 TAACTTCA--TTTCCATATCCAAATTTTATATATGTAAGTATTTATTTATTAAGTAA 6990
Db      899 TACTCTCACTTCCATTAATCAGTACTTATTTATTAATGATTTATTTATTTATTA 958
Qy      6991 -----CATTTATTTATGTCAGTTTATTAATATGATTTATTTATTAAGAAACATTAATCTGC 7045
Db      959 GACTGCATTTTATTTATATCATTTTATTTATTAATGATTTATTTATTAAGAAACATTAATCTGA 1018
Qy      7046 TATTGATA--TTTGTATTAAGCAAAATA---ATATTATGCAATAATCTATG---AAAC 7097
Db      1019 TATTGCTACTTGAGTGAAGGCTTAATTTATTTATTTATTAAGCAATAATTTATGAGCTATA 1078
Qy      7098 AAGATATCTTAGCCTTTAATTAACACATGATATCATTA 7135
Db      1079 CATGTTTATTGACCTCAATTAACACTTGATATCTTA 1116

RESULT 11
US-10-090-365-14
; Sequence 14, Application US/10090365
; Publication No. US2003007706A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindesvogel, Wayne
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: Mouse Cytokine Receptor
; FILE REFERENCE: 01-08
; CURRENT APPLICATION NUMBER: US/10/090,365
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/273,035
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/279,232
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (21)...(557)
US-10-090-365-14

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Query Match 2.9%; Score 215.6; DB 15; Length 1116;
 Best Local Similarity 70.8%; Pred. No. 2.3e-38;

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Matches 452; Conservative 0; Mismatches 149; Indels 37; Gaps 11;
Qy      6535 ATAGCTTGAGAGAGTGGAGAGATCAAGCAATTGGAGAACTGGATTGCTGTTATGTC 6594
Db      479 AAAGCTTGAGAGAGTGGAGAGATCAAGCAATTGGAGAACTGGATTGCTGTTATGTC 538
Qy      6595 TCTGAGAAATGCTTGGCGTGTGACCGAGAAAGAGTGAAGAAACAGAACTGCTCTTCCT 6654
Db      539 TCTGAGAAATGCTGATTTGACAGAGCAAGAGCTGAAATGATTAATCAACCCCTT 598
Qy      6655 GCCTTTTAAAGAAACAATAAGATCCCTGAATGACTTTT---ACTAAGAAAGT 6710
Db      599 CCTGCTAGAAATTAAGATAGATGCCCAAGCCGATTTTAAACCAAGAGAAAGT 658
Qy      6711 AGAAGTAAAGTCCATCATCATTAAGAAATTCACATGAACCTGGCTCAGTTGAAG 6770
Db      659 GGAAGCAAACTCCATCATGATGAGGATGCCAAATGAACCCCTGGTGTAGTACAAAG 718
Qy      6771 AAAATAGTCA--GTGTCCATGAGACGAG--AGGTAGACTTGATTAACACAAAGTTC 6827
Db      719 GAAACCAATGCCACTTTGTTTATAGACCAAGAGTGAAGCTTTAGCATAGATATT 778
Qy      6828 ATTGAACAATTTTATTTGTCAGTGAAG---ATACACAGAAATAATAGTACTTTAAA 6883
Db      779 ATTGAACAATTTTATTTGTAAGTGTGTCTATACAGAAACAAATTAATTTTAAAT 838
Qy      6884 AATTGTTT-----GAAAGAGGTACCTCTCATTCCTTTA---GAAAAAAGCTTATG 6933
Db      839 AATTGCTTTTCCATTAAGAAATTAATTTTCCATTCCTTTAGGGGAAAAACCCCTAAA 898
Qy      6934 TAACTTCA--TTTCCATATCCAAATTTTATATATGTAAGTATTTATTTATTAAGTAA 6990
Db      899 TACTCTCACTTCCATTAATCAGTACTTATTTATTAATGATTTATTTATTTATTA 958
Qy      6991 -----CATTTATTTATGTCAGTTTATTAATATGATTTATTTATTAAGAAACATTAATCTGC 7045
Db      959 GACTGCATTTTATTTATATCATTTTATTTATTAATGATTTATTTATTAAGCAATTAATCTGA 1018
Qy      7046 TATTGATA--TTTGTATTAAGCAAAATA---ATATTATGCAATAATCTATG---AAAC 7097
Db      1019 TATTGCTACTTGAGTGAAGGCTTAATTTATTTATTTATTAAGCAATAATTTATGAGCTATA 1078
Qy      7098 AAGATATCTTAGCCTTTAATTAACACATGATATCATTA 7135
Db      1079 CATGTTTATTGACCTCAATTAACACTTGATATCTTA 1116

RESULT 12
US-10-104-919-14
; Sequence 14, Application US/10104919
; Publication No. US2003009608A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindesvogel, Wayne
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 01-12
; CURRENT APPLICATION NUMBER: US/10/104,919
; PRIOR FILING DATE: 2002-03-23
; PRIOR APPLICATION NUMBER: US 60/279,222
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (21)...(557)
US-10-104-919-14

```


Query Match 2.9%; Score 215.6; DB 15; Length 1116;
Best Local Similarity 70.8%; Pred. No. 2,3e-38;
Matches 452; Conservative 0; Mismatches 149; Indels 37; Gaps 11;

QY 6535 ATAGCTTGAGAGAGAGAGATCAAGCGATTGGGAACTGAGACCTGCTGTTATGTC 6594
DB 479 AAGCTTGAGAGAGAGAGATCAAGCGATTGGGAACTGAGACCTGCTGTTATGTC 538
QY 6595 TCTGAGAAATGCTGCTGCTGAGCGAGAAAGCTGAGAAACGAGAACTGCTCTTCT 6654
DB 539 TCTGAGAAATGCTGCTGCTGATTCAGAGAAAGCTGAGAAATGATTAACCTCTT 598
QY 6655 GCCTTCTAAAGAAACAATPAAGTCCCTGATGAGACTTTT---ACTPAAGAAAGTG 6710
DB 599 CCTGCTAAGAAATPAACAATTAGATGCCCAAGCCGATTTTTPAACCAAGAAAGATG 658
QY 6711 AGAAGCTAACGTCATCATCATTAAGAAATTCACATGAAACCTGGCTGAGTGAAG 6770
DB 659 GGAAGCAAACTCCATCATGATGAGTGGATTCCAAATGAACCCCTGCTGATTAAG 718
QY 6771 AAAATAGTCA--GTGTCATGAGACAG--AGTAGACTTGATTAACCAAGATTC 6827
DB 719 GAAGCAATGCCACTTTGTTTATAGACCAAGATGAGCTTTCTAGATGATATT 778
QY 6828 ATGACAAATTTTATGTCATGATG---ATPACAAGAAATPAATGACTTTAAA 6883
DB 779 ATGATPAACATTTGATGTAAGTGTCTATPACAGAAACAATTTATTTTAAAT 838
QY 6884 AATTGTT-----GAAAGAGTACCTCTCATTCCTTA---GAAAAAGCTTATG 6933
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DB 899 TACCTCATGTTTCCATTAACAGTACTTTTATTTATTAATGATTTATTTATTTAA 958
QY 6991 ----CATTTATTTATGTCAGTTTATTAATGATTTTATTAAGAAACATTAATGTC 7045
DB 959 GACTGCATTTTATTTATATCATTTTATTAATGATTTTATTAAGAAACATTCGA 1018
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DB 1019 TATTGCTACTGAGTGAAGCTPAATATTGATTTTATGCAATTAATTAAGACTTAA 1078
QY 7098 AAGATATCTTAGGCTTTAATPAACAGATGATATCA 7135
DB 1079 CATGTTTATTGACCTCAATPAACACTTGATATCTTA 1116

RESULT 13
US-09-870-574-1
Sequence 1, Application US/09870574
Patent No. US20020102723A1
GENERAL INFORMATION:

APPLICANT: Gurney, Austen L.
APPLICANT: Xie, Ming-Hong
APPLICANT: Maruoka, Ellen M.
APPLICANT: Foster, Jessica S.
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: INTERLEUKIN-22 POLYPEPTIDES, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: THE SAME AND METHODS FOR THE TREATMENT OF PANCREATIC DISORDERS
FILE REFERENCE: P2806-1(US)
CURRENT APPLICATION NUMBER: US/09/870, 574
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: US 60/169, 495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 7
SEQ ID NO 1
LENGTH: 1152
TYPE: DNA
ORGANISM: Homo Sapien
US-09-870-574-1

Query Match 2.9%; Score 214.2; DB 11; Length 1152;
Best Local Similarity 70.9%; Pred. No. 4,8e-38;
Matches 450; Conservative 0; Mismatches 148; Indels 37; Gaps 11;

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DB 516 AAGCTTGAGAGAGAGAGATCAAGCGATTGGGAACTGAGACCTGCTGTTATGTC 575
QY 6595 TCTGAGAAATGCTGCTGCTGAGCGAGAAAGCTGAGAAACGAGAACTGCTCTTCT 6654
DB 576 TCTGAGAAATGCTGCTGCTGATTCAGAGAAAGCTGAGAAATGATTAACCTCTT 635
QY 6655 GCCTTCTAAAGAAACAATPAAGTCCCTGATGAGACTTTT---ACTPAAGAAAGTG 6710
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DB 696 GGAAGCAAACTCCATCATGATGAGTGGATTCCAAATGAACCCCTGCTGATTAAG 755
QY 6771 AAAATAGTCA--GTGTCATGAGACAG--AGTAGACTTGATTAACCAAGATTC 6827
DB 756 GAAGCAATGCCACTTTGTTTATPAAGCAAGATGACTTTCTAAGCAATGATATT 815
QY 6828 ATGACAAATTTTATGTCATGATG---ATPACAAGAAATPAATGACTTTAAA 6883
DB 816 ATGATPAACATTTGATGTAAGTGTCTATPACAGAAACAATTTATTTTAAAT 875
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QY 7098 AAGATATCTTAGGCTTTAATPAACAGATGATATC 7132
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RESULT 14
US-10-063-588-153
Sequence 153, Application US/10063588
Publication No. US20030130483A1
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.
APPLICANT: Flivaroff, Ellen
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Maruoka, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P323081C1

RESULT 15
US-10-006-667-153
Sequence 153, Application US/10006667
Publication No. US20020119130A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gunney, Aubin L.
APPLICANT: Macanabe, Colin K.
APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEI
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P23230R1C1
 CURRENT APPLICATION NUMBER: US/10/006,867
 CURRENT FILING DATE: 2001-12-06
 PRIOR APPLICATION NUMBER: 60/063435
 PRIOR FILING DATE: 1997-10-29
 PRIOR APPLICATION NUMBER: 60/064215
 PRIOR FILING DATE: 1997-10-29
 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/083495
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/088021
 PRIOR FILING DATE: 1998-06-04
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 PRIOR APPLICATION NUMBER: 60/097979
 PRIOR FILING DATE: 1998-08-26
 PRIOR APPLICATION NUMBER: 60/098749
 PRIOR FILING DATE: 1998-09-01
 PRIOR APPLICATION NUMBER: 60/099741
 PRIOR FILING DATE: 1998-09-10


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Db      936 TAGCTTCAGTGTCCATAATCAGTACTTATATTAATAATGATTTATTATTATAA 995
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Db      996 GACTGCATTTTATTATATCATTTTATTATATGATTTATTATAGAAACATCATTCGA 1055
QY      7046 TATTGATA-TTAGTATAAGGCAATA--ATATTAGACAATAACTATG---AAAC 7097
Db      1056 TATTGCTACTGAGTGAAGGCTAATATTGATTTATGACAATAATATAGAGCTATAA 1115
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Mon Jul 21 05:36:15 2003

us-09-751-797-25.rn1

Page 21

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129	GTCGGCCACAGGAGGCAAAATGGCGTCCCTCAACACCGGTGTAAGCTTGAAGGTGTCCAA	188			
209	CTTCACGAGCCCTTATATACCAACCGCACTTTCATGCTGGCTAAAGAGC	258			
189	CTTCAGGAGCGTACATCGTATACCGCACTTTATGCTGGCGCAAGAGG	238			

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Job time : 189.24 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:07:55 ; Search time 234.726 Seconds
(without alignments)
9727.122 Million cell updates/sec

Title: US-09-751-797-8

Perfect score: 7445
Sequence: 1 gttctacaccgtcttaagat.....gatttaattatgtgtat 7445

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
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6: /cgn2_6/ptodata/1/ina/backlist.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	7445	100.0	7445	4	US-09-354-243B-8
4	4245.2	57.0	5935	4	US-09-178-973B-17
5	4245.2	57.0	5935	4	US-09-419-568F-29
6	4245.2	57.0	5935	4	US-09-354-243B-29
7	686	9.2	4797	4	US-09-419-568F-25
8	686	9.2	4797	4	US-09-354-243B-25
9	601.4	8.1	1119	4	US-09-178-973B-7
10	601.4	8.1	1119	4	US-09-419-568F-7
11	601.4	8.1	1119	4	US-09-354-243B-7
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13	555.2	7.5	1111	4	US-09-419-568F-9
14	555.2	7.5	1111	4	US-09-354-243B-9
15	126	1.7	690	4	US-09-419-568F-24
16	126	1.7	690	4	US-09-354-243B-24
17	75.8	1.0	48974	4	US-08-920-422-17
18	73.8	1.0	7218	1	US-08-233-463-14
19	70	0.9	7218	1	US-08-233-463-14
20	68.8	0.9	16442	3	US-08-781-891-208
21	59.2	0.8	96050	4	US-09-245-041-5
22	57.8	0.8	10409	3	US-08-772-440-33
23	57.6	0.8	10614	1	US-08-135-511-35
24	57.6	0.8	10614	1	US-08-187-453-35
25	57.2	0.8	2272	3	US-08-147-592A-3
26	57.2	0.8	2272	3	US-08-292-694A-3
27	56.8	0.8	48974	4	US-08-920-422-17

C	28	56.8	0.8	90050	4	US-09-245-041-5	Sequence 5, Appl
	29	56.2	0.8	4765	3	US-08-936-135-21	Sequence 21, Appl
	30	56.2	0.8	4760	3	US-08-936-135-23	Sequence 23, Appl
	31	56.2	0.8	37950	4	US-09-338-907-183	Sequence 183, App
	32	56.2	0.8	37950	4	US-09-218-207-183	Sequence 183, App
	33	55	0.7	5852	4	US-07-667-106-2	Sequence 2, Appl
	34	55	0.7	17056	4	US-09-245-041-5	Sequence 3, Appl
C	35	54.8	0.7	3205	4	US-09-661-768A-3	Sequence 3, Appl
	36	54.8	0.7	5109	4	US-08-930-055A-2	Sequence 2, Appl
	37	54.8	0.7	7874	4	US-09-780-175-96	Sequence 96, Appl
	38	54.2	0.7	13011	2	US-08-791-849A-14	Sequence 14, Appl
C	39	53.2	0.7	169998	4	US-09-676-610B-24	Sequence 5, Appl
	40	53.2	0.7	6727	3	US-08-629-643A-5	Sequence 5, Appl
	41	53.2	0.7	6727	3	US-09-280-799-1	Sequence 1, Appl
	42	53.2	0.7	6727	4	US-09-155-884-5	Sequence 5, Appl
	43	53	0.7	586	4	US-09-227-357-103	Sequence 103, App
	44	52.6	0.7	4526	1	US-07-855-412B-4	Sequence 4, Appl
	45	52.6	0.7	4526	2	US-08-308-887A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1									
US-09-178-973B-8									
Sequence 8, Application US/09178973B									
Patent No. 6274710									
GENERAL INFORMATION:									
APPLICANT: Dumoutier, Laure									
APPLICANT: Renauld, Jean-Christophe									
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F									
TITLE OF INVENTION: (TIFFS)									
FILE REFERENCE: LIND 5543									
CURRENT APPLICATION NUMBER: US/09/178, 973B									
CURRENT FILING DATE: 1998-10-26									
NUMBER OF SEQ ID NOS: 17									
SEQ ID NO: 8									
LENGTH: 7445									
TYPE: DNA									
ORGANISM: Mus musculus									
US-09-178-973B-8									
Query Match									
Best Local Similarity 100.0%; Score 7445; DB 4; Length 7445;									
Matches 7445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	181	TGAATGTATGCTTAAACAATCTTCAAGCTCTTAATATGCTTAACGACTGAGTCG	240						
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Qy 1321 TCTGTGGCAATGGAGCTGTGAAGAAAGCAATTTCTTATTTAAATTTTAAATTTTGA 1380
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Qy 2161 CAGAGGCAAAATGGCTGCTGCTGCAACCCGCTGCAAGCTTGAAGTGTCCAACTTCCAG 2220
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Db 4081 TTAACATTTTATTTGATCTGTCTATATCTGTCTCAATTAATCTGCTGACCTGATATC 4140
QY 4141 TTAGCTGGGTCTATAGTCTTTCAATCTGTCTAAATTTTGAAGTACAATTTGAGAGCT 4200
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NUMBER OF SEQ ID NOS: 29
SEQ ID NO 8
LENGTH: 7445
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-354-243B-8

Query Match 100.0%; Score 7445; DB 4; Length 7445;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCAACGAGACGATATTATAGCATGTGTTCTGACCATGACAGTACAGAGTGAATGG 120
DB 61 GCAACGAGACGATATTATAGCATGTGTTCTGACCATGACAGTACAGAGTGAATGG 120

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QY 181 TGAATATATGCTTAAACAATCTTCAAGCTCTTAATATAGTGTAAAGAGTCCG 240
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QY 5701 TTCTTGGAACATCTAGAGATGATGATTAAGTATGAGAGGAGGAGCTTGTTCAT 5760
DB 5701 TTCTTGGAACATCTAGAGATGATGATTAAGTATGAGAGGAGGAGCTTGTTCAT 5760
QY 5761 TTGAATCTGGGTTTGTCTCTCATGAGTTGAAAGCTCACCTTTTATACCTCGAA 5820
DB 5761 TTGAATCTGGGTTTGTCTCTCATGAGTTGAAAGCTCACCTTTTATACCTCGAA 5820
QY 5821 TGGAGAGGAAAGAGGAGTGTATGACTCTCACTGAGATTTACTAGTTAGCAATG 5880
DB 5821 TGGAGAGGAAAGAGGAGTGTATGACTCTCACTGAGATTTACTAGTTAGCAATG 5880
QY 5881 GAACAGACACTCGGAGCTCTCTTGAACAAACAAATGAAACCTGTGTTGTCTGTT 5940
DB 5881 GAACAGACACTCGGAGCTCTCTTGAACAAACAAATGAAACCTGTGTTGTCTGTT 5940
QY 5941 TGTCTTTTGTGAAGAAAGCAGGCAAGCCGACACATGGGTGAAATGTGGGTCTTT 6000
DB 5941 TGTCTTTTGTGAAGAAAGCAGGCAAGCCGACACATGGGTGAAATGTGGGTCTTT 6000
QY 6001 GAGTCAAGGCTTTGAGTGTGAGCACTCATCAATGTTGATCATAGTCAAGTGAAGGCTA 6060
DB 6001 GAGTCAAGGCTTTGAGTGTGAGCACTCATCAATGTTGATCATAGTGAAGGCTA 6060
QY 6061 CTTGTCAAGGCTTGTGAGTGTGAGCACTCATCAATGTTGATCATAGTGAAGGCTA 6120
DB 6061 CTTGTCAAGGCTTGTGAGTGTGAGCACTCATCAATGTTGATCATAGTGAAGGCTA 6120
QY 6121 CTGCTACTTGAAGAGTGAAGAGTGAAGAACTTTTTCACACCCCACTAAATTT 6180
DB 6121 CTGCTACTTGAAGAGTGAAGAGTGAAGAACTTTTTCACACCCCACTAAATTT 6180
QY 6181 AATTGACAAAAGATGTGATTTTGGGAAATGAGTGAATGATCTATGATGAT 6240
DB 6181 AATTGACAAAAGATGTGATTTTGGGAAATGAGTGAATGATCTATGATGAT 6240
QY 6241 TGTGCAAGGTTCAATTAAGATTAATAGGCCATCAACAGCTTTAATGGGTGAATG 6300
DB 6241 TGTGCAAGGTTCAATTAAGATTAATAGGCCATCAACAGCTTTAATGGGTGAATG 6300
QY 6301 CAAGTAAATATGATGATGCTGTGTGCTTGAAGTCAAGAAAGCATATTTAAGTC 6360
DB 6301 CAAGTAAATATGATGATGCTGTGTGCTTGAAGTCAAGAAAGCATATTTAAGTC 6360
QY 6361 TTTGGCAATCATTTTACTCATGTAATAATGATGATGATTTAATCTTTAG 6420

[illegible][illegible]

Db 952 CACTTAGGGTTTCTCTCTTTACAGCCAGCCTTGACAGATAACAACACAGAGCTCCGGCTC 1011
Qy 2691 ATCGGGAGAAACTGTTCCGAGAGTCAGTGTAAAGTCTCTCACTGTGATGACAGAGGCTAG 2750
Db 1012 ATCGGGAGAAACTGTTCCGAGAGTCAGTGTAAAGTCTCTCACTGTGATGACAGAGGCTAG 1071
Qy 2751 CTGCGGGAGCTGGGAGACCCCTGCGGATAGTCTGACGATAGACCCCTGCTCTTGTGTC 2810
Db 1072 CTGCGGGAGCTGGGAGACCCCTGCGGATAGTCTGACGATAGACCCCTGCTCTTGTGTC 1131
Qy 2811 TACCTGAGAGCTAAAGATCAGTGTACCTGATGAGCAGTGTCTCACTTGACCCCTGGA 2870
Db 1132 TACCTGAGAGCTAAAGATCAGTGTACCTGATGAGCAGTGTCTCACTTGACCCCTGGA 1191
Qy 2871 GACGTTTCTGCTCCCCCAGTCAGACAGGTTCCAGCCCTACATGACAGAGGTGTACCTTTC 2930
Db 1192 GACATTCCTGCTCCCCCAGTCAGACAGGTTCCGCGCCCTACATGACAGAGGTGTGCTTTC 1251
Qy 2931 CTGACCAAACTCAGCAATCAGCTCAGCTCCGTGTAAAGTCTGACCTGCGCTACCTAGCT 2990
Db 1252 CTGACCAAACTCAGCAATCAGCTCAGCTCCGTGTAAAGTCTGCGCTACCTAGCT 1311
Qy 2991 CCTCA 3050
Db 1312 CCTCA 1371
Qy 3051 AGAGTGAAGAGGAGGCTCAGACCAACACATCATAGGCACTTGAAATAGGTCACAAGG 3110
Db 1372 AGAGTGAAGAGGAGGCTCAGACCAACACATCATAGGCACTTGAAATAGGTCACAAGG 1431
Qy 3111 CTTTGGCTCTCAATTGAGTAATATCTTGAAGTTGTATGATGAGTAAGCTTTATTTGTTATC 3170
Db 1432 CTTTGGCTCTCAATTGAGTAATATCTTGAAGTTGTATGATGAGTAAGCTTTATTTGTTATC 1491
Qy 3171 CATGGAAGAAGTAATCACTCAAAATCTGTAGATGAGAAAGATGTTGGGAAGCAAAAAAGG 3230
Db 1492 CATGGAAGAAGTAATCACTCAAAATCTGTAGATGAGAAAGATGTTGGGAAGCAAAAAAGG 1551
Qy 3231 CCTAGATAGAGAAACAGATCTGCTGAGTATAGTACTTAT---GGGGGAGACAGGGGCG 3286
Db 1552 CCTAGATAGAGAAACAGATCTGCTGAGTATAGTACTTATGGGGGAGAGGCGAGGGGCG 1611
Qy 3287 ATATCCACTGAGTACAGTACTTGTGGGAGAGAAATCACTGAGTAAAGTACTTGTG 3346
Db 1612 ATATCCACTGAGTACAGTACTTGTGGGAGAGAAATCACTGAGTAAAGTACTTGTG-- 1669
Qy 3347 GCATGAGATCCACTGAGTACAAGTACTGTGGGGGAGGGAATGGCAGAGCAAAAGT 3406
Db 1670 -----GGGGGAAGGAATGGCAGAGCAAAAGT 1697
Qy 3407 TGAAGGCA---AGGAAGATGAGAGAGCCTCATGTGGGGGTGTGAAAGTCACTCC--TT 3462
Db 1698 TGAAGGGAAGGAAGATGAGAGAGCCTCATGTGGGGGTGTGAAAGTCACTCCCTT 1757
Qy 3463 TTCCATGTGATGAGAGATTAAAGAAAACCAAGTGTGTGATTGATGTCTTACAGACACCC 3522
Db 1758 TTCCATGTGATGAGAGATTAAAGAAAACCAAGTGTGTGATTGATGTCTTACAGACACCC 1817
Qy 3523 CAACATATAAATATCCAGAGAGAGGGGAGACGTGAGGAGACCTGGCAATTTAGGGAA 3582
Db 1818 AA-----CTATGGCAGACTGTGGAGAGACCTGGCAATTTAGGGAA 1855
Qy 3583 GGGCGGCTTTTTCACAGAGAACTTTATGCTCATCTGTGTCTACACTCCACCTTTG 3642
Db 1856 GGGCGGCTTTTTCACAGAGAACTTTATGCTCATCTGTGTCTACACTCCACCTTTG 1915
Qy 3643 ATGAGGTTCAAGTCAAGGTTGTTCTTCTACCGTTCTTGTCTACGTGTGAAAATTCAAGTAG 3702
Db 1916 ATGAGGTTCAAGTCAAGGTTGTTCTTCTACCGTTCTTGTCTACGTGTGAAAATTCAAGTAG 1975
Qy 3703 ATTCCCAAGAGCAGAGCAGCTTCTGTAAAGGAGGAGCTGTGATTTCAAGTGTCTAG 3762
Db 1976 ATTCCCAAGAGCAGAGCAGCTTCTGTAAAGGAGGAGCTGTGATTTCAAGTGTCTAG 2035

Qy 3763 AGAAGCAATATAGCTCAGAGAAATCAGGTCAACGNGAAATCTAGATCAACAGGGCAAAAA 3822
Db 2036 AGAAGCAATATAGCTCAGAGAAATCTAGGTCAACGNGAAATCTAGATCAACAGGGCAAAAA 2095
Qy 3823 TGAAGTGAAGCCTCTATATCCAGGTGAACGGTCAAGTCCAGATATATAGGTATTTGG 3882
Db 2096 TGAAGTGAAGCCTCTATATCCAGGTGAACGGTCAAGTCCAGATATATAGGTATTTGG 2155
Qy 3883 GCTCCACCGGATTAAGTCTGTAGTGTGAGTCTGTCTTTATTTTGCAGCAATCAGCGGT 3942
Db 2156 GCTCCACCGGATTAAGTCTGTAGTGTGAGTCTGTCTTTATTTTGCAGCAATCAGGTGT 2215
Qy 3943 GACGACCAAGAACTCCAGAGAAATGTGAGAAAGTGAAGAGCAGTGAAGAAAGGTACTA 4002
Db 2216 GACGACCAAGAACTCCAGAGAAATGTGAGAAAGTGAAGAGCAGTGAAGAAAGGTACTA 2275
Qy 4003 TTGGCAAGCCACAATACTAAGCCATTGAGAGAGAGCTGGGGATTTCTTCTCTGCTTC 4062
Db 2276 TTGGCAAGCCACAATACTAAGCCATTGAGAGAGAGCTGGGGATTTCTTCTCTGCTTC 2335
Qy 4063 CCACTCCCTCTACTTTGTAAACATTTTATTTGACTGTCTACTATCTGTCCATTACTCG 4122
Db 2336 CCACTCTCTCTACTTTGTAAACATTTTCTTGAATGTCTACTGTCTGTCCATTACTCA 2395
Qy 4123 CTTAGCTGACCTGTATCTAGCTGGGTCTATAGATCTTTCAATCTGTCTAAATTTGTA 4182
Db 2396 CTTAGCTGACCTGTATCTAGCTGGGTCTATAGATCTTTCAATCTGTCTAAATTTGTA 2455
Qy 4183 AGTCAAAATCTGAGGTACAGAAAGCTTAGCTCAGCCAGTCTCATGAGCACTGTGCTG 4242
Db 2456 AGTCAAAATCTGAGGTACAGAAAGCTTAGCTCAGCCAGTCTCATGAGCACTGTGCTG 2515
Qy 4243 GAGGATGCTGTGTGACAGATCAATGTCTAAGACAGATCCCTGATTTCCAGCTCTGCA 4302
Db 2516 GAGGATGCTGTGTGACAGATCAATGTCTAAGACAGATCCCTGATTTCCAGCTCTGCA 2575
Qy 4303 CTTGCTTAAGTGGCCATGTGTATTACTTTGGCTGTATTAAGTATTTGGGAAGCCAGTTC 4362
Db 2576 CTTGCTTAAGTGGCCATGTGTATTACTTTAGCCGTATTAAGTATTTGGGAAGCCAAATTC 2635
Qy 4363 CCACGACCTACATATCTGAAAGACATGATGAAACCTAGAAAGCTGGGCAAAACT 4422
Db 2636 CCACGACCTACATATCTGAAAGACATGATGAAACCTAGAAAGCTGGGCAAAACT 2695
Qy 4423 TACTAGAGATGATTTTGAAGTCTATTAACGATGCTCTGAAATGTGCAAAATCAAACC 4482
Db 2696 TACTAGAGATGATTTTGAAGTCTATTAACGATGCTCTGAAATGTGCAAAATCAAACC 2755
Qy 4483 AGAATTAACAACAAAGAGCTGAGATTGCAAAATAGACAAAGTATTAATCACTGTATTT 4542
Db 2756 AGAATTAACAACAAAGAGCTGAGATTGCAAAATAGACAAAGTATTAATCACTGTATTT 2815
Qy 4543 AATGATCATATCTTAATTAATAATAGGGCTATATA---TATATTAAGATTAAACA 4598
Db 2816 AATGATCATATCTTAATTAATAATAGGGCTATATAAGTCTATTTAAGTCTATTTAAGTAACA 2875
Qy 4599 CAAGAGTGAATAGCTCCCAATTTACTTGGCTGGTGTTCAAAAGAGTAAAAATATCAGTC 4658
Db 2876 CAAGAGTGAATATTTCCCAATTTACTGAGGCTGGTGTTCAAATAGTAATAAATATCAGTC 2935
Qy 4659 ATGATTAATTAATAGTGTATGAGAAAGTATGAGTGAAGAACTTTCTTACTTTTACT 4718
Db 2936 ATGATTAATTAATAGTGTATGAGAAAGTATGAGTGAAGAACTTTCTTACTTTTACT 2995
Qy 4719 TCAATTTCTAGT-----TTTTTTTCTTCAACCTGTATCAAGCACTAGTAAGCACT 4773
Db 2996 TCAATTTCTAGTATTAATTTTCTTCAACCTGTATCAAGCACTAGTAAGCACT 3055
Qy 4774 ATCTGCTGTAGCTATTAATATGACTTTAACAAGCAAAACAATTTGCTGTGTGCTCTTTGG 4833
Db 3056 ATCTGCTGTAGCTATTAATATGACTTTAACAAGCAAAACAATTTGCTGTGTGCTCTTTGG 3115

QY	483	GGAAAGGCAACAGANATAGAGAGAGCTCAGGCTAGCAAGTCT-GACTTGCCCTTAAAGCCAG	4832
Db	3116	GGAAAGGCAACAGANATAGAGAGAGCTCAGGCTAGCAAGTCTGACTCAACTAAAGCCAG	3175
QY	4893	AGGCATGGTTATATAGCAGAGAAAGGAGAGCTCTTCGCAAGGAGGAGGCTTAAGTAATCA	4952
Db	3176	AGGCATGGTTATATAGCAGAGAAAGTGAAGCTCTTCACAGAGGAGGAGCTTAAGTAATCA	3235
QY	4953	GAACACAGAAAGCTCCGGTTGATGGAATTAATCAGTAAGATATCTAACCTTATCTC---CT	5009
Db	3236	GAACACAGAAAGCTCTGGTTGATGGAATTAATCAGTAAGATATCTAACCTTATCTCCTCT	3295
QY	5010	TCTATCGAAGCTAAATGCTCTCTTTTCTTGCTGTAGAGCTGATPAACACACTGTTTTC	5069
Db	3296	TCTATGAGAGCTAAACCGCTCTCTCTCTTGCTGTAGAGCTGATPAACACCGCTGTTTTC	3355
QY	5070	TTTGAAGGTCATAGGCTTTTGAGATTTTATGTGCTCTCGCAAGTCTTGTAGAGGGTT	5129
Db	3356	TTTGAAGGTCATAGGCTTTTGAGATTTTATGTGCTCTCGCAAGTCTTGTAGAGGGTT	3415
QY	5130	GTTACCTTGCACCTGGGCTTGATGTGTAGCATGCCAAAGGCACACACTTCTGATGCT	5189
Db	3416	GTTACCTTGCACACCTGGGCTTGATGTGTAGCATGCCAAAGGCACACACTTCTGATGCT	3475
QY	5190	GTTGPAAGGTTATTAATTCATTACTTGTCTTTGGAAAGGTGAAGCGTGTGAGAAAG	5249
Db	3476	GTTGPAAGGTTATTAATTCATTACTTGTCTTTGGAAAGGTGAAGCGTGTGAGAAAG	3535
QY	5250	AACCTCACAGAGATGTGTTCTCTGAGAGAAACCTTTTTTCCCTTAAATGCTCTTAA	5309
Db	3536	AACCTCACAGAGATGTATCTCTGAGAGAAAC-TTTTTTTTCCCTTAAAGCTCTTAA	3594
QY	5310	TCCACTTTCACATCAATCTTGACTTTTATACCATCTGTGCATAGAAAGAGTTTAGGC	5369
Db	3595	TCCACTTTCACATCAACTTTGACTTTTATACCATCTGTGCATAGAAAGAGTTTAGGC	3654
QY	5370	CGCTCTCATGCGCTCTGGGAAAGACCAATATGGGAGAGAAATTTATGCTGAGAAATCTG	5429
Db	3655	CGCTCTCATGCGCTCTGGGAAAGACCAATATGGGAGAGAAATTTATGCTGAGAAATCTG	3714
QY	5430	ACCGGACAGGGAACCTGGTCAGAGCTCCCCGGAACACCAACAGTGTTAAGTAGAACA	5489
Db	3715	ACTGGACAGGGAACCTGGGTCAAGCTCCCCAAAGACCACTACAGTGTTAAGTAGAACA	3774
QY	5490	GTCACAGGCTGGGCTCATGTAATAGATGGAACAGAGCAGGAGAAATAGCTACAAAGTT	5549
Db	3775	GTCACAGGCTGGGTTTCATATATAGATGGAACAGAGGAGGAAAGATAGCTACAAAGTT	3834
QY	5550	TCATATGGGTCGCGAGTCTTAAAGATACAAATAGCTGTTGGGCTTCATACAAAGAG	5609
Db	3835	TCATATGGGTCCTTAAGTCTTTAAAGATACAAATAGCTGGTTCATACAAAGAG	3894
QY	5610	TCTGGGAAGGAGAG---TGACAGGGAATTGGAAAGGGAAGAAACAGATGTAGAGA	5666
Db	3895	TCTGGGAAGGAGACAGCATTGACAGGAGATGGAAGGAAAGAAAC-ATGTAGAGA	3952
QY	5667	CTTGAACAGCTACAAATCTCTACACAGATTTTTCTTGGACAAATCTAGAA---GGT	5722
Db	3953	TTTGAAGAGCTCAAAATCTCTACAGAGAGATTTTTCTTGGAGAAATCTAGAACAGGAT	4012
QY	5723	AGTGAGTTAGGT-GATTGACAGGAGGACTTGCCTTTCGCAATTTGAAATCTGGGTTTTGTCTC	5781
Db	4013	GGTGAGTTAGGTGATGCGACAGAGACTTGCCTTTCGCAATTTGAAATCTGGGTTTTGTCTC	4072
QY	5782	TCCATATGAGTTGAAAGGCTCAACC-TTTTATACCTCGAATGAGAGAGAGAAAGGGGT	5840
Db	4073	TCCATATGAGTTGAAAGGCTCAACCTTTTTTACCCTGATGAGAGAGAGAAAGAGGGGT	4132
QY	5841	GTTATGATCTCCACCTGAGATTTTACTAGTTTACGAATGGAAACGACACTCGGGAACCTC	5900
Db	4133	GTTTGAATCTCTACTCTGAGATTTTACTAGTTTACGAATGGAAACGACACTCGGGAACCTC	4192
QY	5901	CTCTTGAC-----AAAAAATGAAACCTGTGTTGCTCTGTTGTTGTTGCTCTTTG	5950

[illegible]

Db 1312 CCTCTCTCTCTCTTATTTCAGTAAGAACCCGAGGCTCCGCCCTCTCTCTCTCA 1371
Qy 3051 AGAGGAGAGAGGAGGCTCAGCACACACCATCATATGAGCACTTGAAATAGTCACAAG 3110
Db 1372 AGAGGAGAGAGGAGGCTCAGCACACACCATCATATGAGCACTTGAAATAGTCACAAG 1431
Qy 3111 CTGTCCTTCAATTAGTAATATCTTGAGTTTGTAGAGTGAAGCTTTATTTGTTATC 3170
Db 1432 CTGTCCTTCAATTAGTAATATCTTGAGTTTGTAGAGTGAAGCTTTATTTGTTATC 1491
Qy 3171 CATGGAAGAAATCACTCAATTTCTGAGATGAGAAAGATGTTGGAGCAAGAAAAAG 3230
Db 1492 CATGGAAGAAATCACTCAATTTCTGAGATGAGAAAGATGTTGGAGCAAGAAAAAG 1551
Qy 3231 CCTAGATGAGAAACAGATCTGCTGAGATATGACTTAT---GGGGGAGCAGGGGCG 3286
Db 1552 CCTAGATGAGAAACAGATCTGCTGAGATATGACTTATGAGGGGGGGGAGGGGCG 1611
Qy 3287 ATATCACTGATGACAACTACTGTCGGGAGAGAAATCCACTGAGTCAAGTACTGTTG 3346
Db 1612 ATATCACTGATGACAACTACTGTCGGGAGAGAAATCCACTGAGTCAAGTACTGTTG- 1669
Qy 3347 GCATGAGATCACTGATGACAACTGTTGTCGGGAGAGAAATGCAAGAGCAAAAGT 3406
Db 1670 -----GGGGGAAGGAAATGCAAGAGCAAAAGT 1697
Qy 3407 TGAAGGA---AGGAAGTGAAGAGGCTCATGTTGGGGGTGTAAGGTCACTCC-TT 3462
Db 1698 TGAAGGGAAGAGGAAGTGAAGAGGCTCATGTTGGGGGTGTAAGGTCACTCCCTT 1757
Qy 3463 TTTCATGATGAGAGATTAAGAAAAACAGTGTGTAGTTGATGTCTTACAGACCCC 3522
Db 1758 TTTCATGATGAGAGATTAAGAAAAACAGTGTGTAGTTGATGTCTTACAGACCCC 1817
Qy 3523 CAACATGAAACATATCCAGAGAGCGGGAGAGCTGTGGAGAGCCTGGCATTTAGGGA 3582
Db 1818 AA-----CTATGAGAGAGCTGTGGAGAGCCTGGCATTTAGGGA 1855
Qy 3583 GGGCGGCTTTTCAACAGAGAACTTATGCTCATCTTGTGCTACACTCCACTTTG 3642
Db 1856 GGGCGGCTTTTCAACAGAGAACTTATGCTCATCTTGTGCTACACTCCACTTTG 1915
Qy 3643 ATGAGTTCAGCTCAGGTTTGTCTTCTACCGTCTTGTCTACTGTGGAACTTCAGTAG 3702
Db 1916 ATGAGTTCAGCTCAGGTTTGTCTTCTACCGTCTTGTCTACTGTGGAACTTCAGTAG 1975
Qy 3703 ATTCGCCAAGACGAGACAGCTCTTCTGTAGGAGAGAGCCTGGATTTCTAGTGTCTAG 3762
Db 1976 ATTCGCCAAGACGAGACAGCTCTTCTGTAGGAGAGAGCCTGGATTTCTAGTGTCTAG 2035
Qy 3763 AGAAGCAATAGCTCAGAGAACTAGGTCAACGTGAATCTAGGTCAACGGCGCAAAA 3822
Db 2036 AGAAGCAATAGCTCAGAGAACTAGGTCAACGTGAATCTAGGTCAACGGCGCAAAA 2095
Qy 3823 TGACTGAACGCTCTATTTCCAGGTGAACGTGCTCAGATATCTAGAGTATTG 3882
Db 2096 TGACTGAACGCTCTATTTCCAGGTGAACGTGCTCAGATATCTAGAGTATTG 2155
Qy 3883 GCTCCACCGGATAGATTTCTGTAGTGTGCTTTATTTTGGACACATACAGCGCT 3942
Db 2156 GCTCCACCGGATAGATTTCTGTAGTGTGCTTTATTTTGGACACATACAGTGT 2215
Qy 3943 GAGGACGAAATCAGAGAAATGTCAAGAGCTGAAGAGAGACAGTGAAGAAAGTACTA 4002
Db 2216 GAGGACGAAATCAGAGAAATGTCAAGAGGCTGAAGAGAGACAGTGAAGAAAGTACTA 2275
Qy 4003 TTGGCAAGCCACATATCAATCAATCTAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 4062
Db 2276 TTGGCAAGCCACATATCAATCAATCTAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 2335
Qy 4063 CCAAGTCCCTTCTATCTTATTAATTTATTTGATCTGTCTATCTGCTCATTAATCTG 4122
Db 2336 CCAAGTCCCTTCTATCTTATTAATTTCTTTGATCTGTCTATCTGCTCATTAATCTG 2395

Qy 4123 CTGAGTGCACCTGATATCTAGCTGGGTCTATAGATCTTTTCAATGTGTCTAAATTTGTA 4182
Db 2396 CTGAGTGCACCTGATATCTAGCTGGGTCTATAGATCTTTTCAATGTGTCTAAATTTGTA 2455
Qy 4183 AGTCACAATCTGAGCTAGCAGAAAGCTTATGCTCAGCAGTCTCATAGAGCACTTGCTG 4242
Db 2456 AGTCACAATCTGAGCTAGCAGAAAGCTTATGCTCAGCAGTCTCATAGAGCACTTGCTG 2515
Qy 4243 GAGATGCTGTGACAGAGTCAATGCTAGAGAGACAGATCCCTGATTCAGGCTTGCA 4302
Db 2516 GAGATGCTGTGACAGAGTCAATGCTAGAGAGACAGATCCCTGATTCAGGCTTGCA 2575
Qy 4303 CTGCTAGTGGCCATGATATTAATCTTTGCTGATTAATTTTGGAAAGCCAGTTC 4362
Db 2576 CTGCTAGTGGCCATGATATTAATCTTTGCTGATTAATTTTGGAAAGCCAGTTC 2635
Qy 4363 CCAAGGACCTAATATCTGAGAGACATGATGAATGAATCTAGAAAGCTGGGCAAACT 4422
Db 2636 CCAAGGACCTAATATCTGAGAGACATGATGAATGAATCTAGAAAGCTGGGCAAACT 2695
Qy 4423 TACTAGAGATGATTTTGAAGCTCAATTAAGGATGCTGTAATGTGGCAAAATCAACC 4482
Db 2696 TACTAGAGATGATTTTGAAGCTCAATTAAGGATGCTGTAATGTGAATCAATCAACC 2755
Qy 4483 AGAATTAACAAGAAAGCTGAGATTTGCAAAATAGACAGATATTAGATCACTGTAAT 4542
Db 2756 AGAATTAACAAGAAAGCTGAGATTTGCAAAATAGACAGATATTAGATCACTGTAAT 2815
Qy 4543 AATAGCTATATCTTAATTTAAATATAGGCTTAATA---TATATTAAGATTAACA 4598
Db 2816 AATAGCTATATCTTAATTTAAATATAGGCTTAATAAGCTTAATTAAGATTAACA 2875
Qy 4599 CAAGAGTGAATAGGCTCCCAATTTTACTGAGCTGCTTCAAAAGATTAATAATCAATC 4658
Db 2876 CAAGAGTGAATAGGCTCCCAATTTTACTGAGCTGCTTCAAAAGATTAATAATCAATC 2935
Qy 4659 ATGATTAATTAATAGTCAATGAAGATAGATGAAGAACCTTTCTTACTTTTAACT 4718
Db 2936 ATGATTAATTAATAGTCAATGAAGATAGATGAAGAACCTTTCTTACTTTTAACT 2995
Qy 4719 TCATTTCTTAACT-----TTTTTTTTTTCTTCAACCTCGATCAAGCCTAGTAGCACT 4773
Db 2996 TCATTTCTTAACTTTTATTTTCTTCAACCTCGATCAAGCCTAGTAGTAGCACT 3055
Qy 4774 ATGCTGTGATTAATTAATAGATTTTACAGCAAAACAATGCTGTGTGGCTCTTTG 4833
Db 3056 ATGCTGTGATTAATTAATAGATTTTACAGCAAAACAATGCTGTGTGGCTCTTTG 3115
Qy 4834 GAAAGGAAAGATAGCAGAGAGCTCAGGCTAGCAAGTCT-GACTTGCCCTAAAGCCAG 4892
Db 3116 GAAAGGAAAGATAGCAGAGAGCTCAGGCTAGCAAGTCTGACTCAACTAAAGCCAG 3175
Qy 4893 AGGATATGATTAATAGCAGAGAGAGAGGCTTTTCCAGTGGGTGTCTTAATTAATCA 4952
Db 3176 AGGATATGATTAATAGCAGAGAGAGAGGCTTTTCCAGTGGGTGTCTTAATTAATCA 3235
Qy 4953 GAAACAGAAAGGCTCGGTTGATGGAATTAATCAGTATGATATCACTTATCTCCT 5009
Db 3236 GAAACAGAAAGGCTCGGTTGATGGAATTAATCAGTATGATATCACTTATCTCCT 3295
Qy 5010 TCTATCAACCTAATATGCTCTTTTCTTGTGTGAGGCTGATTAACACACTTTGTTTC 5069
Db 3296 TCTATCAACCTAATATGCTCTCTCTCTTGTGTGAGGCTGATTAACACAGCTTTGTTTC 3355
Qy 5070 TTTTGAATGTTCAATGCTTTTGTAGATTTTATAGTCTTCCAGTCTTTTGTAGAGGTTT 5129
Db 3356 TTTTGAATGTTCAATGCTTTTGTAGATTTTATAGTCTTCCAGTCTTTTGTAGAGGTTT 3415
Qy 5130 GTTACCTTGACACCTGGGCTTGAATGTTAGATCCAAAGGACACACTCTGAATGCT 5189
Db 3416 GTTACCTTGACACCTGGGCTTGAATGTTAGATCCAAAGGACACACTCTGAATGCT 3475

5190	GTGTAAGAAGTATATATTCATTTACTTTGCTTGTCTTTGGAAAGGTGAAGGTGTGTGAGAAG	5249
3476	GTGTAAAGGTTATATTATTCATTACTTGTCTTTGGAAAGGTGAAGGTGTGTGAGAAG	3535
5250	AACACACAGAGGATGTGTCTCTGTAGAGAAAACCTTTTTCCTTAAATGCTCTATA	5309
3536	AACACACAGAGGATGTATTTCTGTAGAGAAAC-TTTTTCCTTAAAGCTCTATA	3594
5310	TCACCTTTCAGTCAACTTTGACTTTTATPACATGCTGTCAACATGAAGAGTGTAGGCC	5369
3595	TCCACTTTCAGTCAACTTTGACTTTTATPACATGCTGTCAACATGAAGAGTGTAGGCC	3654
5370	CGCTCTAATGAGCTCTGGGAAAAGACAATPAGGGAGAGATGTATATGTAGAGAACTGT	5429
3655	CGCTCTGATGCTCTGGGAAAAGACAATPAGGGAGAGATGTATATGTAGAGAACTGT	3714
5430	ACCAGCAGAGGAAACTGTGTACAGAGCTCCCGGAAACACACACAGAGTTTAAGTAGAACA	5489
3715	ACTGAGCAGAGGAAACTGTGTGTACAGAGCTCCCGGAAACACACATPAGGTGTAGAGACA	3774
5490	GTCCAGAGGTGGCTCATGTAAATAGAAATGAAACAGAGCGAGGAGATPAGCTACAAAGTT	5549
3775	GTCCAGAGGTGGCTCATGTAAATAGAAATGAAACAGAGCGAGGAGATPAGCTACAAAGTT	3834
5550	TCATATGGGTCCGAGGTCTTAAAGTACAAAATAGCTGTTGGGCTTTATAACAAGAGAG	5609
3835	TCATATGGGTCTTAAGTCTTTAAGTATCAAAATAGCTGTTGGGCTTTATAACAAGAGAG	3894
5610	TCTGGGAAAGGACAGCAAG--TGAGAGGGAATGGAAGGGAAGAAACAGAAATPAGAGGA	5666
3895	TCTGGGAAAGGACAGCAAGCATTTGAGAGGAGATGGAAGGGAAGAAAC-ATATPAGAGGA	3952
5667	CTTGAACAGCTACAAATCCTCTACAGACGATTTTTCCTTGGACATCTAGAA----GGT	5722
3953	TTTGAAGAAAGCTACAAATCCTCTACAGAGAGATTTTTCCTTGGAGAACTAGAAACAAGGT	4012
5723	AGTGGATTAGGT-GATTGACAGGGGACTTCTCTTGGCAATTTGAATCTGGGTTTGTCTC	5781
4013	GGTGATTAGGTGATCGCAGAAAGACTTGTCTTGGCAATTTGAATCTGGGTTTGTCTC	4072
5782	TCCATTGAGGTGGAAGCGTCAGCC-TTTTATACCTGCATGGAAGGAGGAAGAAAGGGGT	5840
4073	TCCATTGAGGTGAGAGCGTCACCCCTTTTATACCTGTATGAGAGGAGGAAGAAAGGGGT	4132
5841	GTTATGACTCTACCTGTGAGTTTACTAGTTTACGCAATGGAACAGACACTCGGACCTC	5900
4133	GTTTGACTCTCCTACTGAGTTTACTAGTTTACGCAATGGAACAGACACTCGGACCTC	4192
5901	CTCTTGAC-----AAAAAATGAAAACCTGTGTGTGTCTGTGTCTTTTG	5950
4193	CTCTTGACAGAAAAAATAAAAAAAGAAACCTGTGTGTGTCTGTGTCTTTTG	4252
5951	TTAAGAAAGACA-----	5963
4253	TTAAGAAAGACAAGGACAGCTGGGCAATGGGCCATGCTTTAATCCAGCATTTGGAG	4312
5964	-----	5963
4313	GCAGAGCAGATGACTTTCTTAATTCAGAGCAGCCTGTCTACAAATGATTCAGGA	4372
5964	-----	5963
4373	CAGCAGGCTATACAGAAAACTGTCTCGGAAAAAATAAAAAAAGAAAGAAAG	4432
5964	-----	5963
4433	AAAAGAAAGAAAG	4492
5964	-----	5963
4493	GAA	4555
5964	-----	5963

[illegible]

Db	593	GGATCTCTTCTGCTCCATACACCGCCCTTGCCA-TTTCTCTGAAGCACTTGCAAACTCTTTAG	651
QY	2331	GGGCGCTTTATCTCCGACAGTCTCACTACCTATGTTTCTGTCTCTTTAGAGACTCTTTA	2390
Db	652	GGGCGCTTTATCTCCGACAGTCTCACTACCTATGTTTCTGTCTCTTTAGAGACTCTTTA	711
QY	2391	AGGATGGGTCCTTTTCTATTTCTAATTTCAATTCAGAGTCTACGACCAATTCCTATCTTTGGCT	2450
Db	712	AGGATGGATCTTTTCTATTTCTAATTTCAATTCAGAGTCTACGACCAATTCCTATCTTTGGCT	771
QY	2451	TCAGACACATATACTGAATTTTATCTACAGAGGCGATTAGAAAGCACCCAGACTG	2510
Db	772	TCAGACACATATACTGAATTTTATCTACAGAGGCGATTAGAAAGCACCCAGACTG	831
QY	2511	CAATACCTTCCATTTCTCTGTGCTCTCTTTGAACTCATACCTCTTGGTACTACTGAG	2570
Db	832	CAATACCTTCCATCTGTGTGTGTCTCTCTTGAACCTATACCTCTTGGTACTACTGAG	891
QY	2571	ACCCACTGGGACATACATCTCTACTTACAGGCTTTTCTTCATCTCTCTTGTCAACCAAG	2630
Db	892	ACCCACTGGGACATACATCTCTACTTACAGGCTTTTCTTCATCTCTCTTGTCAACCAAG	951
QY	2631	CACTTAAGGSGTTTCTCTCTTTACAGGCCAGCCTTTCACATATACACACAGAGTCCGCTC	2690
Db	952	CACTTAAGGSGTTTCTCTCTTTACAGGCCAGCCTTTCACATATACACACAGAGTCCGCTC	1011
QY	2691	ATCCGGGGAGAAACTGTTTCCGAGAGTCAGTGTAAAGTCTCTCACTGTGATGACAGGCTAG	2750
Db	1012	ATCCGGGGAGAAACTGTTTCCGAGAGTCAGTGTAAAGTCTCTCACTGTGATGACAGGCTAG	1071
QY	2751	CTGCGGGAGCTGTGGAACCTCTGGGATAGCTTGACGTATGACCCCTGTGCTTCTTGTG	2810
Db	1072	CTGCGGGAGCTGTGGAACCTCTGGGATAGCTTGACGTATGACCCCTGTGCTTCTTGTG	1131
QY	2811	TACCTGCAAGGTAAAGATCAAGTGTACTCTGTATGAAGCAGTGTCTCAACTTCACCTTGAA	2870
Db	1132	TACCTGCAAGGTAAAGATCAAGTGTACTCTGTATGAAGCAGTGTCTCAACTTCACCTTGAA	1191
QY	2871	GACGTTCTGCTCCCCCAGTACAGAGGTTCCAGCCCTACATGACAGAGGTGTACCTTTC	2930
Db	1192	GACATTTCTGCTCCCCCAGTACAGAGGTTCCAGCCCTACATGACAGAGGTGTGTCTTTC	1251
QY	2931	CTGACCAAACTCAGCAATCAAGCTCAGCTCTGTGTAAAGTGTGACTCTGAGTACCTATGCT	2990
Db	1252	CTGACCAAACTCAGCAATCAAGCTCAGCTCTGTGTAAAGTGTGACTCTGAGTACCTATGCT	1311
QY	2991	CCTCTCTCTTCTCTTCTTATTCAGTAAGAACCCGAGGTCCTGCGCTCTCTCTTTCACA	3050
Db	1312	CCTCTCTCTTCTCTTCTTATTCAGTAAGAACCCGAGGTCCTGCGCTCTCTCTTTCACA	1371
QY	3051	AGAGTGAAGGCGCTCAGACACCAACCATATAGGCCACTTGAAATAGTCAACAAAG	3110
Db	1372	AGAGTGAAGGCGCTCAGACACCAACCATATAGGCCACTTGAAATAGTCAACAAAG	1431
QY	3111	CTTTGGCTTCAATTGAATTAATCTTTGAGTTTGTATGAGGAAGCTTATTTGTTTATC	3170
Db	1432	CTTTGGCTTCAATTGAATTAATCTTTGAGTTTGTATGAGGAAGCTTATTTGTTTATC	1491
QY	3171	CATGGAAGAAATCACTCAAAATTTCTGTAGATGAGAAAGATGTTGGAGCGAAGAAAG	3230
Db	1492	CATGGAAGAAATCACTCAAAATTTCTGTAGATGAGAAAGATGTTGGAGCGAAGAAAG	1551
QY	3231	CCATGATAGAGAAACAGATCTGTGAGTATATAGTACTTAT---GGGGGAGCAGGGGGCG	3286
Db	1552	CCATGATAGAGAAACAGATCTGTGAGTATATAGTACTTAT---GGGGGAGCAGGGGGCG	1611
QY	3287	ATATCCACTAGTACAAGTACTTGTGGGAGAGAAATCCACTAGTACAAGTACTTGTG	3346
Db	1612	ATATCCACTAGTACAAGTACTTGTGGGAGAGAAATCCACTAGTACAAGTACTTGTG--	1669
QY	3347	GCATGAGATCCACTGATGACAAATCTTGTGGGGGAGGGAATGGCACAGACAAAGT	3406
Db	1670	-----GGGGGAGAGGAATGGCACAGACAAAGT	1697

QY 3407 TGAAGGA---AGGAAGTGAAGAGGCTCATGGTTGGGGGTGTGAAAGGCTACTCC-TT 3462
Db 1698 TGAAGGAAAGAGAAATGAGAGGCTCAATGTGTGGGGGTGGAAGGCTACTCCTTT 1757
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QY 3523 CAACATATGAAACATATCCAGAGAGCGGGCAGACTGTGGAGACCTGGCATTTAGGAA 3582
Db 1818 AA-----CTATGGCAGACTGTGGAGACCTGGCATTTAGGAA 1855
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Db 1856 GGGGGGCTTTTTCACAGAGAACTTTATGTCTATCTTGTGTCTACACTCCACTTTG 1915
QY 3643 ATGAGGTTCAAGCTAGGTTTCTTCTACGCTTCTGTCTACTGGTGGAACTTCAGTAG 3702
Db 1916 ATGAGGTTAAAGCTAGGTTTCTTCTACGCTTCTGTCTACTGGTGGAACTTCAGTAG 1975
QY 3703 ATTCCCAAGAGCAGAGACAGCTCTTCTGTAAAGGAGAGACCTGGATTTCAAGTCTAG 3762
Db 1976 ATTCCCAAGAGAGAGACAGCTCTTCTGTAAAGGAGAGACCTGGATTTCAAGTCTAG 2035
QY 3763 AGAAGAAATAGCTCAAGAAATCTAGCTCAAGTAAATCTAGCTCAAGCGGCAAAA 3822
Db 2036 AGAAGAAATAGCTCAAGAAATCTAGCTCAAGTAAATCTAGCTCAAGCGGCAAAA 2095
QY 3823 TGAAGTAAAGCTCTATTTCCAGAGAAAGGTCAGTGTCTAGATATCTAGAGTATTTG 3882
Db 2096 TGAAGTAAAGCTCTATTTCCAGAGAAAGGTCAGTGTCTAGATATCTAGAGTATTTG 2155
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Db 2216 GACGACCAAGAACTCCAGAAATGTCAAGAGCTGAAGGAGACAGTAAAGAGTACTA 2275
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Db 2276 TTGGCAAGCCCAATTAAGCCATTCAGTAGAGAGCTGGGAACTTTCTTCTGCTTC 2335
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Db 2336 CCAAGTCCCTCTACTTTGAAATTTATTTGACTGTCTACTACTGTCCATTAATCTCG 2395
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QY 4183 AGTACAAATTTGTGAGCTAGAGAAAGTTAGCTCAGCACTCTCAGAGCACTTGTCTCG 4242
Db 2456 AGTACAAATTTGTGAGCTAGAGAAAGTTAGCTCAGCACTCTCAGAGCACTTGTCTCG 2515
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Db 2696 TACTAGAGATGATTTTGTAGCTCAATTAACGAGATGCTGAAATGTGGCAAAATCAACC 2755

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QY 4599 CAAGATGATTAAGCTTCCCAATTTACTGCGCTGTGTTTCAAAAGAGTAAATATCAGTC 4658
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QY 4719 TCAATTTCTTACT-----TTTTTTTTTCTTCAACCCCTGATCAAGCCATAGTAAGCACT 4773
Db 2996 TCAATTTCTTACTTATTAATTTTCTTCTTCAACCCCTGATCAAGCCATAGTAAGCACT 3055
QY 4774 ATCTGCTGAGCTATTAATTAATGACTTTACAGAAACAATCTGCTGTGGCTCTTTGG 4833
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QY 4893 AGGATGATGATAGCAGAGAAAGTGAAGCTCTTCCGAAATGGGATGCTTAAATATCA 4952
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QY 5190 GTGTAAAGGTTATTAATTTACTTTGCTTTGTGAAAGTGAAGGCTGTGAGAAAG 5249
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Db 3536 AACTCAGAGAGATGCTCTCTGAGAGAAACCTTTTTCCTTAAATAGCTTAA 3594
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Sequence 25, Application US/09419568F
Patent No. 6331613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
TITLE OF INVENTION: (Tifs) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 25
LENGTH: 4797
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-419-568F-25
Query March 9.2% Score 686; DB 4; Length 4797;
Best Local Similarity 53.8%; Pred. No. 1.9e-164;
Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;
QY 2034 CTCCTCTCTCATATCACTGTTGACACTTGTGCATCTGTATGGCTGTCTGCAGAA 2093
DB 29 CTCCTCTCTCATATCACTGTTGACACTTGTGTGAAATGTCTCAATGGCCGCTGCAGAA 88
QY 2094 ATCTATGAGTTTTCCTTATGGGAACTTTGGCCGACGCTGCTTCTCATATGCTT 2153
DB 89 ATCTGATGAGCTTCTTCTTATGGGAACTTGGCCGACGCTGCTTCTTCTTGGCCCT 148
QY 2154 GTGGGCCAGAGGCAATGCGCTGCGTCAACCCGCGCAAGCTTGAAGTGTCCAA 2213
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DB 209 CTTCCAGAGCCGTATATACCAACCGACCTTCACTGCTGATAGAGGATATCATCTC 268
QY 2274 TCTCTTCTCTCATACCGCTTGGCACTTTCTCTGAAGCACTTGCAACTCTTTAGGG 2333
DB 269 AATCTGTCTCTTCTGCTGTGATCTACTGTGAATCAATAGTCTTAACTTTCTTCA 328
QY 2334 CGCTTATCTCCGAGGCTCATCACTATGTTT-----TCTGTCTCTTGAAG 2382
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QY 2383 ACTCTTAAAGACTGGGCTTTTCTATTTCTATTTCAAGCTTCTAGAGCAATTTCTAT 2442
DB 389 TTTTTCAGAGACTCTTGGGAATCTGGCTTTTCTTCTTGAATCTTCTCTTCTCAT 448
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QY 2501 CCCAGCATGCAATATCTTCTCATCTTCTGAGCTCTCTTCTGAATCTCATCTCTTGGC 2560
DB 509 CTGATGATTTTCTTCTTATGCTTATGCTCTGAGCATTTTCTTAACTCATGACATCTG 568
QY 2561 TACTC-----CTGAGACCCACTGCGGACATATCATCTCTAC 2595
DB 569 AATCTGCTTTAATCTTATGATGCTGTGGGAGACGGGATGGGGACATATCTAT 628
QY 2596 TTACAGGCTTTCTTCTCATCTCTTGTACCCAGGCACTTAAAGGTTTC-TCTCTTCA 2654
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QY 2762 GGTGAGCCCTTGGGATAG-----TCTGAGCTATAGCCCTGCTCTTGTGTACTCTG 2817
DB 809 GGTGATGATAGTGTAGGTCTTATGCTTATGACCTTCTGTTTCTTCTTCACTG 868
QY 2818 AGCTTAAGATCACTGCTATCTATGAGAGGCTCTCACTTCACTTCTGAAAGCTTC 2877
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DB 929 TGTCTCCCTCACTGATGAGGTCCAGCTTATATGACAGAGGTGTACTTCTTCA 988
QY 2938 AACTCAGATCACTGCTGCTCTGATGATGATGATGATGATGATGATGATGATGAT 2997
DB 989 GGTCTACGACAGGCTTACGACATGTGTATGATGATGATGATGATGATGATGATGAT 1048
QY 2998 CTTCTCTCTATTCAGTATGAGAACCCGAGCTCTGCTCTCTCTCTCTCTCTCTCT 3057
DB 1049 CTCCT 1108
QY 3058 GAGAGGCTTACGACACCACTCATAGGCTCTTGAATAGTCTCAAAAGCTTTGGC 3117
DB 1109 TAACTGACAGAGAGAGTGTCTGGCAGAGGTTATGAGAGTCA-----TTTGGG 1161
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DB 1162 ATCATTAAGTATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1221
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DB 1222 GGTCTGGAATCTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1281
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QY 3298 GTACAGTACTTGGGGAGAGAAATCCACTGATGATGATGATGATGATGATGATGATGAT 3357
DB 1310 GAAACATCTAGCTGTGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1369
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DB 1416 -----GTGGGTGTGGGTGCGGACACTGTGCTCTGTTGATGATGAGGA 1460
QY 3478 AGTTAAGAAAACA-GTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3536
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QY 3537 ATCCAGAGAGACCGGAGACTGTGGAGACTTGGCAATTAAGGAGGCGC--GCTTTT 3594
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QY 3655 TCAGATTGCTTCT-----ACCTTGTGCTACTGTGTAAC 3693
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QY 3814 GGGCAAAATAGCTGAAGCCCTCTATTCAGGTGAACGGTCACTGCTCAGATATCTG 3873
DB 1821 TGGGCAAAATTAATAAGAGCTTAAATCCAGGTGAATGTACTGATCCATGGGTGG 1880
QY 3874 AGGTATTGGGCTCCACCGGATTAATCTGTAGTGA-GTGTGCTTTATTTTCAGCA 3932
DB 1881 GAGGTTCATMAAGTTTCAGACACATTAAGATATGTATGCTTTATTTATTTATCA 1940
QY 3933 CATCAGCGGTGACGACCAAGATCATCCAGAGAATGTCAAGAGGCTGAAGAGACATGA 3992
DB 1941 TATTGAAGGTATGATGCTGATATTCAGAGAAATGTCAAAAAGCTGAAGACACATGA 2000
QY 3993 AAAGGTACTATTGGACCAACCAATATTAAGCATTCAAGTAG-GAGAAGTGGGATTTG 4050
DB 2001 AAAGGTAGGACTGATTAATGTCATATGCTAATGATGCAATAGAGACAAATGTTT 2060
QY 4051 TTTCCTGCTTCCAGTCCCTTTCTATCTTTGATCACTTTATTTGACTTGTCTACTATG 4110
DB 2061 TTCTTCTCTTCTTCTTCCATCACTTTGATTTTTCATCTGATTTCTCTACACAG 2120
QY 4111 GTCCATTAAGCTGAGTGAACCTGATCTAGTGGGTATATGATTTTCAATCTGTG 4170
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QY 4171 TCTAATTT---GTAACTCACAATTTCTGAGCTAGCAGAAAGCTTAGCTCAGCCAGTCT 4227
DB 2177 TCCAAATCTGCAATGTAGATTTCTAAGATCTGTTGGATCTTAGTGTCTAGTAC 2236
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DB 2357 TAGGAAATTTCAATCTCTATGATCTAATCTGAAGAACTGTTTAAAAACA 2416
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QY 4521 AGATTTAGAACTAGTATTAATAGTATCATCTTAATTAATATAGGCTATATA 4580
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QY 4581 TATTTTAAGATTAACAAGAGTGAATAGCTTCCCAATTAATCTGCTGCTTTTCAA 4640
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QY 4753 TCAAGCACTAGTGAAGCACTATCTGCTAGATTAATATGACTTTACGCAAAACAC 4812
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QY 4813 ATTGCTGTGCTCTTTTGGGAAAGGAAACAGATAGCAGAGGCTCAGGCTAGCAAGT 4872
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QY 4873 CTGACTGCTTAAAGCAGAGGATGTTGATAGCAGAGAAATGAGCTTCTTGCAG 4932
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QY 4933 TGGGTGCTTAAGTATCAGAAAACAGAGAGCTCCGTTATGGAATTAATCAGTAAG- 4991
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QY 4992-----TATCAACCTTATCTCTCTATGCAACCTTAATGCTCTTTCTGTG 5042
DB 3006 GCTTAACCTTAATTTCCCTTTTCTTCTCTTGACTTTTAAAAAGCTTTCTCTAG 3065
QY 5043 TGTAGGCTGATMAACACACTTGT--TTCTTTAGAGTTCATGCTTTGTAGATTTTA 5100
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QY 5101 GTGCTTGGCAGTCTTGT--TAGAGGTTTGTATCCTTGACACCTGGGCTTGATGTTA 5158
DB 3126 TTGTGAAGCCAGTCTCTGTTATAGAACTATATCTAGACATGAGGAGGCTGAATGTTA 3185
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QY 5271 CTGTAGAAAACCTTTTTCCTTAAATGCTTATATCACTTCACTGA- --ACTT 5327
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QY 5603 AAGGAAGTCTGGGAGGACAGCAAGTGAAGGAAATGAAGAAAGGAAACAGATGAG 5662
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QY 5663 AGAGCTGAACAGTCAAAATCCCTACAGAGATTTTCTTGAACATCTGAAGGT 5722
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QY 5723 AGTGAATAGATATGACAGGGGACTGTTTGCATTTGAATCTGGGTTTGTCTCT 5782
DB 3749 ATAGATTAAGGAATTTCAATAGGAATGCTTTTCACTTAATTTGGGTTTCTCT---T 3805
QY 5783 CAATGAGTTGAAAGGCTCAACCTTTTAACTCGAATGAGAGAGAAAGAGGCTGT 5842
DB 3806 CGATTAAGTTGGGATCTCATCTGCAATTTGACT---TGAAGAGAAAGAAATGATGT 3861
QY 5843 TATGACTCCTACCTGAGGTTTACTAGTAAAGAAAGACACTGGGAGCTCTCT 5902

Db	809	GGTGGTGTAGTAGGTTTAGTGTCTTAAATCCCTATACACCTTTCTCTTTCCCTCCACCTGC	868
QY	2818	AGCGTAAAGATCAGTGGCTACTGATGAAGCAGGTGCTCAACTTCACCTCGAGACGTTG	2877
Db	869	AGATGAGTGAACGGCTGCTATCTGATGAAGCAGGTGCTGAACCTTCACCTTGAAGATGTC	928
QY	2878	TGCTCCCCCAGTCAAGACAGGTTCCAGCCCTTCATGCAAGAGAGGTGTAACCTTTCTGACCA	2937
Db	929	TGTTCCCTCAATCTGATAGGTTTCCAGCCTTATATGCAAGAGAGTGTGCCCTCTCTTGCCCA	988
QY	2938	AACTCAGCAATCAGCTCAGCTCCTGTGTAAATGTCATCTGGCTACCTATAGTCTCTCT	2997
Db	989	GGCTCAGCAACAGGCTAAGACACATGTGTAATTGACGCTTCAGCCTATGCCCACTACCC	1048
QY	2998	CTTCCTCTTCTAATTCAGTAAGAAACCCGAGGTCTGCTCTCTCTCTTCAACAAGTGA	3057
Db	1049	CTTCCTCTCTCTCTTCCACAGAGACCCCTTACCCCACTCTCTCTCTCCCTCAACCC	1108
QY	3058	GGAGGGCCCTCAGCAACACCACTATATAGGCCACTTGAATAGGTCAAAAAGGTTGGC	3117
Db	1109	TAACTGACAGAAAGAAAGTGTCTTGGCAGCAGTGTATCAGAGATCA-----TTTGGG	1161
QY	3118	TTCAATTGAGTAATACTTGTAGTTTGTATGATGAGAGCTTATTTGTGTTTATTCATGGA	3177
Db	1162	ATCATAGAGTATTTGCTTTTGTCTTGTGACTGATGTCACATCTTGAATTATATGTGTGATG	1221
QY	3178	AGAAATCAACTCAAAATTTCTGTAGATGAGAAAGATGTTGGAGCAAAAAGGCTGAT	3237
Db	1222	GGGTCTGAACTTAAAGTGTACAGAAAGCCGCACTGGTTGTCTTGCGAAAAAGGCACTC	1281
QY	3238	AGAGAAACAGATCTGCTGAGTATATGTAATATGCGGGGAGCAGGGGCCGATATCAGTA	3297
Db	1282	A-----GGTTGCGTAAGATAGAAAGGTGTGG	1309
QY	3298	GTACAGTACTTGTGGGGAGAGAAATCCACTGATACAAAGTACTGTTGGCATGCAATC	3357
Db	1310	GAAACATCTAGCTGTGGAATGGAATCCATTGATCTTAAAGTTGTGAGGGAGGGATGG	1369
QY	3358	CAGTAGTCAAGTACTTGTGGGGGAGAGGAATGGCAACAGCAAAAGTTGAAGGGAGG	3417
Db	1370	CATGAGAGAAATTAGAAAGAAAGTGGAAATGGAAAGGTTAAA-----	1415
QY	3418	AAGATGGAAGAGGCTCATGTTGGGGGTGTGAAGGTCACTCTTTTCCATGTGATGGAG	3477
Db	1416	-----GTGCGGTGTGGGTGGGCAACATGTTGCCCTGTGTGATGTATGGGA	1460
QY	3478	AGTTAAGAAAAACA-GTGTGTGAGTTTGAATGCTTGAGACACCCCAACTATGAAACAT	3536
Db	1461	AGCCACAAATTCGAGGGGTGTGAATTGATGCGCGCTGAACATTTGAACCTATGAAAAA	1520
QY	3537	ATCCACGAGGACCGGGGAGACTGTGGGAGACTGGGCACTTTAAGGAAAGGCG--GGCTTTT	3594
Db	1521	AGTTTGAAGTGAAGTGGGCCAGTAAAGGCCCTTAGACCTTACTGAAAGAGGCTTAAATTT	1580
QY	3595	CACACGAGAACTTTATGCTCATCTCTTGTGCTACACTCCCACTTGTATGAGTTGACG	3654
Db	1581	CACATGAGATTTTATGTAATCTTTCTGTCTAAGATCACAATTTTCTGAGATAGAT	1640
QY	3655	TCAGTTTCGTTT-----ACCGTTCTTGCTACTGTGTGAAC	3693
Db	1641	TGAAGTTTATTTCTTTCACAGAAATTTGCATAAATACTACTCCGCTCTTTTCACAAAATGCAAC	1700
QY	3694	TTCAAGTAGATTTCCCAAGACAGAGCAGCTCTTCTGTAAAGGAGGAGCCTGGATTTC	3753
Db	1701	CTCAGTAGATTTCCCAAGATGAAGAGAGGTCTCTTGTAAAGGAGTGACTGGATTTCTG	1760
QY	3754	GTGTCTTAGAAGCAAAATAGCTCAGAGAACTTAGTCAACGTGAAATCTTAGTCAAGC	3813
Db	1761	GCATCCAAAGGAATTCNAAGACTCAGGAATACTAGTGTCACTGTTGAATCTAAGTCAATTG	1820
QY	3814	GGGCAAAAATACCTGAAGCCTCTAATTCAGGTGAACGGTCACTGCTCTCAGATATACCTG	3873
Db	1821	TGGGCAAAATTAACAGACTTTTAATTCACAGGTAAATTTGACTGTATCCTCATGGGTGTG	1880

QY	3874	AGGATTTGGGCTCCACCGGATAGATTCGTGTGTA-GTCCGCTTTATTTTGGACA	39923
Db	1861	GAGGTCATPAAAGTTTAGCAACAACATTAAATAGTATGCTGTATTGTTTATPACA	19440
QY	3933	CATCAGCGGTGACGACCGAACAATCCAGAAAGATGTGAGAAGGCTGAAGACAGTGA	39923
Db	1941	TATTGAAGGTGATGCTCGCATATCCAGAGGAAATGTGCAAAAAGCTGAAGACAGTGA	20000
QY	3993	AAAGTACTATTGGCAAGCCACATCTACGCCATTCAATG--GAGACGTGGGATTC	40582
Db	2001	AAAGGTAGCATGTAACTGTCAATGCTAAATGCAATGAGAGAGCAAAATGTGTTT	20600
QY	4051	TTTCGTGCTCCCAAGTCCCTTCTACTTTGAAACATTTTATTTACTGTCTACTATCG	41100
Db	2061	TTCTTCTCTTCTTCTTCCCATCACTTTGTGATTTTTCACCTTGATCTCTCAACACAG	21220
QY	4111	GTCCATTACTCGCTTACGTGCACCTGTACTAGCTGGGTCTATAGATCTTCAATCTGTG	41700
Db	2121	GGCAGATTA---CTTTGGTGTCTGTGATGTAGATATATCTATATATCTAGATGTCAGTT	21760
QY	4121	TCTAAATTT---GTAGTCACAATTCAGACCTAGACGAAGAAGCTAGCTGACGAGTGC	42220
Db	2177	TCCAATTTTGCAAAATTGTAAATTTTGAATCTGATGGATCTTAAGTTGCTCTAGTAC	22380
QY	4228	ATGACACTTGCTCGAGGATGCGCTTGTCAGACAGTCATGCTAGAAACGACATCCCTG	42870
Db	2237	ATAACCTCAGATTCGGGGATGTGTCAGTGGCAGAGATAGGGCTAGAAATGCAAGTCTCTG	22960
QY	4288	ATTCCACGCTGTGAC--TTGCTGTGTGGCATGTGTATTAATCTTTGGCTTATTAAGAT	43460
Db	2297	AATCCCAAGCAGACATTTTCCCGTGGTGTATCAGATTAGTTTGGTACCATTAATCT	23560
QY	4347	TTGGGAAA--GCCAGTTCGCCAGGACCTACATATCTGAAACACATGATCTGAAAACTA	44040
Db	2357	TAGGGAATTTCAATTCCTATTATCATCATGATTAATCTGMAAGATCTGTTTAAAAACA	24160
QY	4405	GAAAGCTGGGCA---CAACTTACTAGAGATGATTTTGGCTCATTTAAACGATGCTC	44660
Db	2417	GAAAAATGCCATGCGGCAATTTTATGAAAGTCAATTTTGAAGCATTAATGACATTCGTT	24760
QY	4461	TGAATGTGGCAAAATCAACCCACAATPAAACAACAAAAGAGCTGATTTGCAATAGGACA	45200
Db	2477	TGAAACTTGGAAATTAATCTCAACACATGAGAAAGAGCTGACCTTGCAATATAGGCT	25360
QY	4521	AGATATTAGATCACTGGTATTAATAGCTATCATCTTAATTAAATATAGGCGCTATATA	45800
Db	2537	AATTTCTGGA-----GTAAATAACAATTATTTGAAATTAATCAATTAATCTACAGATA	25890
QY	4581	TATATTTAAGATTAAACAAGAAGTGTAGTACCTCCCAATTTACTTGGCTGTGTTCAA	46400
Db	2590	TTGATTTTAGTTTAAAGCAAGACAAACAACC--CCGATCTCTTTTATACAGGTTCAAT	26480
QY	4641	AGAGTAAAAAATATCAGTCATGATGATTAATTTATAGTGTATGAAATATAGATGAAAAACC	47000
Db	2649	AGAGTAAAAAATATAGTATAGTATTAATTAATAGTAAATGGAATCTGAAATGGTAAAGT	27080
QY	4701	TTTCTTACTTTTAACTTCA-----TTTCTAGATTTTTCTTCTTCAACCTGCA	47520
Db	2709	TTTTTTTCTTCTCTCTCCCATCAAGACCTTCCATTCAGTTTCTTCTTCACTCCCTCA	27680
QY	4753	TCAGGCACTAGTAGACACCTATGCTGTGAGATTAATTAATGACTTTACGAAACAAC	48120
Db	2769	ACAAATCCCTTAGGAGCATTTATCATAGTGTGGCTGGGTGATCAATTTCTATAGTGAAT	28280
QY	4813	ATTGCTGTGTGCTCTTTTGGGGAAGGAACAGATATGACAGAGGCTCAGGCTAGCAGT	48720
Db	2829	ACCATCATGTGGCTTAATTTGGTGAAGAAACA--ACAATGGAAGCTTAAGCTAAACATA	28860
QY	4873	CTGACTTGCCCTAAAGCCAGAGCATGTGTTATATGCAAGAAATGAGGCTTCTTGCAGG	49320
Db	2887	GTGACTCACCCCCAAAACCGAGGAATATATTAGAGCATGTGAATGTACGCTCTT--GCAGG	29450

QY 4933 TGGGTGCTTAAGTAATCAGAAACAGAGAGCTCCGGTGTAGTGAATTATCAGTAAGA- 4991
 DB 2946 CAGGTACAACTAAATTAATCTCAGAAACATGAAAGCTCCAGTTGATGAAATTTTCAGTAACAA 3005
 QY 4992 -----TATCTAACCTTATCTCCTTATCGAAGCTAAATGCTCTTTTCTGTG 5042
 DB 3006 GCTTAACCTTAATTCCTCCCTTTTCCCTCTGACCTTTTAAAAAGCCTTCTCTAG 3065
 QY 5043 TGTAGGCTGATTAACACACTTGT- TTCTTTAGAGTGTCAAGCTTTGTAGATTTTA 5100
 DB 3066 CATCATTTAATAGATGTGACTGTTCTCTTTGATTAATGAAAGCTTTGAGTTTAA 3125
 QY 5101 GTGCTGCGCAGTCTGT- TAGAGGTTTGTATCTTGACCTGGGCTTGTGATTTA 5158
 DB 3126 TTGTGAAGCCCAAGTCTCTGTGTATGAACTTAATCAGACATGAGAGGCTGAAATGTTA 3185
 QY 5159 GCATGCCAAAGGACACACTCTGTAATGCTGTGTAAGTAAAGTTATTAATCTTACT- 5215
 DB 3186 GCATGCCACAGACAAAGGATCTTTACATCTTCTTAAAAAATTAATCTGATTTGATCTT 3245
 QY 5216 -----TTGTCTTTGAAAGGTGAAGCGTGTGTGAAGAAACTCAAGAGATGTGTTCT 5270
 DB 3246 GCTTGTGCTTTTGAAGAAAGTGAAGTGAAGAGAGAAATCTGATGTA----- 3296
 QY 5271 CTGTAGGAAACTTTTTCCTTAAATGCTTATATCACTTTCACTCA- ACTT 5327
 DB 3297 -----TCTGTGTGATTTTCAGACCTTTAATCACTTTTGAAGAAATCAATT 3342
 QY 5328 TGACTTTTATCAATGCTGTCAATGAAGAGTGTGAAGCCGCTCATAGGCTCTGG 5387
 DB 3343 TCATATTTGCAATGGGTTGCCATGTGAAGAGTATATGCTTTTTCGTGTGACTTCA 3402
 QY 5388 AAAAGCAACAATAGGAGAGAAATGTTATGCTGAAGAACTGACCGCAGGAGAACTGT 5447
 DB 3403 GAAAGCA- CAGAGAGAGAGAAATGTTGTTCAAGAAAGATCAACAGAGAGAAACGT 3461
 QY 5448 CAGAGCTCCCGAAGACCA-----CCACAGGTGTTAATGAG 5485
 DB 3462 CAGAGCTGTGAATAGGAGTGTGTTGAGAGCATTAATTCCTCTGTGGGGTAAA 3521
 QY 5486 AACAGTCCAGGTTGGCTCATGTAATGAATGAAGACAGAGAGAGAGATAGCTAA 5545
 DB 3522 AGCAGAAACGAGTTGTGATTAAT- GCATGACAGACAGTGAAGGAGATTAATTTAA 3580
 QY 5546 AGTTTCATAGGCTC- CGAGTCTTAAAGATACAAATAGCTGC- TTGGGCTTCTAACA 5602
 DB 3581 AATTTCTTATAGTCTTGAAGTCTTGAATGAAAGAAATATCTTTTGGCTTATGCA 3640
 QY 5603 AAGGAGTCTGGAAGGACAGCAAGTGAAGAGGAAATGAAAGGAAAGAAAGAAATGTA 5662
 DB 3641 AAGAGATGTAAGAG-----TGAAAGGCGGAAAGAAAGCAAGAAAGAAAG 3688
 QY 5663 AGGACTGGAACAGTCAAAATCTCTACAGACATTTTCTTGAAACAATCTAGAAGT 5722
 DB 3689 AACCATGTATATATAGAGCAATGTGTGACAAAGTTTCTGTGAATAATGCAAAATATG 3748
 QY 5723 AGTGAATTAGGTGATGACAGGGGAGCTTGTGCAATTTGATGTGGATTTTGTCTCT 5782
 DB 3749 ATATATTAAGAGAAATTTAGTAGGGAATGCTTTTCACTTGAATTTGGGTTCTCT- T 3805
 QY 5783 CCATTGAGTTGAAAGGCTCACTTTTACCTCGAATGAGAGAGAAAGAGGGGTGT 5842
 DB 3806 CGATTTAAGTTGGGATCTCATCTGCAATTTGACT- TGAGAGAGAAAGAAATGATATG 3861
 QY 5843 TATGACTCTACCTGGAATTTTACTAGTTTACGAAATGAAAGACACTCGGAGCTCTCT 5902
 DB 3862 TAGAGCCTATATCTGGTTTCTATTAAGCAAGAGTGAAGAAAGACTTATTTGTATTT 3921
 QY 5903 CTGACAAAAAATGAAACCTGTGTTGTTCTGTTGTTCTTTGTTAAGAAAGAC 5962
 DB 3922 TTCCACAAAGAGTAAATCTTTTCTTTTACTGTTTGTCAAAAGGTGAAATAGAAAG 3981
 QY 5963 AGGAAAGCCGACCAATGAGTGTGATGTGGGCTTTGAGTCAAGGCTTTGAGTTGAG 6022

DB 3982 CCTTAATGTATGTGTAATACATGTCTCAAAAGTATTTAGTAGATGTTTAAATCAG 4041
 QY 6023 CACTCATCAATAGTT-----GATCATGTGTAGGTGAGAGGC 6058
 DB 4042 GAGTGTCAATCATTTTGGCTTCCCTGAGCACTTGAAGAAATGTTCTGTGTACACAT 4101
 QY 6059 TACTGTGAGGCGAGCCCTGTGCTTCCGACTTAAATCTCCAGGTCTTATGATCACT 6118
 DB 4102 AAAATACAGAAACATAGCTGATGAGCTAAAGAAAGTCCATGACATTAATCTCATCTGTT 4161
 QY 6119 TCTGTACTATGACAGACTGATGAGTGTGAGAAACCTTTTCTC----- 6163
 DB 4162 TAAGAAAGTTTATGAATTTCTGTTAGGTTGATTTCAAAAGCTGTCTGGCCATGTGGGC 4221
 QY 6164 -----AACCCCACTAAATTTAATGACAAAGACTGTGTAATTTG 6205
 DB 4222 CTGTGGGCTGAGGTGTGACAGCTCCTTAATTAATATCTGTATGATTTTGGAGC 4281
 QY 6206 TGGATACAGTGTGATTAATGA----- 6227
 DB 4282 TGCAAAACAGGCCAAGGCATATATGTTGTCACCTGGGATCCCGAGATCCAGCCTCACT 4341
 QY 6228 -----TCTATGTGTGATTTGCAAGGTTCAATAGATGATTAATAGGCCATCAAGC 6283
 DB 4342 TCACTCTCTTGTCTGTGTGTAAGAGGGGTGTCACTCTGCCCAGCTTTTAAACAGC 4401
 QY 6284 TTATGTGGTGTGAATGCAAGTAATATAGTATGATGCTGTGTGCTCTTATAGTACAGAA 6343
 DB 4402 TTCTATGTGTGAGGTGACCTGAAATTTGATGCTGTGTGTGCT- CTCAGTCCAGGA 4460
 QY 6344 GGCATGATTTTAAAGTCTTGGGCAATCATTTATCTCATGCTTAAATTAATTAATGTT 6403
 DB 4461 GCGCTCATTTTAACTCTTTGCAATCATTAATCAATCAATCAATCAATCAATCAAT 4508
 QY 6404 GATTTATATCTTTTAAAGAGGCTGATCTGTGTTTGTGTGCTCAGAGAACCAATGTCA 6463
 DB 4509 TACTATGAATGTTTAAACAAATGCTTAAACCTGTTTGTGTCTCATCACTAATCTGTG 4568
 QY 6464 CCAGCTCTTCTAATCTGTGTACCACTTATAGAAATGCTACCTGCTCAATTTGTTGTA 6523
 DB 4569 CAATTTCT- AATTTGTTACTTTAGAAACATGAGATTAATCTCAATTTGTTGCA 4625
 QY 6524 TTCTATTTTCAATAGCTTGAAGAGTGAAGATCAAGGAGTTGGGAACTGAGCCTG 6583
 DB 4626 TTCTATTTTCAAGCTTGGAGAGAGTGAAGATCAAGGAACTGGAGACTGGAATTTG 4685
 QY 6584 CTGTTATGTCTTGAAGAAATGCTTGTGCTGTGAGCGAGAAAGACTAGAAACGAAAGAC 6643
 DB 4686 CTGTTATGTCTTGAAGAAATGCTTGTGATTTGACAGGCAAAAGCTGAAATGAAATTAAC 4745
 QY 6644 TGCTCTTCTCCGCTTCTTAAAGAAACATTAAGATCCCTGAATGAGACTTTT 6695
 DB 4746 TAACCCCTTCTCCGTGTAAGAAATTAATTAATGATGCCCCAAAGCAATTTT 4797

RESULT 9
 US-09-178-973B-7
 ; Sequence 7, Application US/09178973B
 ; Patent No. 6274710
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumoutier, Laure
 ; APPLICANT: Lohued, Jamila
 ; APPLICANT: Renaud, Jean-Christophe
 ; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
 ; TITLE OF INVENTION: (Tifs)
 ; FILE REFERENCE: LUD 5543
 ; CURRENT APPLICATION NUMBER: US/09/178, 973B
 ; CURRENT FILING DATE: 1998-10-26
 ; NUMBER OF SEQ ID NOS: 17
 ; SEQ ID NO 7
 ; LENGTH: 1119

TYPE: DNA
ORGANISM: Mus musculus
US-09-178-973B-7

Query Match
Best Local Similarity 99.8%; Pred. No. 3e-143;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6535 ATAGCTTGAGAGAGATGAGAGATCAAGCGCATTTGGGAACTGGACCTGCTTTATGTC 6594
DB 510 AAAGCTTGAGAGAGATGAGAGATCAAGCGCATTTGGGAACTGGACCTGCTTTATGTC 569
QY 6595 TCTGAGAAATGCTGGCTGAGCGGAGAGAACTAGAAACGAAAGTCTCTCTCT 6654
DB 570 TCTGAGAAATGCTGGCTGAGCGGAGAGAACTAGAAACGAAAGTCTCTCTCT 629
QY 6655 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGAGACTTTTACTTAAAGAAAGTGA 6714
DB 630 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGAGACTTTTACTTAAAGAAAGTGA 689
QY 6715 GCTAAGCTTCATCATCATTAGAGATTTGACATGAAACCTGGCTCAGTTGAAAAA 6774
DB 690 GCTAAGCTTCATCATCATTAGAGATTTGACATGAAACCTGGCTCAGTTGAAAAA 749
QY 6775 TAGTGTCAAGTTGTCATGAGACCAAGAGTGAAGTGAACCAAAAGTTCATTGACA 6834
DB 750 TAGTGTCAAGTTGTCATGAGACCAAGAGTGAAGTGAACCAAAAGTTCATTGACA 809
QY 6835 ATATTATTATGTCATGATGATACACAGAAATTAATGATTTAAATTTGTTGA 6894
DB 810 ATATTATTATGTCATGATGATACACAGAAATTAATGATTTAAATTTGTTGA 869
QY 6895 AGAGAGTACCTCTCATTCCTTTAGAAAAAGCTTATGTAATTCATTCATTCGA 6954
DB 870 AGAGAGTACCTCTCATTCCTTTAGAAAAAGCTTATGTAATTCATTCATTCGA 929
QY 6955 TATTTATATATGTAAGTTTATTTATTAAGTATACATTTATTTATGTCATTATTA 7014
DB 930 TATTTATATATGTAAGTTTATTTATTAAGTATACATTTATTTATGTCATTATTA 989
QY 7015 ATATGATTTATTTATTAAGAAATATCTGATTTAGTATTAAGCAATTAATA 7074
DB 990 ATATGATTTATTTATTAAGAAATATCTGATTTAGTATTAAGCAATTAATA 1049
QY 7075 TTTATGACATTAATGTAAGAAACAAATATCTTAGGCTTTAATAACATGATATCAT 7134
DB 1050 TTTATGACATTAATGTAAGAAACAAATATCTTAGGCTTTAATAACATGATATCAT 1109
QY 7135 AAA 7137
DB 1110 AAA 1112

RESULT 10
US-09-419-568F-7

Sequence 7, Application US/09419568F
Patent No. 631613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 7
LENGTH: 1119

TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-419-568F-7

Query Match
Best Local Similarity 99.8%; Pred. No. 3e-143;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6535 ATAGCTTGAGAGAGATGAGAGATCAAGCGCATTTGGGAACTGGACCTGCTTTATGTC 6594
DB 510 AAAGCTTGAGAGAGATGAGAGATCAAGCGCATTTGGGAACTGGACCTGCTTTATGTC 569
QY 6595 TCTGAGAAATGCTGGCTGAGCGGAGAGAACTAGAAACGAAAGTCTCTCTCT 6654
DB 570 TCTGAGAAATGCTGGCTGAGCGGAGAGAACTAGAAACGAAAGTCTCTCTCT 629
QY 6655 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGAGACTTTTACTTAAAGAAAGTGA 6714
DB 630 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGAGACTTTTACTTAAAGAAAGTGA 689
QY 6715 GCTAAGCTTCATCATCATTAGAGATTTGACATGAAACCTGGCTCAGTTGAAAAA 6774
DB 690 GCTAAGCTTCATCATCATTAGAGATTTGACATGAAACCTGGCTCAGTTGAAAAA 749
QY 6775 TAGTGTCAAGTTGTCATGAGACCAAGAGTGAAGTGAACCAAAAGTTCATTGACA 6834
DB 750 TAGTGTCAAGTTGTCATGAGACCAAGAGTGAAGTGAACCAAAAGTTCATTGACA 809
QY 6835 ATATTATTATGTCATGATGATACACAGAAATTAATGATTTAAATTTGTTGA 6894
DB 810 ATATTATTATGTCATGATGATACACAGAAATTAATGATTTAAATTTGTTGA 869
QY 6895 AGAGAGTACCTCTCATTCCTTTAGAAAAAGCTTATGTAATTCATTCATTCGA 6954
DB 870 AGAGAGTACCTCTCATTCCTTTAGAAAAAGCTTATGTAATTCATTCATTCGA 929
QY 6955 TATTTATATATGTAAGTTTATTTATTAAGTATACATTTATTTATGTCATTATTA 7014
DB 930 TATTTATATATGTAAGTTTATTTATTAAGTATACATTTATTTATGTCATTATTA 989
QY 7015 ATATGATTTATTTATTAAGAAATATCTGATTTAGTATTAAGCAATTAATA 7074
DB 990 ATATGATTTATTTATTAAGAAATATCTGATTTAGTATTAAGCAATTAATA 1049
QY 7075 TTTATGACATTAATGTAAGAAACAAATATCTTAGGCTTTAATAACATGATATCAT 7134
DB 1050 TTTATGACATTAATGTAAGAAACAAATATCTTAGGCTTTAATAACATGATATCAT 1109
QY 7135 AAA 7137
DB 1110 AAA 1112

RESULT 11

US-09-354-243B-7

Sequence 7, Application US/09354243B
Patent No. 6359117
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 7
LENGTH: 1119

TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-354-243B-7

Query Match 8.1%; Score 601.4; DB 4; Length 1119;
Best Local Similarity 99.8%; Pred. No. 3e-143;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6535 ATAGCTTGGAGAGAGTGAAGATCAAGGCGATTGGGAACTGCACTGCTGTTATATGTC 6534
DB 510 AAAGCTTGGAGAGAGTGAAGATCAAGGCGATTGGGAACTGCACTGCTGTTATATGTC 569
QY 6595 TCTGAGAAATGCTTGGCTGAGCGAGAAAGTAGAAAACGAAAGACTGCTCTCTCT 6654
DB 570 TCTGAGAAATGCTTGGCTGAGCGAGAAAGTAGAAAACGAAAGACTGCTCTCTCTCT 629
QY 6655 GCCCTTCTAAAAGAACATAGATCCCTGATGAGACTTTTCTAAAGAAAGTAGAAA 6714
DB 630 GCCCTTCTAAAAGAACATAGATCCCTGATGAGACTTTTCTAAAGAAAGTAGAAA 689
QY 6715 GCTAACGTCATCATCTTGAAGATTTCACATGAAACCTGCTCAGTTGAAAAAGAAA 6774
DB 690 GCTAACGTCATCATCTTGAAGATTTCACATGAAACCTGCTCAGTTGAAAAAGAAA 749
QY 6775 TAGGTCAAGTTGTCATGAGACGAGAGTAGACTGATTAACCAAAAGATTCAATGACA 6834
DB 750 TAGGTCAAGTTGTCATGAGACGAGAGTAGACTGATTAACCAAAAGATTCAATGACA 809
QY 6835 ATATTATTATGTCACATGATGATACACAGAAAAATATGACTTTAAATAATGTTGAA 6894
DB 810 ATATTATTATGTCACATGATGATACACAGAAAAATATGACTTTAAATAATGTTGAA 869
QY 6895 AGAGAGTTACCTCTCATCTCTTTAGAAAAAAAGCTTATGTAACCTTCCATATCCAA 6954
DB 870 AGAGAGTTACCTCTCATCTCTTTAGAAAAAAAGCTTATGTAACCTTCCATATCCAA 929
QY 6955 TATTTTATATATGTAAGTTATTTATATATAGTAACTTTTATTTATGTCAGTTATTA 7014
DB 930 TATTTTATATATGTAAGTTATTTATATATAGTAACTTTTATTTATGTCAGTTATTA 989
QY 7015 ATATGATTTATTTATATGAAACATTTATCTGCTATTTAGTATTAAGCAATATA 7074
DB 990 ATATGATTTATTTATATGAAACATTTATCTGCTATTTAGTATTAAGCAATATA 1049
QY 7075 TTATGACAAATACATGAGAAACAGATATCTTAGGCTTTAATAAACAATGATATCAT 7134
DB 1050 TTATGACAAATACATGAGAAACAGATATCTTAGGCTTTAATAAACAATGATATCAT 1109
QY 7135 AAA 7137
DB 1110 AAA 1112

RESULT 12

US-09-178-973B-9
Sequence 9, Application US/09178973B
Patent No. 6274710
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
FILE REFERENCE: LUD 5543
CURRENT APPLICATION NUMBER: US/09/178,973B
PRIORITY FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus

US-09-178-973B-9

Query Match 7.5%; Score 555.2; DB 4; Length 1111;
Best Local Similarity 96.0%; Pred. No. 1.7e-131;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

QY 6535 ATAGCTTGGAGAGAGTGAAGATCAAGGCGATTGGGAACTGCACTGCTGTTATATGTC 6594
DB 508 AAAGCTTGGAGAGAGTGAAGATCAAGGCGATTGGGAACTGCACTGCTGTTATATGTC 567
QY 6595 TCTGAGAAATGCTTGGCTGAGCGAGAAAGTAGAAAACGAAAGACTGCTCTCTCTCT 6654
DB 568 TCTGAGAAATGCTTGGCTGAGCGAGAAAGTAGAAAACGAAAGACTGCTCTCTCTCT 627
QY 6655 GCCCTTCTAAAAGAACATAGATCCCTGATGAGACTTTTCTAAAGAAAGTAGAAA 6714
DB 628 GCCCTTCTAAAAGAACATAGATCCCTGATGAGACTTTTCTAAAGAAAGTAGAAA 687
QY 6715 GCTAACGTCATCATCTTGAAGATTTCACATGAAACCTGCTCAGTTGAAAAAGAAA 6774
DB 688 GCTAACGTCATCATCTTGAAGATTTCACATGAAACCTGCTCAGTTGAAAAAGAAA 747
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DB 808 ATATTATTATGTCACATGATGATACACAGAAAAATATGACTTTAAATAATGTTGAA 867
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QY 7015 ATATGATTTATTTATATGAAACATTTATCTGCTATTTAGTATTAAGCAATATA 7073
DB 988 ATATGATTTATTTATATGAAACATTTATCTGCTATTTAGTATTAAGCAATATA 1047
QY 7074 ATATGACAAATACATGAGAAACAGATATCTTAGGCTTTAATAAACAATGATATCA 7133
DB 1048 ATATGACAAATACATGAGAAACAGATATCTTAGGCTTTAATAAACAATGATATCA 1107
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DB 1108 TAAA 1111

RESULT 13

US-09-419-568F-9
Sequence 9, Application US/09419568F
Patent No. 6331613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
PRIORITY FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIORITY FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus

FEATURE:
US-09-419-568F-9

Query Match 7.5%; Score 555.2; DB 4; Length 1111;
Best Local Similarity 96.0%; Pred. No. 1.7e-131;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

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QY 6595 TCTGAGAAATGCTTGGCTGAGCGAGAAAGCTAGAAAGAAAGAAAGTCTCTTCT 6654
DB 568 TCTGAGAAATGCTTGGCTGAGCGAGAAAGCTAGAAAGAAAGAAAGTCTCTTCT 627
QY 6655 GCCTTCTAAAAAGAAACATTAAGATCCCTGAATGAGACTTTTACTTAAGAAAGTAGAA 6714
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QY 6715 GCTAAGCTCATCATATTAGAAAGATTGACATGAAACCTGGCTCAGTTGAAAAAGAAA 6774
DB 688 GCTAAGCTCATCATATTAGAAAGATTGACATGAAACCTGGCTCAGTTGAAAAAGAAA 747
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DB 1108 TAAA 1111
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RESULT 14
US-09-354-243B-9

Sequence 9, Application US/09354243B

Patent No. 6359117

GENERAL INFORMATION:

APPLICANT: Dumoutier, Laure

APPLICANT: Louhed, Jamila

APPLICANT: Renaud, Jean-Christophe

TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Pe

TITLE OF INVENTION: (TIPI) The Proteins Encoded, and Uses Thereof

FILE REFERENCE: LUD 5543.1

CURRENT APPLICATION NUMBER: US/09/354,243B

CURRENT FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US09/178,973

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 9

LENGTH: 1111

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:
US-09-354-243B-9

Query Match 7.5%; Score 555.2; DB 4; Length 1111;
Best Local Similarity 96.0%; Pred. No. 1.7e-131;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

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QY 6535 ATAGCTTGGAGAGAGATCAAGCGATTGGGGAAGTGGAGACTGGCTGCTTTATATGTC 6594
DB 508 AAAGCTTGGAGAGAGAGAGATCAAGCGATTGGGGAAGTGGAGACTGGCTGCTTTATATGTC 567
QY 6595 TCTGAGAAATGCTTGGCTGAGCGAGAAAGCTAGAAAGAAAGAAAGTCTCTTCT 6654
DB 568 TCTGAGAAATGCTTGGCTGAGCGAGAAAGCTAGAAAGAAAGAAAGTCTCTTCT 627
QY 6655 GCCTTCTAAAAAGAAACATTAAGATCCCTGAATGAGACTTTTACTTAAGAAAGTAGAA 6714
DB 628 GCCTTCTAAAAAGAAACATTAAGATCCCTGAATGAGACTTTTACTTAAGAAAGTAGAA 687
QY 6715 GCTAAGCTCATCATATTAGAAAGATTGACATGAAACCTGGCTCAGTTGAAAAAGAAA 6774
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DB 1108 TAAA 1111
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RESULT 15
US-09-419-568F-24

Sequence 24, Application US/09419568F

Patent No. 6331613

GENERAL INFORMATION:

APPLICANT: Dumoutier, Laure

APPLICANT: Louhed, Jamila

APPLICANT: Renaud, Jean-Christophe

TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible p

TITLE OF INVENTION: (TIPI) The Proteins Encoded, and Uses Thereof

FILE REFERENCE: LUD 5543.2

CURRENT APPLICATION NUMBER: US/09/419,568F

CURRENT FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: US09/354,243

PRIOR FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US09/178,973

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 24

LENGTH: 690

TYPE: DNA

ORGANISM: Mus musculus

ORGANISM: Homo sapiens
FEATURE:
US-09-419-568F-24

Query Match 1.7%; Score 126; DB 4; Length 690;
Best Local Similarity 71.7%; Pred. No. 2.2e-22;
Matches 165; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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QY 2094 ATCTATGAGTTTTCCTTATGGGGACTTGGGCGCCAGCTGGCTTTCATGCCCCCT 2153
Db 89 ATCTGAGCTCTTCTCTTATGGGGAGCCCTGGCCACACAGCTGCTCTCTTGGCCCT 148
QY 2154 GTGGGCCAGAGGCAATGCGCTGCGCTCAACACCGGTGCAAGTTGAGGTGCCAA 2213
Db 149 CTGTGACAGGAG 208
QY 2214 CTTCAGAGCGGTACATGTCACACCGACCTTTATGCTGGCCAAAGAGG 2263
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Job time : 308.726 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:03:00 ; Search time 1155.93 Seconds

(without alignments)
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Title: US-09-751-797-24

Perfect score: 690
Sequence: 1 tgcacacagacagatcttcag.....gatgcccaagcgattttt 690

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	690	100.0	690	6 AR201414	AR201414 Sequence
2	690	100.0	690	6 AX459971	AX459971 Sequence
3	690	100.0	690	6 HSA277247	AJ277247 Homo sapi
4	676	98.0	1152	6 AX092422	AX092422 Sequence
5	676	98.0	1152	6 AX358990	AX358990 Sequence
6	676	98.0	1152	6 AX362483	AX362483 Sequence
7	676	98.0	1152	6 AX392477	AX392477 Sequence
8	676	98.0	1152	6 AX403770	AX403770 Sequence
9	676	98.0	1152	6 AX454768	AX454768 Sequence
10	676	98.0	1152	6 AX491246	AX491246 Sequence
11	676	98.0	1167	6 AF279437	AF279437 Homo sapi
12	671	97.2	1139	6 AX054620	AX054620 Sequence
13	669	97.0	1132	6 AX048204	AX048204 Sequence
14	639	92.6	1116	6 AX151713	AX151713 Sequence
15	639	92.6	1116	6 AX179578	AX179578 Sequence
16	639	92.6	1116	6 AX468783	AX468783 Sequence
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21	407.6	59.1	1111	6 AX179614	AX179614 Sequence
22	407.6	59.1	1111	6 AR165228	AR165228 Sequence
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24	407.6	59.1	1111	6 AX459955	AX459955 Sequence
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26	380	55.1	537	6 AX054622	AX054622 Sequence
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ALIGNMENTS

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LOCUS AR201414 690 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 24 from patent US 6359117.
ACCESSION AR201414
VERSION AR201414.1 GI:20252302
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 690)
AUTHORS Dumoutier,L., Lohued,J. and Renaud,J.-C.
TITLE Isolated nucleic acid molecules which encode T cell inducible factors (TIFs), the proteins encoded, and uses therefor
JOURNAL Patent: US 6359117-A 24 19-WAR-2002;

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source location/Qualifiers
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BASE COUNT 182 a 176 c 167 g 165 t
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Best Local Similarity 100.0%; Pred. No. 1.6e-180;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 661 ATTAACAATTAGATGCCCCCAAGCGATTTT 690

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LOCUS
DEFINITION Sequence 25 from Patent WO0210393.
ACCESSION AX459971
VERSION AX459971.1 GI:21725707
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Dumoutier, L. and Renaud, J.C.
Isolated nucleic acid molecules which encode c cell inducible

JOURNAL
Patent: WO 0210393-A-25 07-FEB-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
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BASE COUNT 182 a 176 c 167 g 165 t
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Best Local Similarity 100.0%; Pred. No. 1.6e-180;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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LOCUS
DEFINITION Homo sapiens mRNA for interleukin 22 (IL-22 gene).
ACCESSION AJ277247
VERSION AJ277247.1 GI:3968293
KEYWORDS IL-22 gene; interleukin 22.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 690)
 AUTHORS Dumortier, L., Van Roost, E., Colau, D. and Renaud, J.C.
 TITLE Human interleukin-10-related T cell-derived inducible factor:
 molecular cloning and functional characterization as an
 hepatocyte-stimulating factor
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (18), 10144-10149 (2000)
 JOURNAL 20420346
 PUBMED 10954742
 REFERENCE 2 (bases 1 to 690)
 AUTHORS Renaud, J.C.
 TITLE Direct Submission
 JOURNAL Submitted (10-APR-2000) Renaud J.C., UCL 74-59, Ludwig Institute
 for Cancer Research, Avenue Hippocrate, 74, B-1200 Brussels,
 Belgium

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BASE COUNT 182 a 176 c 167 g 165 t
 ORIGIN

Query Match 100.0%; Score 690; DB 9; Length 690;
 Best Local Similarity 100.0%; Pred. No. 1.6e-180;
 Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 541 AGAGTGGAGAGATCAAAAGCAATGGAGAGTGAATTTGCTTTATGTCTCTGAGAAATG 600
 DB 541 AGAGTGGAGAGATCAAAAGCAATGGAGAGTGAATTTGCTTTATGTCTCTGAGAAATG 600
 QY 601 CCTGCATTTGACACAGACAAAGCTGAAAAATGATTAACATCCCTTTCCCTGCTAGAA 660
 DB 601 CCTGCATTTGACACAGACAAAGCTGAAAAATGATTAACATCCCTTTCCCTGCTAGAA 660
 QY 661 ATTAACATTAATGATGCCCCCAAGCGATTTT 690
 DB 661 ATTAACATTAATGATGCCCCCAAGCGATTTT 690

RESULT 4
 AX092422
 LOCUS AX092422 1152 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 153 from Patent WO0116318.
 AX092422
 ACCESSION AX092422
 VERSION AX092422.1 GI:13444525
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo;
 Baton, D.L., Pilvaroff, E., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and
 Wood, W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0116318-A 153 08-MAR-2001;
 Gentech, Inc. (US)

FEATURES
 source location/Qualifiers
 1..1152
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 342 a 244 c 228 g 338 t
 ORIGIN

Query Match 98.0%; Score 676; DB 6; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 1.3e-176;
 Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTCGAAAGAGTTCTCTTCCCGAGTACCAAGTGTGAGTTAGAAATGTCTGCAATG 74
 DB 1 CTTCGAAAGAGTTCTCTTCCCGAGTACCAAGTGTGAGTTAGAAATGTCTGCAATG 74
 QY 75 GCGGCGTGCAGAAATCTGTAGCTCTTCCATTAGGGAGACCTGGCCACAGAGTGCCTC 134
 DB 75 GCGGCGTGCAGAAATCTGTAGCTCTTCCATTAGGGAGACCTGGCCACAGAGTGCCTC 134
 QY 135 CTTCCTTGGCCCTTGTGTACAGGAGAGAGAGTGCAGCCATCAGCTCCACATGACAG 194
 DB 135 CTTCCTTGGCCCTTGTGTACAGGAGAGAGAGTGCAGCCATCAGCTCCACATGACAG 194
 QY 194 GCTCCAGTGCAGGCTTGAACAAGTCCAACTTCCAGAGAGCTTATACCAACCGACCT 240
 DB 194 GCTCCAGTGCAGGCTTGAACAAGTCCAACTTCCAGAGAGCTTATACCAACCGACCT 240
 QY 241 TCATGTGAGTAAAGAGAGCTGAGTGGTGTATACAAACAGAGCTTGTCTGATTTGGGG 300
 DB 241 TCATGTGAGTAAAGAGAGCTGAGTGGTGTATACAAACAGAGCTTGTCTGATTTGGGG 300
 QY 301 AGAGTCAATGATGAGAGAGCTGATCTGATGAAGAGAGTGTGAACCTTGA 374
 DB 301 AGAGTCAATGATGAGAGAGCTGATCTGATGAAGAGAGTGTGAACCTTGA 374
 QY 375 GAAGTGTGTTCCCTCAATCTGATAGTTCCAGCTTATATGACAGAGAGTGTGCTTC 434
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Db 361 GAACTGCTGTTCCCTCAATCTGATAGTTCAGGCTTATATGACAGAGGTGTCCTTC 420
 QY 435 CTGGCCAGGCTCAGCAACAGGCTAAGACATGTCATATTAAGGTGATGACCTGCATATC 494
 Db 421 CTGGCCAGGCTCAGCAACAGGCTAAGACATGTCATATTAAGGTGATGACCTGCATATC 480
 QY 495 CAGAGGAATGTGCAAAAGCTGAAGAGACACAGTGAAGAAAGCTTGGAGAGATGAGAGATC 554
 Db 481 CAGAGGAATGTGCAAAAGCTGAAGAGACACAGTGAAGAAAGCTTGGAGAGATGAGAGATC 540
 QY 555 AAGCAATTTGAGAAATGATGATTTGCTTTATGTCCTGAGAAATGCTGATTTGACCA 614
 Db 541 AAGCAATTTGAGAAATGATGATTTGCTTTATGTCCTGAGAAATGCTGATTTGACCA 600
 QY 615 GAGCAAGCTGAAGAAATGAATTAACCTCCCTTCTGAGAAATGAATTAACCTGATG 674
 Db 601 GAGCAAGCTGAAGAAATGAATTAACCTCCCTTCTGAGAAATGAATTAACCTGATG 660
 QY 675 CCCCAGGATTTT 690
 Db 661 CCCCAGGATTTT 676

RESULT 5
 AX358990 1152 bp DNA linear PAT 13-FEB-2002
 LOCUS AX358990
 DEFINITION Sequence 243 from Patent WO0193983.
 AX358990
 VERSION AX358990.1 GI:18675396
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
 Watanabe, C.K. and Wood, W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0193983-A 243 13-DEC-2001;
 Genentech Inc. (US)
 FEATURES
 source Location/Qualifiers
 1. .1152
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 342 a 244 c 228 g 338 t
 ORIGIN

Query Match 98.0%; Score 676; DB 6; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 1.3e-176;
 Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 CTTAGAACAGGTTCTCTTCCAGTACAGGTTGCTGAGTTGAATGTCTGCATG 74
 Db 1 CTTAGAACAGGTTCTCTTCCAGTACAGGTTGCTGAGTTGAATGTCTGCATG 60
 QY 75 GCGCCCTGAGAAATCTGTAGCTCTTCTTATGGGAGACCTGGACACAGCTGCTC 134
 Db 61 GCGCCCTGAGAAATCTGTAGCTCTTCTTATGGGAGACCTGGACACAGCTGCTC 120
 QY 135 CTTCTTGGCCCTCTTGTATCAGGAGAGACAGCTGCGCCATCAGCTCCACTGAGG 194
 Db 121 CTTCTTGGCCCTCTTGTATCAGGAGAGACAGCTGCGCCATCAGCTCCACTGAGG 180
 QY 195 CTTAGAACAGTCACTTCCAGACAGCTTATATCAACGACAGCTTCAATGCTGCTAG 254
 Db 181 CTTAGAACAGTCACTTCCAGACAGCTTATATCAACGACAGCTTCAATGCTGCTAG 240
 QY 255 GAGGCTAGCTTGGCTATACACACAGAGCTTGTCTCATTTGGGAGAAATGTTCCAC 314
 Db 241 GAGGCTAGCTTGGCTATACACACAGAGCTTGTCTCATTTGGGAGAAATGTTCCAC 300

QY 315 GAGGCTAGTATGAGTACAGGCTGCTATCTGATGAGACAGGTGCTGAATCTTACCTTGA 374
 Db 301 GAGGCTAGTATGAGTACAGGCTGCTATCTGATGAGACAGGTGCTGAATCTTGA 360
 QY 375 GAAGTCTGTCCTCCATCTGTATGATGTCAGACCTTATATGACAGAGGTGCTGCTC 434
 Db 361 GAAGTCTGTCCTCCATCTGTATGATGTCAGACCTTATATGACAGAGGTGCTGCTC 420
 QY 435 CTGGCCAGGCTCAGCAACAGGCTAAGACATGTCATATTAAGGTGATGACCTGCATATC 494
 Db 421 CTGGCCAGGCTCAGCAACAGGCTAAGACATGTCATATTAAGGTGATGACCTGCATATC 480
 QY 495 CAGAGGAATGTGCAAAAGCTGAAGAGACACAGTGAAGAAAGCTTGGAGAGATGAGAGATC 554
 Db 481 CAGAGGAATGTGCAAAAGCTGAAGAGACACAGTGAAGAAAGCTTGGAGAGATGAGAGATC 540
 QY 555 AAGCAATTTGAGAAATGATGATTTGCTTTATGTCCTGAGAAATGCTGATTTGACCA 614
 Db 541 AAGCAATTTGAGAAATGATGATTTGCTTTATGTCCTGAGAAATGCTGATTTGACCA 600
 QY 615 GAGCAAGCTGAAGAAATGAATTAACCTCCCTTCTGAGAAATGAATTAACCTGATG 674
 Db 601 GAGCAAGCTGAAGAAATGAATTAACCTCCCTTCTGAGAAATGAATTAACCTGATG 660
 QY 675 CCCCAGGATTTT 690
 Db 661 CCCCAGGATTTT 676

RESULT 6
 AX362483 1152 bp DNA linear PAT 15-FEB-2002
 LOCUS AX362483
 DEFINITION Sequence 243 from Patent WO0208288.
 AX362483
 VERSION AX362483.1 GI:18694699
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
 Watanabe, C.K. and Wood, W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0208288-A 243 31-JAN-2002;
 Genentech, Inc. (US)
 FEATURES
 source Location/Qualifiers
 1. .1152
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 342 a 244 c 228 g 338 t
 ORIGIN

Query Match 98.0%; Score 676; DB 6; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 1.3e-176;
 Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 CTTAGAACAGGTTCTCTTCCAGTACAGGTTGCTGAGTTGAATGTCTGCATG 74
 Db 1 CTTAGAACAGGTTCTCTTCCAGTACAGGTTGCTGAGTTGAATGTCTGCATG 60
 QY 75 GCGCCCTGAGAAATCTGTAGCTCTTCTTATGGGAGACCTGGACACAGCTGCTC 134
 Db 61 GCGCCCTGAGAAATCTGTAGCTCTTCTTATGGGAGACCTGGACACAGCTGCTC 120
 QY 135 CTTCTTGGCCCTCTTGTATCAGGAGAGACAGCTGCGCCATCAGCTCCACTGAGG 194
 Db 121 CTTCTTGGCCCTCTTGTATCAGGAGAGACAGCTGCGCCATCAGCTCCACTGAGG 180
 QY 195 CTTAGAACAGTCACTTCCAGACAGCTTATATCAACGACAGCTTCAATGCTGCTAG 254
 Db 181 CTTAGAACAGTCACTTCCAGACAGCTTATATCAACGACAGCTTCAATGCTGCTAG 240

Db 181. CTGACAAAGTCCAACTTCCAGCAGCCCTATATACCAACGACCTTCATGCTGGCTAG 240
QY 255 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTGTCTCATTTGGGAGAACTTTCCAC 314
Db 241 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTGTCTCATTTGGGAGAACTTTCCAC 300
QY 315 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTGTCTCATTTGGGAGAACTTTCCAC 374
Db 301 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTGTCTCATTTGGGAGAACTTTCCAC 360
QY 375 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTGTCTCATTTGGGAGAACTTTCCAC 434
Db 361 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTGTCTCATTTGGGAGAACTTTCCAC 420
QY 435 CTGGCCAGGCTCAGCAACAGGCTAAGCAATGTCTATATGAGAGTGAATGACCTGCATATC 494
Db 421 CTGGCCAGGCTCAGCAACAGGCTAAGCAATGTCTATATGAGAGTGAATGACCTGCATATC 480
QY 495 CAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAGAAAGCTTGAGAGAGTGAAGATC 554
Db 481 CAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAGAAAGCTTGAGAGAGTGAAGATC 540
QY 555 AAGCAATTGGAGAACTGATTTGCTGTTATATGCTCTGAGAAATGCTGCAATTTGACCA 614
Db 541 AAGCAATTGGAGAACTGATTTGCTGTTATATGCTCTGAGAAATGCTGCAATTTGACCA 600
QY 615 GAGCAAAAGCTGAAATGAATTAATACTAACCCCTTTCCCTGCTAGAAATTAACAATTAGATG 674
Db 601 GAGCAAAAGCTGAAATGAATTAATACTAACCCCTTTCCCTGCTAGAAATTAACAATTAGATG 660
QY 675 CCCCAGGAGATTTT 690
Db 661 CCCCAGGAGATTTT 676

RESULT 7
AX392477 1152 bp DNA linear PAT 23-MAR-2002
LOCUS AX392477
DEFINITION Sequence 1 from Patent WO021611.
ACCESSION AX392477
VERSION AX392477.1 GI:19700776
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 Aggarwal, S., Foster, J. S., Goddard, A., Gurney, A. L., Maruoka, E. M.,
AUTHORS Wood, W. I., and Xie, M. H.,
TITLE Interleukin-22 polypeptides, nucleic acids encoding the same and
JOURNAL methods for the treatment of pancreatic disorders
Genentech, Inc. (US)
Patent: WO 021611-A 1 28-FEB-2002;
FEATURES
Location/Qualifiers
source 1..1152
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 342 a 244 c 228 g 338 t
Query Match 98.0%; Score 676; DB 6; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.3e-176;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAAAGGTTCTCTCCAGTCAACAGTGTGCTCGAGTAGAATTGCTGCATG 74
Db 1 CTTGAGAAAGGTTCTCTCCAGTCAACAGTGTGCTCGAGTAGAATTGCTGCATG 60
QY 75 GCCGCCCTGAGAAATCTGTAGAGCTCTTCTTATGAGGACCTTGCCACAGCTGCCTC 134
Db 61 GCCGCCCTGAGAAATCTGTAGAGCTCTTCTTATGAGGACCTTGCCACAGCTGCCTC 120
QY 135 CTTCTTTGGCCCTCTTGTGTAAGAGGAGAGAGAGCTGCCCATCAGCTCCCATGAGG 194

Db 121 CTTCTTTGGCCCTCTTGTGTAAGAGGAGAGAGAGCTGCCCATCAGCTCCCATGAGG 180
QY 195 CTTGAGAAAGGTTCTCTCCAGTCAACAGTGTGCTCGAGTAGAATTGCTGCATG 254
Db 181 CTTGAGAAAGGTTCTCTCCAGTCAACAGTGTGCTCGAGTAGAATTGCTGCATG 240
QY 255 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTGTCTCATTTGGGAGAACTTTCCAC 314
Db 241 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTGTCTCATTTGGGAGAACTTTCCAC 300
QY 315 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTGTCTCATTTGGGAGAACTTTCCAC 374
Db 301 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTGTCTCATTTGGGAGAACTTTCCAC 360
QY 375 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTGTCTCATTTGGGAGAACTTTCCAC 434
Db 361 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTGTCTCATTTGGGAGAACTTTCCAC 420
QY 435 CTGGCCAGGCTCAGCAACAGGCTAAGCAATGTCTATATGAGAGTGAATGACCTGCATATC 494
Db 421 CTGGCCAGGCTCAGCAACAGGCTAAGCAATGTCTATATGAGAGTGAATGACCTGCATATC 480
QY 495 CAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAGAAAGCTTGAGAGAGTGAAGATC 554
Db 481 CAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAGAAAGCTTGAGAGAGTGAAGATC 540
QY 555 AAGCAATTGGAGAACTGATTTGCTGTTATATGCTCTGAGAAATGCTGCAATTTGACCA 614
Db 541 AAGCAATTGGAGAACTGATTTGCTGTTATATGCTCTGAGAAATGCTGCAATTTGACCA 600
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Db 601 GAGCAAAAGCTGAAATGAATTAATACTAACCCCTTTCCCTGCTAGAAATTAACAATTAGATG 660
QY 675 CCCCAGGAGATTTT 690
Db 661 CCCCAGGAGATTTT 676

RESULT 8
AX403770 1152 bp DNA linear PAT 14-JUN-2002
LOCUS AX403770
DEFINITION Sequence 125 from Patent WO0077037.
ACCESSION AX403770
VERSION AX403770.1 GI:21437200
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 Ferrera, N., Fong, S., Gao, W. Q., Gerber, H., Gerritsen, M. E.,
AUTHORS Goddard, A., Godowski, P., Gurney, A., Kijavits, I. J., Mather, D.,
Napier, M., Pan, J., Paoni, N., Roy, M., Tumas, D., Watanabe, C.,
Williams, P. M., Wood, W. I., and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
JOURNAL the same
Patent: WO 0077037-A 125 21-DEC-2000;
Genentech Inc. (US)
FEATURES
Location/Qualifiers
source 1..1152
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 342 a 244 c 228 g 338 t
Query Match 98.0%; Score 676; DB 6; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.3e-176;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAAAGGTTCTCTCCAGTCAACAGTGTGCTCGAGTAGAATTGCTGCATG 74

D6		1	CTTCAGAAACAGATTCTCCTTCCCAAGTACCAGATGCTCGAGATTAGATTGTCTGCATATG	69
OY		75	GCCCACCTGCAGAAAATCTGTAGAGCTCTTTCTTAATGAGGAAGATGGCCCTCCAGCTCTCTC	134
D6		61	GCCGCCCTGCAGAAATCTGTAGAGCTCTTTCTTAATGAGGAAGATGGCCCTCCAGCTCTC	120
OY		135	CTTCTCTTGAGCCCTCTTGATACAGAGGAGAGACAGCTGGGCCCATCAGTCCCATCTGCAGS	194
D6		121	CTTCTCTTGAGCCCTCTTGATACAGAGGAGAGACAGCTGGGCCCATCAGTCCCATCTGCAGS	180
OY		195	CTTGCAAGTCCAACTTCCAGAGCCCTATATACCAACCGCACCTTCATGCTGGCTAAG	254
D6		181	CTTGCAAGTCCAACTTCCAGAGCCCTATATACCAACCGCACCTTCATGCTGGCTAAG	240
OY		255	GAGGCTAGCTTGGCTGATMACACAACAGACCTTGTCTCATTTGGGAGAAACTGTTCCAC	314
D6		241	GAGGCTAGCTTGGCTGATMACACAACAGACCTTGTCTCATTTGGGAGAAACTGTTCCAC	300
OY		315	GGAGTCAATATGAGTAGAGCGCTGCTATCTGATGAAGAAGGTGCTGAACCTTGAAC	374
D6		301	GGAGTCAATATGAGTAGAGCGCTGCTATCTGATGAAGAAGGTGCTGAACCTTGAAC	360
OY		375	GAAGTCTGTTTCCCTCATCTGATAGTTTCCAGCCTTATATGCAAGAGAGTGGTGGCTTC	434
D6		361	GAAGTCTGTTTCCCTCATCTGATAGTTTCCAGCCTTATATGCAAGAGAGTGGTGGCTTC	420
OY		435	CTGGCCAGGCTCAGCAACAGGCTAACATGTCAATATTGAAGGTATGACTGCATATC	494
D6		421	CTGGCCAGGCTCAGCAACAGGCTAACATGTCAATATTGAAGGTATGACTGCATATC	480
OY		495	CAGAGGAATGTGCAAAAGCTGAGAGACAAGTGA AAAAGCTTGAGAGAGTGAAGATC	554
D6		481	CAGAGGAATGTGCAAAAGCTGAGAGACAAGTGA AAAAGCTTGAGAGAGTGAAGATC	540
OY		555	AAAGCAATTGAGAACTGATTTGCTGTTTTATGTCTTGAGAAATGCTGCATTTGACCA	614
D6		541	AAAGCAATTGAGAACTGATTTGCTGTTTTATGTCTTGAGAAATGCTGCATTTGACCA	600
OY		615	GAGCAAACTGAAAAAATGAATACTAACCCCCCTTCCCTGCTAGAAATPACAATAGATG	674
D6		601	GAGCAAACTGAAAAAATGAATACTAACCCCCCTTCCCTGCTAGAAATPACAATAGATG	660
OY		675	CCCCCAAAGCGATTTTT 690	
D6		661	CCCCCAAAGCGATTTTT 676	
RESULT 9				
AX454768				
LOCUS		1152 bp	DNA	linear
DEFINITION		Sequence 353 from Patent WO0208284.		PAT 06-JUL-2002
ACCESSION		AX454768		
VERSION		AX454768.1		GI:21714008
KEYWORDS				
SOURCE				
ORGANISM				
				human.
				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
				Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE				
AUTHORS				Baker,K.P., Ferreira,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
				Godowski,P.J., Guney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
				Paoletti,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
				and Ye,W.
TITLE				
JOURNAL				
				Compositions and methods for the diagnosis and treatment of
				disorders involving angiogenesis
				Patent: WO 0208284-A 353 31-JAN-2002;
				Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferreira, Napoleone
				(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
				Audrey (US) ; Godowski, Paul J. (US) ; Guney, Austin L. (US) ;
				Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)
				; Paoletti, Nicholas F. (US) ; Stephan, Jean-Philippe S. (US) ;
				Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William

FEATURE	1 (US)	Location/Qualifiers
Source	1. 1152	/Organism="Homo sapiens"
		/db_xref="taxon:9606"
BASE COUNT	342 a 244 c 228 g 338 t	
ORIGIN		
Query Match	98.0%; Score 676; DB 6; Length 1152;	
Best Local Similarity	100.0%;	Pred. No. 1.3e-176;
Matches 676; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
15	CTTCAGAAACAGGTCTCTCCCTCCAGACACAGTGTCTCAGTTAGTAATGTCTGCATG	74
1	CTTAGAAACAGGTCTCTCTCCAGACACAGTGTCTCAGTTAGTAATGTCTGCATG	60
75	GCCGCCCTGCAGAAATCTGTAGGCTCTTCTTATGGGAGCCCTGGCACAGTGTCTC	134
61	GCCGCCCTGCAGAAATCTGTAGGCTCTTCTTATGGGAGCCCTGGCACAGTGTCTC	120
135	CTTCTCTTGGCCCTCTTGTATCAGGAGGAGACAGCTGCCCATCAGCTCCCATGCAAG	194
121	CTTCTCTTGGCCCTCTTGTATCAGGAGGAGACAGCTGCCCATCAGCTCCCATGCAAG	180
195	CTTACCAAGTCCCACTTCCAGACGCCCTATATACCAACCGACCTTCATGCTGGCTAAG	254
181	CTTACCAAGTCCCACTTCCAGACGCCCTATATACCAACCGACCTTCATGCTGGCTAAG	240
255	GAGGCTAGCTTGGCTGATTAACAACACAGACGTTGCTCATATGGGAGAAACTGTTCCAC	314
241	GAGGCTAGCTTGGCTGATTAACAACACAGACGTTGCTCATATGGGAGAAACTGTTCCAC	300
315	GAGTCTAGTATGATGAGACGCTGCTATCTGATGAAGACAGGTGCTGAACTTACCTTGA	374
301	GAGTCTAGTATGATGAGACGCTGCTATCTGATGAAGACAGGTGCTGAACTTACCTTGA	360
375	GAGTCTGCTTCTCCCTCATCTGATAGTGTCCAGCTTATATGACAGAGGTGTGCCCTTC	434
361	GAGTCTGCTTCTCCCTCATCTGATAGTGTCCAGCTTATATGACAGAGGTGTGCCCTTC	420
435	CTGGCCAGGCTCAGCAACAGGCTAAGCAATGTGATTTGAAGGTGATGACCTGCATATC	494
421	CTGGCCAGGCTCAGCAACAGGCTAAGCAATGTGATTTGAAGGTGATGACCTGCATATC	480
495	CAGAGGATGTGCAAAAGCTGAGAGACACAGTGAATAAGCTTGAAGAGGTGAGAGATC	554
481	CAGAGGATGTGCAAAAGCTGAGAGACACAGTGAATAAGCTTGAAGAGGTGAGAGATC	540
555	AAAGCAATTTGAGAACTGTGATTTGCTGTTATGTCTGAGAAATGCTGCATTTGACCA	614
541	AAAGCAATTTGAGAACTGTGATTTGCTGTTATGTCTGAGAAATGCTGCATTTGACCA	600
615	GAGCAAGCTGAATAATGAATTAACATCCCTTCTCCGTAGAAATTAACATTAAGT	674
601	GAGCAAGCTGAATAATGAATTAACATCCCTTCTCCGTAGAAATTAACATTAAGT	660
675	CCCCAAAGCGATTTT 690	
661	CCCCAAAGCGATTTT 676	
RESULT 10		
AX491246	1152 bp	linear
LOCUS	AX491246	Sequence 353 from Patent WO2006090.
DEFINITION	AX491246	
ACCESSION	AX491246.1	GI:22323960
VERSION		
KEYWORDS		
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1	

AUTHORS Baker, K. P., Ferrara, N., Gerber, H., Gertlisen, M. E., Goddard, A., Godowski, P. J., Gurney, A. L., Hillan, K. J., Maierster, S. A., Pan, J., Paoni, N. F., Stephan, J. P., Watanabe, C. K., Williams, P. M., Wood, W. I., and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis

JOURNAL Patent: WO 0200690-A 353 03-JAN-2002;

FEATURES Genentech, Inc. (US)

source Location/Qualifiers

BASE COUNT 342 a 244 c 228 g 338 t

ORIGIN

Query Match 98.0%; Score 676; DB 6; Length 1167;
 Best Local Similarity 100.0%; Pred. No. 1.3e-176;
 Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 CTTGAGAACAGGTTCTCTCCAGTCCAGTCCAGTCTGAGTTAGATTGTCTGCAATG 74
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 1 CTTGAGAACAGGTTCTCTCCAGTCCAGTCCAGTCTGAGTTAGATTGTCTGCAATG 60

75 GCGGCCCTGAGAAATGTGAGCTCTTCTTATGAGGAGCCCTGGCCACAGCTGCTC 134
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 61 GCGGCCCTGAGAAATGTGAGCTCTTCTTATGAGGAGCCCTGGCCACAGCTGCTC 120

135 CTTCTCTTGGCCCTCTTGTATGAGGAGGAGAGAGCTGCGCCATCAGCTCCCACTGAG 194
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 121 CTTCTCTTGGCCCTCTTGTATGAGGAGGAGAGAGCTGCGCCATCAGCTCCCACTGAG 180

195 CTTGACAAAGTCCAACTTCCAGCAGCCCTATATCAACACGCGACCTTCATGCTGCTAG 254
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 181 CTTGACAAAGTCCAACTTCCAGCAGCCCTATATCAACACGCGACCTTCATGCTGCTAG 240

255 GAGGCTAGCTTGGCTGTAACAACAAGAGGCTGCTCTCTTGGGGAGAACTGTTCCAC 314
 |||||
 241 GAGGCTAGCTTGGCTGTAACAACAAGAGGCTGCTCTCTTGGGGAGAACTGTTCCAC 300

315 GAGTCAATGATGATGAGCGCTGCTATCTGATGAGAGGCTGCTGAATTCACCTTGAA 374
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 301 GAGTCAATGATGATGAGCGCTGCTATCTGATGAGAGGCTGCTGAATTCACCTTGAA 360

375 GAAAGTCTGTTCCCTCAATCTGATAGTTCAGCTTATATGCAAGAGTGTGCTTC 434
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 361 GAAAGTCTGTTCCCTCAATCTGATAGTTCAGCTTATATGCAAGAGTGTGCTTC 420

435 CTGGCCAGGCTCAAGCAAGGCTAAGCAATGTCATATGAAAGTGAATGACCTGATATC 494
 |||||
 421 CTGGCCAGGCTCAAGCAAGGCTAAGCAATGTCATATGAAAGTGAATGACCTGATATC 480

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 481 CAGAGCAATGTGCAAAAAGCTGAAGACAGTGAAGAAAGCTTGGAGAGTGAAGATC 540

555 AAAGCAATGTGCAAAAAGCTGAATTTGCTTATATGCTCTGAGAAATGCTCATTTGACA 614
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 541 AAAGCAATGTGCAAAAAGCTGAATTTGCTTATATGCTCTGAGAAATGCTCATTTGACA 600

615 GAGCAAGCTGGAATAAAGTAATACTAACCCCTTCCCTGTAAGAAATTAATTAATG 674
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 601 GAGCAAGCTGGAATAAAGTAATACTAACCCCTTCCCTGTAAGAAATTAATTAATG 660

675 CCCCAGGATTTT 690
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 661 CCCCAGGATTTT 676

RESULT 11 AF279437 1167 bp mRNA linear PRI 09-OCT-2000
LOCUS AF279437 Homo sapiens interleukin 22 (IL22) mRNA, complete cds.
DEFINITION AF279437
ACCESSION

VERSION AF279437.1 GI:10719561

KEYWORDS Homo sapiens.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1167)
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Xie, W. H., Aggarwal, S., Ho, W. H., Foster, J., Zhang, Z., Stinson, J., Wood, W. I., Goddard, A. D., and Gurney, A. L.

TITLE Interleukin (IL)-22, a novel human cytokine that signals through the interferon receptor-related proteins CRF2-4 and IL-22R

JOURNAL J. Biol. Chem. 275 (40), 31335-31339 (2000)

MEDLINE 20469498

PUBMED 10875937

REFERENCE 2 (bases 1 to 1167)
 Xie, W. H., Aggarwal, S., Ho, W. H., Foster, J., Zhang, Z., Stinson, J., Wood, W. I., Goddard, A. D., and Gurney, A. L.

AUTHORS Direct Submission

TITLE Submitted (16-JUN-2000) Molecular Biology, Genentech Inc., 1 DNA Way, South San Francisco, CA 94080, USA

JOURNAL

FEATURES Location/Qualifiers

source 1. 1167
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BASE COUNT 357 a 244 c 228 g 338 t

ORIGIN

Query Match 98.0%; Score 676; DB 9; Length 1167;
 Best Local Similarity 100.0%; Pred. No. 1.3e-176;
 Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 CTTGAGAACAGGTTCTCTCCAGTCCAGTCCAGTCTGAGTTAGATTGTCTGCAATG 74
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 1 CTTGAGAACAGGTTCTCTCCAGTCCAGTCCAGTCTGAGTTAGATTGTCTGCAATG 60

75 GCGGCCCTGAGAAATGTGAGCTCTTCTTATGAGGAGCCCTGGCCACAGCTGCTC 134
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135 CTTCTCTTGGCCCTCTTGTATGAGGAGGAGAGAGCTGCGCCATCAGCTCCCACTGAG 194
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 121 CTTCTCTTGGCCCTCTTGTATGAGGAGGAGAGAGCTGCGCCATCAGCTCCCACTGAG 180

195 CTTGACAAAGTCCAACTTCCAGCAGCCCTATATCAACACGCGACCTTCATGCTGCTAG 254
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 181 CTTGACAAAGTCCAACTTCCAGCAGCCCTATATCAACACGCGACCTTCATGCTGCTAG 240

255 GAGGCTAGCTTGGCTGTAACAACAAGAGGCTGCTCTCTTGGGGAGAACTGTTCCAC 314
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 241 GAGGCTAGCTTGGCTGTAACAACAAGAGGCTGCTCTCTTGGGGAGAACTGTTCCAC 300

315 GAGTCAATGATGATGAGCGCTGCTATCTGATGAGAGGCTGCTGAATTCACCTTGAA 374
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 301 GAGTCAATGATGATGAGCGCTGCTATCTGATGAGAGGCTGCTGAATTCACCTTGAA 360

375 GAAAGTCTGTTCCCTCAATCTGATAGTTCAGCTTATATGCAAGAGTGTGCTTC 434
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 361 GAAAGTCTGTTCCCTCAATCTGATAGTTCAGCTTATATGCAAGAGTGTGCTTC 420

QY 435 CTGGCCAGGCTCAGAAAGGCTAAGCATATGTCATTTGAGGTGATGACCTGCATATC 494
DB 421 CTGGCCAGGCTCAGAAAGGCTAAGCATATGTCATTTGAGGTGATGACCTGCATATC 480
QY 495 CAGAGGATGTGCAAAAGCTGAAAGGACACAGTGAAGAAAGCTTGAGAGAGTGCAGATC 554
DB 481 CAGAGGATGTGCAAAAGCTGAAAGGACACAGTGAAGAAAGCTTGAGAGAGTGCAGATC 540
QY 555 AAAGCAATTTGAGAACTGATTTGCTTTATGTCCTGAGAAATGCTGCATTTGACCA 614
DB 541 AAAGCAATTTGAGAACTGATTTGCTTTATGTCCTGAGAAATGCTGCATTTGACCA 600
QY 615 GAGCAAGCTGAAAAATGATTAACCTCCCTTCTGCTAGAAATTAACATTAATG 674
DB 601 GAGCAAGCTGAAAAATGATTAACCTCCCTTCTGCTAGAAATTAACATTAATG 660
QY 675 CCCCAAGCGATTTT 690
DB 661 CCCCAAGCGATTTT 676

RESULT 12
LOCUS AX054620 1139 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 1 from Patent WO0073457.
ACCESSION AX054620
VERSION AX054620.1 GI:12228184
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1139)
AUTHORS Parham,C.L., de waal Malefyt,R. and Marehalli,N.L.
TITLE Mammalian interleukin-10 homologs: il-d110 and il-d210
JOURNAL Patent: WO 0073457-A 1 07-DEC-2000;
SHERING CORPORATION (US)
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source location/Qualifiers
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ORIGIN

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Best Local Similarity 99.9%; Pred. No. 3.1e-175;
Matches 671; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 6 AGAAGAGTTCTCTCCCACTGACCAAGTCTGAGTTAGATTTGCTGCAATGGCCG 65
QY 79 CCTCGAGAAATCTGAGAGTCTTTCTTATGGGAGCCCTGGCAACGAGTCCCTCTTC 138
DB 66 CCTCGAGAAATCTGAGAGTCTTTCTTATGGGAGCCCTGGCAACGAGTCCCTCTTC 125
QY 139 TCTTGGCCCTCTTGTGACAGGAGAGAGAGAGTCCCAATGCTCCAGAGCTTG 198
DB 126 TCTTGGCCCTCTTGTGACAGGAGAGAGAGAGTCCCAATGCTCCAGAGCTTG 185
QY 199 ACAAGTCCAACTTCCAGAGAGCCCTATATCAACCAACGACCTTCAATGCTAGAGAG 258

DB 186 ACAAGTCCAACTTCCAGAGAGCCCTATATCAACCAACGACCTTCAATGCTAGAGAG 245
QY 259 CTAGCTTGGCTGTAAACACACAGACAGTTCATTTGGGAGAACTGTCACAGAG 318
DB 246 NTAGCTTGGCTGTAAACACACAGAGTTCATTTGGGAGAACTGTCACAGAG 305
QY 319 TCAGTATGAGTGAAGCGCTGCTATGCTATGAGAGAGTGTGAACCTTGAAGAG 378
DB 306 TCAGTATGAGTGAAGCGCTGCTATGCTATGAGAGAGTGTGAACCTTGAAGAG 365
QY 379 TGGCTTCCCTCAATCTGATAGGTTCCAGCTTATATGAGAGAGTGTGCTTCTGG 438
DB 366 TGGCTTCCCTCAATCTGATAGGTTCCAGCTTATATGAGAGAGTGTGCTTCTGG 425
QY 439 CCAGCTCAGCAACAGGCTAAGACATGTCATATTGAAGGTGATGACCTGCATATCCAGA 498
DB 426 CCAGCTCAGCAACAGGCTAAGACATGTCATATTGAAGGTGATGACCTGCATATCCAGA 485
QY 499 GGAATGTGCAAAAGCTGAGAGACACAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAAG 558
DB 486 GGAATGTGCAAAAGCTGAGAGACACAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAAG 545
QY 559 CAATGGAGAACTGAGATTTGCTTTATGCTCTGAGAAATGCTGATTTGACCAAGC 618
DB 546 CAATGGAGAACTGAGATTTGCTTTATGCTCTGAGAAATGCTGATTTGACCAAGC 605
QY 619 AAAGCTGAAAAATGATTAACCTCCCTTCTGCTAGAAATTAACATTAATGAGTCC 678
DB 606 AAAGCTGAAAAATGATTAACCTCCCTTCTGCTAGAAATTAACATTAATGAGTCC 665
QY 679 AAAGCGATTTT 690
DB 666 AAAGCGATTTT 677

RESULT 13
LOCUS AX048204 1132 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 44 from Patent WO0070049.
ACCESSION AX048204
VERSION AX048204.1 GI:11876994
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1132)
AUTHORS Tang,Y.T., Yue,H., Lal,P., Burford,N., Bandman,O., Baughn,M.R.,
Azimzai,Y., Lu,D.A. and Patterson,C.
TITLE Extracellular signaling molecules
JOURNAL Patent: WO 0070049-A 44 23-NOV-2000;
Incyte Genomics, Inc. (US)
FEATURES
source location/Qualifiers
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BASE COUNT 333 a 240 c 226 g 333 t
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Best Local Similarity 100.0%; Pred. No. 1.1e-174;
Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ACAGTTCTCTCTCCCACTGACCAAGTCTGAGTTAGATTTGCTGCAATGGCCG 60
QY 82 TGCAAGAAATCTGTAGAGTCTTTCTTATGGGAGCCCTGGCAACGAGTCCCTCTCT 141
DB 61 TGCAAGAAATCTGTAGAGTCTTTCTTATGGGAGCCCTGGCAACGAGTCCCTCTCT 120

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QY	202	AGTCAACCTTCCAGACAGCCCTATATACCAACCGACCTTCATCTGGCTTACAGAGGCTA	261
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QY	262	GCTTGGCTGATTAACAACAACAAGCTTGGTCTCATTTGGGAGAAACTGTTCCAGGAGTCA	321
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QY	322	GTATGAGTGAAGCGGTGCTATCTGATGTAAGAGCAGGAGTCAACTTCAACCTTGAAGAAGTGC	381
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QY	382	TGTTCCCTCAATCTGATGTAAGTTCAGGCTTATATGACAGAGTGGTCCCTTCTGAGCA	441
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QY	442	GGCTTCAGCAACAGGCTTAAGCACAATGTCATATTTGAAGTGAATGACTGTCTATCCAGAGGA	501
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QY	502	ATGTGCAAAAGCTGAAGGACACAGTGAAGAAAAGCTTGGAGAGAGTGAAGATCAAAACAA	561
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QY	562	TTGAGAGAATGATTTGGTGTATATGTCCTGAGAAAATGCTGCAATTTGACACAGAGCAA	621
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Db	601	GCTGAAAAATGATTAATCTAACCCCTTTTCCCTGCTAGAAATTAATTAATGATGCCCAA	660
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DEFINITION	Sequence 14 from Patent WO0140467.		
ACCESSION	AX151713		
VERSION	AX151713.1	GI:14533647	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1116)		
AUTHORS	Presnell, S.R., Xu, W., Kindsvogel, W. and Chen, Z.		
TITLE	Human cytokine receptor		
JOURNAL	Patent: WO 0140467-A 14 07-JUN-2001;		
	ZymoGenetics, Inc. (US)		
FEATURES	Location/Qualifiers		
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ORIGIN			

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Qy	112	GGACCTGGCCACCAAGCTGCTCTCTTCTTTGGGCCCTCTTGTTAACAAGGAGAGACTG	171			
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Qy	232	ACCGCACCTTCATGCTGGCTAAGGAGGCTAAGCTTGGCTGATAACACACAGACCTTGCT	291			
Dd	181	ACCGCACCTTCATGCTGGCTAAGGAGGCTAAGCTTGGCTGATAACACACAGACCTTGCT	240			
Qy	292	TCATTGGGGGAAAATCTGTCCACGAGTCAATGATGATGAGCTGCTATCTGATGAAGC	351			
Dd	241	TCATTGGGGGAAAATCTGTCCACGAGTCAATGATGATGAGCTGCTATCTGATGAAGC	300			
Qy	352	AGGTGCTGAATCTTCAACCTTGAAGAAAGTGTCTCCCTCAATCTGATAGGTTCCAGCCT	411			
Dd	301	AGGTGCTGAATCTTCAACCTTGAAGAAAGTGTCTCCCTCAATCTGATAGGTTCCAGCCT	360			
Qy	412	ATAATGACGAGAGTGTGCTCCCTCTGACCAGAGCTCAGCAAACAGGCTAAGCATATGATA	471			
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Qy	472	TTGAAGTGTATGACCTGECATATCCAGAGAAATGTGCAAAAAGCTGAAGACACAGTGA	531			
Dd	421	TTGAAGTGTATGACCTGECATATCCAGAGAAATGTGCAAAAAGCTGAAGACACAGTGA	480			
Qy	532	AGCTTGAAGAAGTGTGAAGATCAAGCAATTGGAGAATCTGATTTGCTTTATGCTC	591			
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Dd	541	TGAAGAAATGCTGCTGATTTGACAGAGCAAAAGCTGAATAATGAATTAACCCCTTTCC	600			
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RESULT 15						
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	DEFINITION	AX179578				
	ACCESSION	AX179578.1 GI:15132010				
	VERSION					
	KEYWORDS	human.				
	SOURCE	Homo sapiens				
	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euarchontia; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1116) Presnell,S.R. and Kindsvogel,W. Cyokine zcyto18 Patent: WO 0146422-A 1 28-JUN-2001; ZymoGenetics, Inc. (US)				
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BASE COUNT 336 a 229 c 222 g 329 t
ORIGIN

Query Match 92.6%; Score 639; DB 6; Length 1116;
Best Local Similarity 100.0%; Pred. No. 2,4e-166;
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 52 TCGAGTTAGAAATGCTGCAATGGCCGCTGCAGAAATCTGTGAGCTTTCTTATAG 111
Db 1 TCGAGTTAGAAATGCTGCAATGGCCGCTGCAGAAATCTGTGAGCTTTCTTATAG 60
Qy 112 GGACCTGGCCACGAGCTGCTCTTCTTGGCCCTCTGTTACAGGAGAGCAGCTG 171
Db 61 GGACCTGGCCACGAGCTGCTCTTCTTGGCCCTCTGTTACAGGAGAGCAGCTG 120
Qy 172 GGCCCATCAGCTCCGCTGAGGCTTGAACAATCCACTCCAGCAGCCCTATATACCA 231
Db 121 GGCCCATCAGCTCCGCTGAGGCTTGAACAATCCACTCCAGCAGCCCTATATACCA 180
Qy 232 ACCGACCTTATGCTGCTAAGAGGCTAGCTGATTAACAACAAGCCTTCTC 291
Db 181 ACCGACCTTATGCTGCTAAGAGGCTAGCTGATTAACAACAAGCCTTCTC 240
Qy 292 TCATTGGGGAGAAATGTTCCACGAGTCAATAGTGAAGGCTGCTATCTGATGAGC 351
Db 241 TCATTGGGGAGAAATGTTCCACGAGTCAATAGTGAAGGCTGCTATCTGATGAGC 300
Qy 352 AGGTGCTGAACCTTCACTTGAAGAAGTGTCTTCTCAATCTGATAGTTCCAGCCTT 411
Db 301 AGGTGCTGAACCTTCACTTGAAGAAGTGTCTTCTCAATCTGATAGTTCCAGCCTT 360
Qy 412 ATATGCAGAGGTGTGCTCTTCTGCGCAGGCTCAGCAAGGCTTAAGCATGTCTA 471
Db 361 ATATGCAGAGGTGTGCTCTTCTGCGCAGGCTCAGCAAGGCTTAAGCATGTCTA 420
Qy 472 TTGAAGGTGATGACCTGCATATCCAGAGAAATGTGCAAAAGCTGAAGGACACAGTGA 531
Db 421 TTGAAGGTGATGACCTGCATATCCAGAGAAATGTGCAAAAGCTGAAGGACACAGTGA 480
Qy 532 AGCTTGGAGAGAGTGGAGATCAAAAGCAATGGAGAACTGATTTGCTGTTATGTCTC 591
Db 481 AGCTTGGAGAGAGTGGAGATCAAAAGCAATGGAGAACTGATTTGCTGTTATGTCTC 540
Qy 592 TGAAGAAATGCTGCTTTGACCAAGCAAAAGCTGAAAAATGATTAACCTCCCTTTCC 651
Db 541 TGAAGAAATGCTGCTTTGACCAAGCAAAAGCTGAAAAATGATTAACCTCCCTTTCC 600
Qy 652 CTGCTAGAAATTAACAATTAGATGCCCAAGGATTTT 690
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Search completed: July 19, 2003, 16:16:17
Job time : 1156.93 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:06:30 ; Search time 604.063 Seconds

(without alignments)
18499.535 Million cell updates/sec

Title: US-09-751-797-24

Sequence: 1 tgcacaagaagaatcttcag.....gatccccaagaagcattttt 690

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Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	70.4	10.2	389	17	AQ104025 HS_3108 B
3	61.2	8.9	562	17	AZ449260 IM0247J21
4	41.2	6.0	507	10	AM074124 XM08b01.x
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ALIGNMENTS

RESULT 1
AK005228
LOCUS
DEFINITION
Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500012D04:interleukin 10-related T cell-derived inducible factor, full insert sequence.
ACCESSION
AK005228
VERSION
AK005228.1 GI:12837639
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (strain: C57BL/6J) adult male cerebellum cDNA to mRNA, clone: lib:RIKEN full-length enriched mouse cDNA library
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
PUBMED
99279253
10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Suganara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL
MEDLINE
PUBMED
20499374
11042159

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AUTHORS

3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Saeki, N., Carninci, P., Komu, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubara, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system -384-format
Genome Res. 10 (11), 1757-1771 (2000)

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4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Komu, H., Yamada, I., Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R., Kadoya, K., Matsuda, H., Ashburner, M., Batilov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stambli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.U., Bulic, C., Flecher, C., Fujita, M., Gariboldi, M., Guetlich, S., Hill, D., Holman, M., Hume, D.A., Kamaya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Rongwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyman-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S. and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

5 (bases 1 to 700)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bulic, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, P., Hiramoto, K., Hirooka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Komu, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamataka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

TITLE
JOURNAL
COMMENT

Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer 15' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence 15' GAGAGAGAGAGCGGCCGATTAATTCGATTAATTAATTAATTAATTCGCGCC 3'. cDNA was cleaved with XhoI and SclI. Cloning sites, 5' end, XhoI; 3'

FEATURES
source

end: SclI. Host: SOLR.
Location/Qualifiers

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BASE COUNT
ORIGIN

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Matches 169; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

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Db 37 CACATCAGCGGTGACGACCAACATCCAGAGATGTCAGAGGCTTAAGACACAGT 96
QY 528 AAAAGCTTGAGAGAGTGAAGATCAAGCAATTGAGAGTCTGCTGTTATG 587
Db 97 AAAAGCTTGAGAGAGTGAAGATCAAGCAATTGAGAGTCTGCTGTTATG 156
QY 588 TCTCTGAGAAATGCTTGATTTGACACAGAGCAAGCTGAAATGATTAACCCCT 647
Db 157 TCTCTGAGAAATGCTTGATTTGACACAGAGCAAGCTGAAATGATTAACCCCT 216
QY 648 TTCCTGCTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 690
Db 217 CTGCTTTTAAAGAACATTAATTAATTAATTAATTAATTAATTAATTAAT 259

RESULT 2
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DEFINITION HS_3108_B1_C01_T7 CIT Approved Human Genomic Sperm Library D Homo
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ACCESSION AO104025
VERSION AO104025.1 GI:3478961
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 389)
Mahaits G.G., Wallace J.C., Smith K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contract: Mahaits CG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector

TITLE
JOURNAL
MEDLINE
COMMENT

Plate: 3108 row: F column: 1
 Class: BAC ends
 High quality sequence stop: 389
 Location/Qualifiers

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 /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 119 a 86 c 65 g 118 t 1 others

ORIGIN

Query Match 10.2%; Score 70.4; DB 17; Length 389;
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QY 464 ATGTCATTTGAAGGTGATGACCTGCATATCCAGAGAAATGTGCAAAAGCTGAGAGAC 523
 |||
 Db 148 ATACCATTTGAAGGTGATGACCTGCATATCCAGAGAAATGTGCAAAAGCTGAGAGAC 89

OY 524 AGTGAAGAAAGCTTGAGAGA 543
 |||
 Db 88 AGTGAAGAAAGGTAGAGACTGA 69

RESULT 3 562 bp DNA linear GSS 04-OCT-2000
 LOCUS AZ449260
 DEFINITION 1M0247J21F Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0247J21 F, DNA sequence.
 AZ449260
 VERSION
 KEYWORDS GSS.
 ACCESSION AZ449260.1 GI:10602872
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
 and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801.585.5606
 Fax: 801.585.7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0247 row: J column: 21
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 562.

FEATURES

Source

1. 562
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0247J21"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource"

BASE COUNT 119 a 155 c 116 g 172 t

ORIGIN

Query Match 8.9%; Score 61.2; DB 17; Length 562;
 Best Local Similarity 73.6%; Pred. No. 7.2e-07;
 Matches 78; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

OY 256 AGCTACTTGGCTGATATACACACAGCTTCTTCATTGGGAGAACTCTTCACG 315
 |||
 Db 305 AGGCACGCTTGCAGATACACACAGATCTCCGCTCCATCGGGAGAACTGTTCCAG 364

OY 316 GAGTCAGTATGATGAGAGCGCTGCTATCTGATGAAGCAGTGCTGA 361
 |||
 Db 365 GAGTCAGTGTATGCTCTGCTGTGATGAGCAGGAGCTGCTGCGGA 410

RESULT 4 507 bp mRNA linear EST 13-OCT-1999
 LOCUS AM074124
 DEFINITION X008001.X1 NCI_CGAP GU1 Homo sapiens cDNA clone IMAGE:2575657 3'
 similar to SW:TCOF_HUMAN Q13428 TREACLE PROTEIN ; mRNA sequence.
 AM074124
 VERSION
 KEYWORDS EST.
 ACCESSION AM074124.1 GI:6029122

SOURCE

ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 507)
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Chris Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
 Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.llnl.gov/bdrp/image/image.html

JOURNAL
 COMMENT

FEATURES
 Source
 Possible reversed clone: polyT not found
 Seq primer: -40UP from Gdbco
 High quality sequence stop: 346.
 Location/Qualifiers

1. 307
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2575657"
 /clone_lib="NCI CGAP GU1"
 /tissue_type="2_pooled high-grade transitional cell
 tumors"
 /lab_host="DH10B"
 /note="Organ: genitourinary tract; Vector: PCMV-SpOrf6;

	Query Match	Similarity	Score	DB	Length
Best Local	5.8%	56.4%	40.2	10	510
Matches	75	Conservative	0	Mismatches	58
				Indels	0
				Gaps	0

```
FEATURES
  source
    Location/Qualifiers
      1..522
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:170117"
        /clone_1ib="Geseler Wilms tumor"
        /sex="pooled (6)"
        /lab_host="DH10B"
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Query Match	5.8%;	Score 40.2;	DB 9;	Length 522;
Best Local Similarity	56.4%;	Pred. No. 1.1;		
Matches	75;	Conservative	0;	Mismatches 58; Indels 0; Gaps 0;
QY	115	CCTGTGCCACAGTGTGCTCTTCTTTGTGGCCCTTTGGTACAGGAGAGAGACAGTGGC	174	
Db	228	CCCCGGCCCCAGCTTCTTCTTCTTGTGCTCCGGGGGTCCTGGACAGCTGGCTGCTC	287	
QY	175	CCATCAGCTCCCATGTGAGGCTTGACAAATGCCAATTCAGACGCCCTATATACCAACC	234	
Db	288	CCGATACCTCCGGCTTCCGGCTCCAGACGCCCTTCGTGCTCTCTTGTGTGTGCCA	347	
QY	235	GCACTTCATGCT	247	
Db	348	CCACTTCTTCTTCT	360	

FEATURES	source
JOURNAL	Genomics Laboratory
COMMENT	Helix Research Institute
TITLE	1532-3 Yana, Kizazazu, Chiba 292-0812, Japan
REFERENCE	Tel: 81-438-52-3975
AUTHORS	Fax: 81-438-52-3986
ORGANISM	Email: genomics@hri.co.jp
	HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
	Research Institute; cDNA library construction; Department of
	Virology; Institute of Medical Science, University of Tokyo, and
	Helix Research Institute.
	Location/Qualifiers
	1..540
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="NT2RP3000357"
	/clone_1lb="NT2RP3"
	/cell_type="leucocarcinoma"
	/cell_line="NT2"
	/note="vector: pWE18SP3; mRNA from NT2 neuronal precursor
	cells after 2-weeks retinoic acid (RA) induction"
	177 t 4 others

was hemimethylated. A modification of Stratagene's

was hemimethylated. A modification of Stragare's first-strand synthesis primer was used. An 'anchor' nucleotide (Y=A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGACATGTGTCAG(18)] to anchor the primer at the 5' end of the poly(A) tract. After

second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently

phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI sites within the first strand synthesis primer was then

all *XhoI* sites in the cDNA would be protected by their restriction by digestion with *XhoI* from Promega (40U/μl); site within the 118c-Brdm4 synthesis primer was chosen

size-fractionated with a 500bp cutoff using [Seahacry] hemimethylated status. The cdna constructs were

S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately 1 ml. The

column eluent was precipitated, redissolved, and ligated into StrataGene's pBluescript II XR Predigested vector

(pBluescript II SK(+)) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). This

library was constructed in the laboratory of Dr. Paul Keim and Dr. Virginia H. Corvett at Northern Arizona

```
University."
a      105 g      177 t
      104 c
```

5.8%; Score 40.2; DB 14; Length 540;
57.6%; Pred. No. 1.1;

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servative 0; Mismatches 53; Indels 0; Gaps 0;

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ACAGCGCTAAGACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATG 504

GGTGGCCACGACATGATAGTTACAGGAGAAGTTTGCCCAATGACCAGAAAAG 102

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AGAGTTCACAGAGGACGCTATACAGCAGAGACAGAGTGTATGATGCTCAGAGGACCACTG 42
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543 bp	mRNA	linear	EST 03-DEC-2001
Gm-c1028	Glycine max cDNA clone	GENOME SYSTEMS CLONE	ID: 1

5'-5031 5' similar to TR:004347 004347 YEAST HYPOTHETICAL
XYDB1_SCHPO ISOLOG. ; mRNA sequence.

1 GI:7924373

max
Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

6 1 to 543)
D walm D vcdlin T Erneldding T Corwell V Khanna

1a, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Underwood, K., Stenroe, M., Theising, B., Allen, M., Bowers

Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
Er, E., Kohn, S., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk

erston, R. and Wilson, R.
 oybean EST Project

Shoemaker R/Public Soybean EST Project

Boybean EST Project
on University School of Medicine

est Park Parkway, Box 8501, St. Louis, MO 63108, USA
286 1800

286 1810

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:02:25 ; Search time 94.6289 Seconds

(without alignments)
16420.772 Million cell updates/sec

Title: US-09-751-797-24

Perfect score: 690
1 tcacacagcagatcttcag.....gatgcccaagcagctttc 690

Sequence: IDENTITY NUC

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	690	100.0	690	21	AAA28839 Human T cell induc
2	690	100.0	690	22	AA314875 Human CDNA encodin
3	690	100.0	690	24	AA030645 Human TIF CDNA. H
4	690	100.0	690	24	AA027150 Human T cell deriv
5	676	98.0	1152	22	AA092134 Human PRO10096 CDN
6	676	98.0	1152	22	AA087053 Nucleotide sequenc
7	676	98.0	1152	24	AB195737 Human angiotensin
8	676	98.0	1152	24	AB118447 CDNA encoding huma
9	676	98.0	1152	24	AB188248 Human PRO10096 CDN

10	676	98.0	1152	24	ABK33657	CDNA encoding huma
11	671	97.2	1139	22	AA028841	Human interleukin-
12	669	97.0	1132	22	AA043310	Human EXCS encodin
13	669	97.0	1177	21	AA081773	Human GIL-19/AB289
14	639	92.6	1116	22	AA090719	Human cytokine, ZC
15	639	92.6	1116	22	AA083741	Human IL-TIF polyp
16	639	92.6	1116	22	ABK10503	Human CDNA encodin
17	410.8	59.5	1166	21	AA091774	Murine GIL-19 prot
18	409.2	59.3	1119	21	AA028815	Murine T cell indu
19	409.2	59.3	1119	22	AA014858	Mouse cDNA encodin
20	409.2	59.3	1119	22	AA014858	Mouse TIF alpha CD
21	409.2	59.3	1119	22	AA027133	Mouse T cell deriv
22	407.6	59.1	1111	24	AA090746	Mouse ZCYTO18 CDNA
23	407.6	59.1	1111	21	AA028817	Murine T cell indu
24	407.6	59.1	1111	22	AA014860	Mouse cDNA for T c
25	407.6	59.1	1111	22	AA030629	Mouse TIF beta CDN
26	407.6	59.1	1111	24	AA027135	Mouse T cell deriv
27	380	55.1	537	22	AA028842	Human interleukin-
28	356.4	51.7	501	22	AA090720	Degenerate sequenc
29	317	45.9	418	24	AA030638	Human TIF DNA frag
30	272.2	39.4	504	21	AA043454	Mouse secreted exp
31	258	37.4	4796	21	AA028840	Human T cell induc
32	258	37.4	4797	22	AA014876	Human partial geno
33	258	37.4	4797	22	AA030646	Human TIF genomic
34	258	37.4	4797	24	AA027151	Human T cell deriv
35	127.6	18.5	5935	21	AA028818	Murine T cell indu
36	127.6	18.5	5935	22	AA014878	Mouse partial geno
37	127.6	18.5	5935	24	AA030660	Mouse TIF beta gen
38	127.6	18.5	5935	24	AA027153	Mouse T cell deriv
39	126	18.3	7444	21	AA028816	Murine T cell indu
40	126	18.3	7445	22	AA014859	Mouse partial geno
41	126	18.3	7445	24	AA030628	Mouse TIF alpha ge
42	126	18.3	7445	24	AA027134	Mouse T cell deriv
43	60	8.7	60	24	ABN38603	Human spliced tran
44	40.2	5.8	4840	24	ABN36926	Gene #3424 used to
45	36.6	5.3	1080	19	AA059719	Human secreted pro

ALIGNMENTS

RESULT 1					
AAA28839					
ID	AAA28839	standard;	CDNA;	690	BP.
XX					
AC	AAA28839;				
XX					
DT	04-SEP-2000	(first entry)			
XX					
DE	Human T cell inducible factor CDNA.				
XX					
XX	TIF-alpha; T cell derived inducible factor; interleukin 9; STAT; IL-9;				
KW	Anti-asthmatic; anti-allergic; cytosolic; inhibitor; antagonist;				
KW	probe; chromosome 12q15; ss.				
XX					
OS	Homo sapiens.				
XX					
FH	Key	Location/Qualifiers			
FT	CDS	72..611			
FT		/*tag= a			
XX					
PN	WO200024758-A1.				
XX					
PD	04-MAY-2000.				
XX					
PF	18-OCT-1999;	99WO-US24424.			
XX					
PR	26-OCT-1998;	98US-0178973.			
PR	16-JUL-1999;	99US-0354243.			
XX					
PA	(LUDWIG) LUDWIG INST CANCER RES.				
XX					
PI	Dumoutier L, Louhed J, Renaud J,				

XX WPI: 2000-422495/36.
 DR P-PSDB; AA192879.
 XX
 PT New nucleic acid molecule encoding a T cell derived inducible factor
 for treating asthma, an allergy or lymphoma
 XX
 XX Claim 1; Page 38; 46pp; English.
 XX
 CC This cDNA encodes a human T cell derived inducible factor (TIF). The gene
 CC was mapped to chromosome 12q15. The human TIF was identified based on
 CC homology to a murine TIF, which was identified by subtraction cloning
 CC from a murine lymphoma cell line BW5147 in the presence or absence of
 CC interleukin 9 (IL-9). BW5147 can be grown in vitro, without the need to
 CC add any cytokines to its culture medium. Many IL-9 activities are
 CC mediated by activation of STAT transcription factors. The novel TIFs were
 CC expressed in the presence of IL-9, but not in its absence. TIFs induce
 CC STAT activation in cells. They can be used, e.g., in the stimulation of
 CC regeneration of targeted tissues. Their inhibitors or antagonists can be
 CC used to retard, prevent or inhibit differentiation of other tissues. The
 CC TIFs and their coding sequences are useful in the treatment of asthma,
 CC allergies and lymphoma (claimed). They are also useful for identifying
 CC compounds that inhibit or activate T cell induced factor activity in a
 CC cell (claimed).
 XX
 SQ Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;
 Query Match 100.0%; Score 690; DB 21; Length 690;
 Best Local Similarity 100.0%; Pred. No. 1.8e-193;
 Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 TGCACAGAGAGATCTTCAGAACAGGTTCTCTCCCAAGTACAGGTTGCTCGAGTTAG 60
 QY 1 TGCACAGAGAGATCTTCAGAACAGGTTCTCTCCCAAGTACAGGTTGCTCGAGTTAG 60
 DB 1 TGCACAGAGAGATCTTCAGAACAGGTTCTCTCCCAAGTACAGGTTGCTCGAGTTAG 60
 QY 61 AATGTCGATGAGGCGCCCTGACAGAAATCTGTGAGCTTCTCCATTAGGGGAGCCCTGG 120
 DB 61 AATGTCGATGAGGCGCCCTGACAGAAATCTGTGAGCTTCTCCATTAGGGGAGCCCTGG 120
 QY 121 CCACAGAGTGCCTCTCTCTTGTGCGCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAG 180
 DB 121 CCACAGAGTGCCTCTCTCTTGTGCGCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAG 180
 QY 121 CCACAGAGTGCCTCTCTCTTGTGCGCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAG 180
 DB 121 CCACAGAGTGCCTCTCTCTTGTGCGCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAG 180
 QY 181 GGTCCCATGAGAGGCTTGAAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 DB 181 GGTCCCATGAGAGGCTTGAAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 QY 241 TCATGCTGCTAAGAGAGGCTAGCTTGTGATTAACAACAACAGAGCTTCTCATTTGGGG 300
 DB 241 TCATGCTGCTAAGAGAGGCTAGCTTGTGATTAACAACAACAGAGCTTCTCATTTGGGG 300
 QY 301 AGAAAGTGTCCAGGAGTCAAGTATGAGAGGCTCTATCTGATGAAGAGAGTGTCTGA 360
 DB 301 AGAAAGTGTCCAGGAGTCAAGTATGAGAGGCTCTATCTGATGAAGAGAGTGTCTGA 360
 QY 301 AGAAAGTGTCCAGGAGTCAAGTATGAGAGGCTCTATCTGATGAAGAGAGTGTCTGA 360
 DB 301 AGAAAGTGTCCAGGAGTCAAGTATGAGAGGCTCTATCTGATGAAGAGAGTGTCTGA 360
 QY 361 ACTTACACCTTGAAGAGTGTCTTCCCAATCTGATAGGTTCCAGCTTATATGACAG 420
 DB 361 ACTTACACCTTGAAGAGTGTCTTCCCAATCTGATAGGTTCCAGCTTATATGACAG 420
 QY 421 AGTGTGCTCTTCTGAGCAGAGCTCAGCAACAGGCTAAGCAATCTATTTGAAGGTG 480
 DB 421 AGTGTGCTCTTCTGAGCAGAGCTCAGCAACAGGCTAAGCAATCTATTTGAAGGTG 480
 QY 481 ATGACCTGATATCCAGAGAGATGTGCAAAAGCTGAAGACACAGTGAAGAAAGCTTGGAG 540
 DB 481 ATGACCTGATATCCAGAGAGATGTGCAAAAGCTGAAGACACAGTGAAGAAAGCTTGGAG 540
 QY 541 AGAGTGAAGAGATCAAGAGATTTGGAATGCTGTTTATGCTCTGAGAAAG 600
 DB 541 AGAGTGAAGAGATCAAGAGATTTGGAATGCTGTTTATGCTCTGAGAAAG 600
 QY 601 CCTGATTTGACCAAGCAAGCTGAAGAAATGATTAACACCCCTTCCCTGATAGAA 660
 DB 601 CCTGATTTGACCAAGCAAGCTGAAGAAATGATTAACACCCCTTCCCTGATAGAA 660

DB 601 CCTGATTTGACCAAGCAAGCTGAAGAAATGATTAACACCCCTTCCCTGATAGAA 660
 QY 661 ATACCAATTAGATGCCCCCAAGCGATTTT 690
 DB 661 ATACCAATTAGATGCCCCCAAGCGATTTT 690
 RESULT 2
 AAS14875
 ID AAS14875 standard; cDNA; 690 BP.
 AC AAS14875;
 XX 19-DEC-2001 (first entry)
 DE Human cDNA encoding T cell derived inducible factor, TIF.
 KW Human; T cell derived inducible factor; TIF; src; antiallergic;
 KW antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;
 KW cancer; lymphoma; immune system disorder; allergy; asthma;
 KW acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
 KW thyroiditis; melanoma; hepatoma.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 72..611
 FT /*tag= a
 FT /product= "TIF"
 FT /transl_except= (pos:159..161,aa:Glu)
 FT /transl_except= (pos:378..380,aa:Ile)
 FT /transl_except= (pos:405..407,aa:Arg)
 FT /transl_except= (pos:519..521,aa:Cys)
 PN US2001024652-A1.
 PD 27-SEP-2001.
 PF 29-DEC-2000; 2000US-0751797.
 XX 18-OCT-1999; 99US-0419568.
 PR 26-OCT-1998; 98US-0178973.
 PR 16-JUL-1999; 99US-0354243.
 PA (DUMO//) DUMOUTIER L.
 PA (LOUA//) LOUAHED J.
 PA (RENA//) RENAUD J.
 PI Dumoutier L, Louahed J, Renaud J;
 XX
 DR WPI: 2001-638496/73.
 DR P-PSDB; AAU09091.
 PT New isolated nucleic acid molecules encoding T cell inducible factors,
 PT useful as markers for expression or effect of interleukin (IL)-9 in a
 PT subject and diagnosing susceptibility to asthma or allergy -
 XX
 PS Claim 1; Page 17; 26pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule, which encodes
 CC a T cell derived inducible factor (TIF) which are upregulated by the
 CC cytokine interleukin-9 (IL-9) and induce STAT transcription factor
 CC activation. The TIF proteins (or their mutants) may be used to test IL-9
 CC ant/agonists for their potency against lymphomas, immune system
 CC disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
 CC autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
 CC or inhibit differentiation of tissue types in which they are active and
 CC therefore be used to develop treatments for melanomas and hepatomas.
 CC The present sequence encodes human TIF.
 SQ Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;
 Query Match 100.0%; Score 690; DB 22; Length 690;

Best Local Similarity 100.0%; Pred. No. 1,8e-193; Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 TGCAACAGCAAAATCTTACAGAGGTTCTCTCCAGCAGTACAGGTTGCTGAGTTAG 60
DB 1 TGCAACAGCAAAATCTTACAGAGGTTCTCTCCAGCAGTACAGGTTGCTGAGTTAG 60
QY 61 AATTGTCTGCAATGGCCCGCTGCAAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGG 120
DB 61 AATTGTCTGCAATGGCCCGCTGCAAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGG 120
QY 121 CCACAGGCTGCTCTTCTTCTTGGCCCTCTTGTACAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 CCACAGGCTGCTCTTCTTCTTGGCCCTCTTGTACAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 GCTCCCACTGACAGGCTTACAGAGTCCAACTTCCAGAGCCCTATATACCAACCCGACCT 240
DB 181 GCTCCCACTGACAGGCTTACAGAGTCCAACTTCCAGAGCCCTATATACCAACCCGACCT 240
QY 241 TCATGCTGCTAAGAGAGCTGAGCTGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAG 300
DB 241 TCATGCTGCTAAGAGAGCTGAGCTGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAG 300
QY 301 AGAAAGCTGCTCAAGAGAGCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 AGAAAGCTGCTCAAGAGAGCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 ACTTACCCCTTGAAGAGAGTGTCTCTCAATCTGATAGAGTTCAGAGCTTATATGACAG 420
DB 361 ACTTACCCCTTGAAGAGAGTGTCTCTCAATCTGATAGAGTTCAGAGCTTATATGACAG 420
QY 421 AGGTGTCCTCTTCTTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 480
DB 421 AGGTGTCCTCTTCTTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 480
QY 481 ATGACCTGCAATATCCAGAGAGATGTCAGAAAGCTGAAAGACACAGTGAAGAGAGAG 540
DB 481 ATGACCTGCAATATCCAGAGAGATGTCAGAAAGCTGAAAGACACAGTGAAGAGAGAG 540
QY 541 AGAGTGAAGAGATCAAGAGCAATTTGAGAACTGATTTGCTGTTATGCTGAGAGATG 600
DB 541 AGAGTGAAGAGATCAAGAGCAATTTGAGAACTGATTTGCTGTTATGCTGAGAGATG 600
QY 601 CCTGCAATTTGACAGAGAGCAAGCTGAAATGAAATGAAATGAAATGAAATGAAATG 660
DB 601 CCTGCAATTTGACAGAGAGCAAGCTGAAATGAAATGAAATGAAATGAAATGAAATG 660
QY 661 ATTAACATTTAGATGCCCCCAAGCGATTTT 690
DB 661 ATTAACATTTAGATGCCCCCAAGCGATTTT 690
```

RESULT 3

AAD30645 ID AAD30645 standard; cDNA; 690 BP.

AAD30645;

21-MAY-2002 (first entry)

Human TIF cDNA.

XX T cell derived inducible factor; TIF; interleukin-21; IL-21; human;
XX STRAT transcription factor; acute phase protein; inflammation;
XX chromosome 12; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
XX CDS 72..611
XX FT /tag= a
XX FT /product= "Human TIF protein"

PN W0200210393-A2.
XX 07-FEB-2002.
XX 27-JUN-2001; 2001WO-US20485.
XX 27-JUL-2000; 2000US-0626617.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Dumoutier L, Renaud J;
XX MPI: 2002-195964/25.
XX P-ESDB; AAE19237.
XX Stimulating expression of STAT transcription factor and inducing
XX production of acute phase protein in a cell. involves contacting a cell
XX capable of expressing STAT with T cell derived inducible factors -
XX Claim 6; Page 55-56; 64pp; English.
XX The invention relates to nucleic acid molecules encoding T cell
XX derived inducible factors (TIFs) also known as interleukin-21 (IL-21).
XX TIF polynucleotides are upregulated by the cytokine, IL-9. IL-TIF or
XX IL-21 molecules are implicated in activation of STAT transcription
XX factors, acute phase proteins and inflammation. The present sequence
XX is human TIF cDNA. The TIF gene is located on chromosome 12.
SQ Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;

Query Match 100.0%; Score 690; DB 24; Length 690;
Best Local Similarity 100.0%; Pred. No. 1,8e-193;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 TGCAACAGCAAAATCTTACAGAGGTTCTCTCCAGCAGTACAGGTTGCTGAGTTAG 60
DB 1 TGCAACAGCAAAATCTTACAGAGGTTCTCTCCAGCAGTACAGGTTGCTGAGTTAG 60
QY 61 AATTGTCTGCAATGGCCCGCTGCAAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGG 120
DB 61 AATTGTCTGCAATGGCCCGCTGCAAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGG 120
QY 121 CCACAGGCTGCTCTTCTTCTTGGCCCTCTTGTACAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 CCACAGGCTGCTCTTCTTCTTGGCCCTCTTGTACAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 GCTCCCACTGACAGGCTTACAGAGTCCAACTTCCAGAGCCCTATATACCAACCGACCT 240
DB 181 GCTCCCACTGACAGGCTTACAGAGTCCAACTTCCAGAGCCCTATATACCAACCGACCT 240
QY 241 TCATGCTGCTAAGAGAGCTGAGCTGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAG 300
DB 241 TCATGCTGCTAAGAGAGCTGAGCTGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAG 300
QY 301 AGAAAGCTGCTCAAGAGAGCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 AGAAAGCTGCTCAAGAGAGCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 ACTTACCCCTTGAAGAGAGTGTCTCTCAATCTGATAGAGTTCAGAGCTTATATGACAG 420
DB 361 ACTTACCCCTTGAAGAGAGTGTCTCTCAATCTGATAGAGTTCAGAGCTTATATGACAG 420
QY 421 AGGTGTCCTCTTCTTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 480
DB 421 AGGTGTCCTCTTCTTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 480
QY 481 ATGACCTGCAATATCCAGAGAGATGTCAGAAAGCTGAAAGACACAGTGAAGAGAGAG 540
DB 481 ATGACCTGCAATATCCAGAGAGATGTCAGAAAGCTGAAAGACACAGTGAAGAGAGAG 540
QY 541 AGAGTGAAGAGATCAAGAGCAATTTGAGAACTGATTTGCTGTTATGCTGAGAGATG 600
DB 541 AGAGTGAAGAGATCAAGAGCAATTTGAGAACTGATTTGCTGTTATGCTGAGAGATG 600
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```
QY 601 CCTGCAATTGACGAGCAAGCTGAATACTAACCCTTCCCTGCTAGAA 660
DB 601 CCTGCAATTGACGAGCAAGCTGAATACTAACCCTTCCCTGCTAGAA 660
QY 661 ATACCAATTAGATGCCCCCAAGCGATTTT 690
DB 661 ATACCAATTAGATGCCCCCAAGCGATTTT 690

RESULT 4
AAD27150 standard; DNA; 690 BP.
AC AAD27150;
XX
XX 09-APR-2002 (first entry)
XX
XX Human T cell derived inducible factor (TIF) beta cDNA.
XX
XX T cell derived inducible factor; TIF; cytokine; interleukin-9; IL-9;
XX protein therapy; STAT activation; differentiation; human; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 72..611
XX FT /*tag= a
XX FT /product= "Human TIF beta"
XX FT /transl_except= (pos:159..161, aa:Glu)
XX FT /transl_except= (pos:378..380, aa:Ile)
XX FT /transl_except= (pos:405..407, aa:Arg)
XX FT /transl_except= (pos:519..521, aa:Cys)
XX
XX US631613-B1.
XX
XX 18-DEC-2001.
XX
XX 18-OCT-1999; 99US-0419568.
XX
XX 26-OCT-1998; 98US-0178973.
XX 16-JUL-1999; 99US-0354243.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Dumoutier L, Louhed J, Renaud J;
XX
XX WPI; 2002-105277/14.
XX P-PSDB; AAE16554.
XX
XX Nucleic acids encoding T cell derived inducible factors useful for
XX inducing STAT activation in cells -
XX
XX Claim 1; Column 31-32; 24pp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule, which
XX encodes a T cell derived inducible factor comprising an amino acid
XX sequence encoded by 6 defined nucleotide sequences. The nucleic acid
XX molecules are shown to be up regulated by the cytokine interleukin-9
XX (IL-9) and are described as T Cell Derived Inducible Factors (TIFs). The
XX invention is used in protein therapy. The nucleic acid molecules encode
XX proteins which induce STAT activation in cells. They can be used, for
XX example, in the stimulation of regeneration of targeted tissues.
XX Further, their inhibitors or antagonists can be used to retard, prevent
XX or inhibit differentiation of other tissues. The present sequence is
XX human TIF beta cDNA.
XX
XX Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;
XX
XX Query Match 100.0%; Score 690; DB 24; Length 690;
XX Best Local Similarity 100.0%; Pred. No. 1,8e-193;
XX Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TGACAGAGAGAAATCTTCAGAAAGGTTCTCTTCCCAAGTACCAAGTTGCTGAGTTAG 60
DB 1 TGACAGAGAGAAATCTTCAGAAAGGTTCTCTTCCCAAGTACCAAGTTGCTGAGTTAG 60
QY 61 AATTGCTGCAATGAGCGCCCTGACAGAAATCTGTAGAGCTTTCTTATGAGGACCTGG 120
DB 61 AATTGCTGCAATGAGCGCCCTGACAGAAATCTGTAGAGCTTTCTTATGAGGACCTGG 120
QY 121 CCACAGCTGCTCCTCTTCTTCTTGGCCCTCTTGGTACAGGAGAGAGAGCTGCGCCATCA 180
DB 121 CCACAGCTGCTCCTCTTCTTCTTGGCCCTCTTGGTACAGGAGAGAGAGCTGCGCCATCA 180
QY 181 GCTCCACAGCTGAGGCTTGAAGTCAAGTCAAGTCCAGAGGCTTATACCAACCGACCT 240
DB 181 GCTCCACAGCTGAGGCTTGAAGTCAAGTCAAGTCCAGAGGCTTATACCAACCGACCT 240
QY 241 TCATGCTGCTAAGAGAGGCTAGCTTGGCTGATACAAACAGAGCTTGGCTGATTTGGG 300
DB 241 TCATGCTGCTAAGAGAGGCTAGCTTGGCTGATACAAACAGAGCTTGGCTGATTTGGG 300
QY 301 AGAACTGTTCCACGAGAGTCAATGATGAGAGGCTGCTATCTGATGAAGCAGGTCCTGA 360
DB 301 AGAACTGTTCCACGAGAGTCAATGATGAGAGGCTGCTATCTGATGAAGCAGGTCCTGA 360
QY 361 ACTTCACTTGAAGAGAGTCTGCTTCCCTCAATCTATAGTTCCAGCCTTATATGCAAG 420
DB 361 ACTTCACTTGAAGAGAGTCTGCTTCCCTCAATCTATAGTTCCAGCCTTATATGCAAG 420
QY 421 AGGTGAGTGCCTTCTGCGCAGGCTCAGCAACAGGCTAAGCATGCTATATTGAAGGTG 480
DB 421 AGGTGAGTGCCTTCTGCGCAGGCTCAGCAACAGGCTAAGCATGCTATATTGAAGGTG 480
QY 481 ATGACCTGCTATCCAGAGAAATGTGCAGAAAGCTGAAGCAACAGTGAAGAAAGCTTGGAG 540
DB 481 ATGACCTGCTATCCAGAGAAATGTGCAGAAAGCTGAAGCAACAGTGAAGAAAGCTTGGAG 540
QY 541 AAGGTGAGAGATCAAAAGCAATTTGAGAACTGATTTGCTTTATGCTCTGAGAAATG 600
DB 541 AAGGTGAGAGATCAAAAGCAATTTGAGAACTGATTTGCTTTATGCTCTGAGAAATG 600
QY 601 CCTGCAATTGACGAGCAAGCTGAAAAATGATTAATAACCCCTTCCCTGCTAGAA 660
DB 601 CCTGCAATTGACGAGCAAGCTGAAAAATGATTAATAACCCCTTCCCTGCTAGAA 660
QY 661 ATACCAATTAGATGCCCCCAAGCGATTTT 690
DB 661 ATACCAATTAGATGCCCCCAAGCGATTTT 690

RESULT 5
AAF92134
ID AAF92134 standard; cDNA; 1152 BP.
XX
XX AAF92134;
XX
XX 15-MAY-2001 (first entry)
XX
XX Human FRO10096 cDNA.
XX
XX Human; PRO protein; mapping; ss.
XX
XX Homo sapiens.
XX
XX WO200116318-A2.
XX
XX 08-MAR-2001.
XX
XX 24-AUG-2000; 2000WO-US23328.
XX
XX 01-SEP-1999; 99WO-US20111.
XX 15-SEP-1999; 99WO-US21090.
XX 07-DEC-1999; 99US-0169495.
XX 09-DEC-1999; 99US-0170262.
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PR	11-JAN-2000; 2000US-0175481.	
PR	18-FEB-2000; 2000WO-US04341.	
PR	18-FEB-2000; 2000WO-US04342.	
PR	22-FEB-2000; 2000WO-US04414.	
PR	01-MAR-2000; 2000WO-US05601.	
PR	03-MAR-2000; 2000US-0187282.	
PR	25-APR-2000; 2000US-0193937.	
PR	22-MAY-2000; 2000WO-US14042.	
PR	05-JUN-2000; 2000US-0209832.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;	
PI	Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;	
XX		
DR	WP1: 2001-183260/18.	
DR	P-PSDB: AAB87602.	
PT	Eighty four nucleic acids encoding PRO polypeptides, useful in	
PT	molecular biology, including use as hybridization probes, and in	
PT	chromosome and gene mapping.	
XX		
PS	Claim 2; Fig 153; 278bp; English.	
XX		
CC	The present sequence is the coding sequence for a human PRO polypeptide	
CC	(secreted and transmembrane). The PRO protein, and PRO agonists, PRO	
CC	antagonists or anti-PRO antibodies are useful for preparation of a	
CC	medicament useful in the treatment of a condition which is responsive to	
CC	the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO	
CC	protein may also be employed as molecular weight markers for protein	
CC	electrophoresis. The PRO coding sequence has applications in molecular	
CC	biology, including use as hybridisation probes, and in chromosome and	
CC	gene mapping.	
XX		
SO	Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;	
Query Match	98.0%; Score 676; DB 22; Length 1152;	
Best Local Similarity	100.0%; Pired. No. 3.1e-189;	
Matches 676; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	15 CTTGAGAACAGGTTCTCTCTCCACAGCAGTGTCTGAGTTAGATTGTCGCAATG 74	
DB	1 CTTGAGAACAGGTTCTCTCTCCACAGCAGTGTCTGAGTTAGATTGTCGCAATG 60	
QY	75 GCCGCCCTGCAGAAATCTGTAGAGCTCTTTCCTTATGAGGAGCCCTGGCCACGAGCTGCTC 134	
DB	61 GCCGCCCTGCAGAAATCTGTAGAGCTCTTTCCTTATGAGGAGCCCTGGCCACGAGCTGCTC 120	
QY	135 CTTCTCTTGGCCCTCTTGTGTACAGGAGAGAGACGCTGGCCCATCAGTCTCCCATCTGCAGG 194	
DB	121 CTTCTCTTGGCCCTCTTGTGTACAGGAGAGAGACGCTGGCCCATCAGTCTCCCATCTGCAGG 180	
QY	195 CTTGCAAGTCCAACTTTCAGAGAGCCCTATATCAACAAACCCGACCTTATGCTGGCTTAG 254	
DB	181 CTTGCAAGTCCAACTTTCAGAGAGCCCTATATCAACAAACCCGACCTTATGCTGGCTTAG 240	
QY	255 GAGGCTAGCTTGAGGATTAACAACAACAAGCTTCTCTCATTTGGGGAGAACTGTTCAC 314	
DB	241 GAGGCTAGCTTGAGGATTAACAACAACAAGCTTCTCTCATTTGGGGAGAACTGTTCAC 300	
QY	315 GGAGTCAGTATGAGTGAAGCGCTGTATCTGATGTAAGAACAGGTCGTAACCTTGA 374	
DB	301 GGAGTCAGTATGAGTGAAGCGCTGTATCTGATGTAAGAACAGGTCGTAACCTTGA 360	
QY	375 GAAAGTCTTTCCTTCAATCTGATAGTTCCAGGCTTATATGCAAGAGTGGTGCCTTC 434	
DB	361 GAAAGTCTTTCCTTCAATCTGATAGTTCCAGGCTTATATGCAAGAGTGGTGCCTTC 420	
QY	435 CTGGCCAGGCTCAGCAACAAGGCTTAAGCATATTTGAAGTGCATGACCTGCATATC 494	
DB	421 CTGGCCAGGCTCAGCAACAAGGCTTAAGCATATTTGAAGTGCATGACCTGCATATC 480	
QY	495 CAGAGAAATGTGCAAAAGCTGAAGACACAGTGAAAAAGCTTGAGAGAGTGAAGATC 554	

Dd		 CAGAGGAATGTGCAAAAGCTGACAGACACAGTGAATAAAGCTTGAGAGAGTGGAGAATGC	540
Oy	481	 AAACGAATTGGAGAACCTGCATTTTGGCTTTATGTCTCGAGAAATGCCCGCATTTGACCA	614
Dd	555	 AAACGAATTGGAGAACCTGCATTTTGGCTTTATGTCTCGAGAAATGCCCGCATTTGACCA	600
Oy	541	 GAGCAAACCTGAAAAATATTAACAACCCCTTCCTGCTAGAAAATTAACAATTAGATG	674
Dd	615	 GAGCAAACCTGAAAAATATTAACAACCCCTTCCTGCTAGAAAATTAACAATTAGATG	660
Oy	601	 CCCCCAAGCGATTTTT	690
Dd	675	 CCCCCAAGCGATTTTT	676
Oy	661	 CCCCCAAGCGATTTTT	676
Db			
RESULT 6			
AAC87053			
ID	AAC87053	standard; cDNA; 1152 BP.	
XX			
AC	AAC87053;		
XX			
DT	20-APR-2001	(first entry)	
XX			
DE	Nucleotide sequence of human polypeptide PRO10096.		
XX			
KM	Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;		
KM	PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;		
KM	PRO1183; PRO1742; PRO1419; PRO1999; PRO1710; PRO248; PRO353; PRO1318;		
KM	PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;		
KM	PRO246; PRO265; PRO941; PRO10936; PRO6003; PRO6004; PRO350; PRO2630;		
KW	PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;		
KX	ss.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	58..597	
FT		/*tag= a	
FT	sig_peptide	58..156	
FT		/*tag= b	
XX			
PN	WO200077037-A2.		
XX			
PD	21-DEC-2000.		
XX			
PF	22-MAY-2000; 2000MO-US14042.		
XX			
XX	15-JUN-1999;	99US-0139695.	
PR	20-JUL-1999;	99US-0145070.	
PR	26-JUL-1999;	99US-0145698.	
PR	17-AUG-1999;	99US-0149396.	
PR	01-SEP-1999;	99WO-US20111.	
PR	08-SEP-1999;	99WO-US20594.	
PR	15-SEP-1999;	99WO-US21090.	
PR	15-SEP-1999;	99WO-US21547.	
PR	30-NOV-1999;	99WO-US28313.	
PR	01-DEC-1999;	99WO-US28301.	
PR	02-DEC-1999;	99WO-US28565.	
PR	07-DEC-1999;	99US-0169495.	
PR	05-JAN-2000;	2000MO-US00219.	
PR	18-FEB-2000;	2000MO-US04341.	
PR	18-FEB-2000;	2000MO-US04342.	
PR	22-FEB-2000;	2000MO-US04414.	
PR	01-MAR-2000;	2000MO-US05601.	
PR	02-MAR-2000;	2000MO-US05841.	
PR	20-MAR-2000;	2000MO-US07377.	
PR	30-MAR-2000;	2000MO-US08439.	
PR	15-MAY-2000;	2000MO-US13358.	
PR	17-MAY-2000;	2000MO-US13705.	
XX			
PA	(GENE) GENENTECH INC.		
XX			

PI Ashkenazi A¹, Baker KP, Botstein DA, Desnovers L, Eaton DL,
 PI Ferrara N, Fong S, Gao W, Gerber H, Gertlsen ME, Goddard A,
 PI Godowski PJ, Gurney AW, Kijavini IJ, Mather JP, Napier MA, Pan J,
 PI Piont NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
 PI Wood WI, Zhang Z;
 XX WPI; 2001-050091/06.
 DR P-PSDB; AAB31210.
 XX
 PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
 PT transmembrane polypeptide is useful for gene therapy and identification
 PT of related polypeptides -
 XX
 PS Claim 2; Fig 63; 244pp; English.
 XX
 CC The present sequence encodes a human secreted and transmembrane
 CC polypeptide. The specification describes human polypeptides, designated
 CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
 CC PRO365, PRO361, PRO1308, PRO183, PRO1272, PRO1419, PRO4999, PRO7170,
 CC PRO248, PRO353, PRO1318, PRO1600, PRO940, PRO533, PRO301, PRO187,
 CC PRO337, PRO411, PRO436, PRO246, PRO285, PRO941, PRO10096, PRO6003,
 CC PRO6004, PRO2630 and PRO6309. The biological activity of cells
 CC can be modulated with agents that bind to these polypeptides, resulting
 CC in the death of the cells. The polynucleotides encoding these
 CC polypeptides are useful in the recombinant production of the
 CC polypeptides, as a hybridisation probe to screen libraries to isolate
 CC homologous sequences, or to map the gene. They may also be used for
 CC analysing genetic disorders, and to produce transgenic animals which are
 CC useful for the development and screening of therapeutically useful
 CC reagents. The polynucleotides can also be used in gene therapy e.g. to
 CC replace a defective gene.
 XX
 SQ Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;

Query Match 98.0%; Score 676; DB 22; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 3.1e-189;
 Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAAAGGTTCTCTTCCCAAGTCCAGTTGCTGAGTATGATGTTCTGCAATG 74
 DB 1 CTTGAGAAAGGTTCTCTTCCCAAGTCCAGTTGCTGAGTATGATGTTCTGCAATG 60
 QY 75 GCCGCCCTGACAAATCTGTGAGCTTTCCCTTATGAGGAGACCTTGGCCACCGCTGCTC 134
 DB 61 GCCGCCCTGACAAATCTGTGAGCTTTCCCTTATGAGGAGACCTTGGCCACCGCTGCTC 120
 QY 135 CTTCTCTTGGCCCTCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
 DB 121 CTTCTCTTGGCCCTCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 QY 195 CTTGACAAAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254
 DB 181 CTTGACAAAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 QY 255 GAGGCTAGCTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 314
 DB 241 GAGGCTAGCTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 QY 315 GAGGCTAGCTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 374
 DB 301 GAGGCTAGCTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 QY 375 GAGGCTAGCTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 434
 DB 361 GAGGCTAGCTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 435 CTGGCAGAGCTCAGCAAG 494
 DB 421 CTGGCAGAGCTCAGCAAG 480
 QY 495 CAGAGGAATGTGCAGAAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 554
 DB 481 CAGAGGAATGTGCAGAAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 540

QY 555 AAGCAATTGGAGAACTGATTTGCTGTTATGCTCTGAGAAATGCTGATTTGACCA 614
 DB 541 AAGCAATTGGAGAACTGATTTGCTGTTATGCTCTGAGAAATGCTGATTTGACCA 600
 QY 615 GAGCAAAAGCTGAAAAATGATTAACCTTCCCTTCTGCTGCTGAAATTAACATTTAGATG 674
 DB 601 GAGCAAAAGCTGAAAAATGATTAACCTTCCCTTCTGCTGCTGAAATTAACATTTAGATG 660
 QY 675 CCCCAAGGCAATTTT 690
 DB 661 CCCCAAGGCAATTTT 676
 RESULT 7
 ABL95737
 ID ABL95737 standard; cDNA; 1152 BP.
 XX
 AC ABL95737;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Human angiogenesis related cDNA PRO10096 SEQ ID NO: 353.
 XX
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiac; cytosolic; antiangiogenic; hypotensive; valvulopathy;
 KW antileukostatic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200208284-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 09-JUL-2001; 2001WO-US21735.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 15-SEP-2000; 2000US-000000P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 22-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06520.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.


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PR 28-JUN-2001, 2001WO-US00000.
XX
PA (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERE/) FERRARA N.
PA (GERE/) GERBER H.
PA (GERE/) GERITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PAN/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX
DR MPI; 2002-171999/22.
XX P-PSDB; ABB95599.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 1; Fig 353; 567bp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention.
XX
SQ Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;
XX
Query Match 98.0%; Score 676; DB 24; Length 1152;
Best Local Similarity 100.0%; Pred. No. 3.1e-189;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 15 CTTGAGAACAGGTTCTCCCTCCAGCAGCAGTGTGCTGAGTTAGAAATGTCTGCAATG 74
Db 1 CTTGAGAACAGGTTCTCCCTCCAGCAGCAGTGTGCTGAGTTAGAAATGTCTGCAATG 60
QY 75 GCCGCCCTGAGAAATCTGTAGCTCTTTCTTATGGGGAACCTGGCCACAGCTGCTC 134
Db 61 GCCGCCCTGAGAAATCTGTAGCTCTTTCTTATGGGGAACCTGGCCACAGCTGCTC 120
QY 135 CTTCTCTTGGCCCTCTTGTGTACAGGAGGAGCAAGCTGCGCCATCAGCTCCCACTGAGG 194
Db 121 CTTCTCTTGGCCCTCTTGTGTGTACAGGAGGAGCAAGCTGCGCCATCAGCTCCCACTGAGG 180
QY 195 CTTGACAAAGTCAACTCCAGAGCCCTATATATCCAAACGACCTTCATGCTGGGCTAG 254
Db 181 CTTGACAAAGTCAACTCCAGAGCCCTATATATCCAAACGACCTTCATGCTGGGCTAG 240
QY 255 GAGGCTAGCTTGGCTGTATTAACAACAAGAGCTTGTCTCATTTGGGGAAGAACTGTTCCAC 314
Db 241 GAGGCTAGCTTGGCTGTATTAACAACAAGAGCTTGTCTCATTTGGGGAAGAACTGTTCCAC 300
QY 315 GAGGTCAGTATGAGTGAGCGCTGTATCTGTATGAAGAGAGTGCTGAACCTTGA 374
Db 301 GAGGTCAGTATGAGTGAGCGCTGTATCTGTATGAAGAGAGTGCTGAACCTTGA 360
QY 375 GAAGTGCTTCCCTCAATCTGATAGGTTCCAGCTATATGACGAGAGGTGCTCCCTTC 434

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Db 361 GAAGTCTGTCCCTCAATCTGATAGATTCCAGCCTTATATGACGAGGTGTGCCCTTC 420
QY 435 CTGGCCAGGCTCAGCAACAGGCTAAGCACATGTGCATATTGAAGTATGACCTGCAATTC 494
Db 421 CTGGCCAGGCTCAGCAACAGGCTAAGCACATGTGCATATTGAAGTATGACCTGCAATTC 480
QY 495 CAGAGAAATGTGCAAAAAGCTGAAAGACACAGTGAAGAAAAGCTTGAGAGAGTGAGATC 554
Db 481 CAGAGAAATGTGCAAAAAGCTGAAAGACACAGTGAAGAAAAGCTTGAGAGAGTGAGATC 540
QY 555 AAGCAATTGAGAACTGATTTGCTGTTATGTCCTGAGAAATGCTGCATTTGACCA 614
Db 541 AAGCAATTGAGAACTGATTTGCTGTTATGTCCTGAGAAATGCTGCATTTGACCA 600
QY 615 GAGCAAAAGCTGAAAAATGAACTAACCCTTTTCCCTGCTTGAATAAATTAAGTGAATG 674
Db 601 GAGCAAAAGCTGAAAAATGAACTAACCCTTTTCCCTGCTTGAATAAATTAAGTGAATG 660
QY 675 CCCCAGGAGATTTT 690
Db 661 CCCCAGGAGATTTT 676

RESULT 8
ABK1847
ID ABK1847 standard; cDNA; 1152 BP.
XX
AC ABK1847;
XX
DT 05-JUN-2002 (first entry)
XX
DE cDNA encoding human interleukin 22 (IL-22) protein.
XX
KW Interleukin 22; IL-22; cytostatic; antiinflammatory; IL-22 antagonist;
KW immunotherapy; PAP; pancreaticitis associated protein; receptor; gene;
KW IL-22R; IL-10Rbeta; bioactive molecule linkage; cell death; pancreaticitis;
KW pancreatic disorder; pancreatic carcinoma; acinar cell carcinoma; human;
KW mixed cell population pancreatic carcinoma; clone DNA15185-2806; 88.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 58..597
FT sig_peptide 58..156
FT sig_peptide /*tag= b
FT sig_peptide 157..594
FT sig_peptide /*tag= c
XX
PN WO200216611-A2.
XX
PD 28-FEB-2002.
XX
PF 30-MAY-2001; 2001WO-US17443.
XX
PR 24-AUG-2000; 2000WO-US23328.
XX
PA (GETH ) GENENTECH INC.
PI Aggarwal S, Foster JS, Goddard A, Gurney AL, Maruoka EM, Wood WI,
PI Xie W,
XX
DR MPI; 2002-280940/32.
XX
DR P-PSDB; AAU78081.
XX
PT Novel isolated interleukin 22 polypeptide useful for identifying IL-22
PT agonists and antagonists that are used for treating acute pancreatitis,
PT chronic pancreatitis, pancreatic carcinoma -
XX
PS Claim 2; Fig 1; 94bp; English.
XX
CC The present invention relates to a new polypeptide having at least 80%

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CC identity to a 101 amino acid interleukin (IL)-22 sequence. The invention
CC is useful for detecting IL-22R (IL-22 receptor) or IL-10Rbeta polypeptide
CC in a sample which involves contacting sample with an IL-22 polypeptide
CC and determining the formation of an IL-22R/IL-22 polypeptide conjugate or
CC an IL-10Rbeta/IL-22 polypeptide conjugate. Preferably, the IL-22
CC polypeptide is labelled with a detectable label or is attached to a solid
CC support. The polypeptide is also useful for linking a bioactive molecule,
CC e.g. toxin, radiolabel or antibody that causes the death of the cell, to
CC a cell expressing IL-22R polypeptide or IL-10Rbeta polypeptide which
CC bioactive molecule and allowing binding of the IL-22 polypeptide with to
CC IL-22R or IL-10Rbeta polypeptide thus linking the bioactive molecules to
CC the cell. The molecules of the invention can also be used for modulating
CC biological activity of cell expressing IL-22R or IL-10Rbeta polypeptide,
CC whereby the cell is killed and the antibody of the invention is useful
CC for inhibiting IL-22 induced expression of PAPI (pancreatitis associated
CC protein) by pancreatic cells. The antibody is also useful for treating a
CC pancreatic disorder such as acute or chronic pancreatitis, pancreatic
CC carcinoma including acinar cell carcinoma or mixed cell population
CC of the pancreas in a mammal. The present nucleic acid sequence encodes
CC the human interleukin 22 (IL-22) protein of the invention. This sequence
CC is a clone designated DNA125185-2806.
XX
XX
SQ Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;
Query Match 98.0%; Score 676; DB 24; Length 1152;
Best Local Similarity 100.0%; Pred. No. 3,1e-189;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CTTGAGAAAGGTTCTCCCTCCCAAGTCACCAAGTCTGAGTGAATGTCGTGCATG 74
DB 1 CTTGAGAAAGGTTCTCCCTCCCAAGTCACCAAGTCTGAGTGAATGTCGTGCATG 60
QY 75 GCCGCCCTGACAAATCTGTGAGCTCTTCCCTTATGAGGAGACCTGGCCACCAAGTCCCTC 134
DB 61 GCCGCCCTGACAAATCTGTGAGCTCTTCCCTTATGAGGAGACCTGGCCACCAAGTCCCTC 120
QY 135 CTTCTCTTGGCCCTCTTGTGACAGGAGGAGAGAGCTGCCCATCAGTCCCACTGCAGG 194
DB 121 CTTCTCTTGGCCCTCTTGTGACAGGAGGAGAGAGCTGCCCATCAGTCCCACTGCAGG 180
QY 195 CTTGCAAGTCCCACTTCCAGAGAGCTTATCACCAGCACTTCAATGCTGCTGATG 254
DB 181 CTTGCAAGTCCCACTTCCAGAGAGCTTATCACCAGCACTTCAATGCTGCTGATG 240
QY 255 GAGGCTAGCTGCTGATATACACAGAGCTTCGCTCATGAGGAGAGAACTGTTCCAG 314
DB 241 GAGGCTAGCTGCTGATATACACAGAGCTTCGCTCATGAGGAGAGAACTGTTCCAG 300
QY 315 GAGGCTAGTATGATGAGGAGCTGCTATCTGATGAAGCAGTCTGCACTTCACTGAA 374
DB 301 GAGGCTAGTATGATGAGGAGCTGCTATCTGATGAAGCAGTCTGCACTTCACTGAA 360
QY 375 GAGGCTGCTGTTCCCTCAATCTATGATGCTCCAGCTTATATGACAGAGGTGTCCTTC 434
DB 361 GAGGCTGCTGTTCCCTCAATCTATGATGCTCCAGCTTATATGACAGAGGTGTCCTTC 420
QY 435 CTGGCCAGGCTCAGCAACAGGCTAAGCAGATGTCTATATTGAAGTGAATGCTGCATATC 494
DB 421 CTGGCCAGGCTCAGCAACAGGCTAAGCAGATGTCTATATTGAAGTGAATGCTGCATATC 480
QY 495 CAGAGGAATGTGCAAAAAGCTGAAGACACAGTGAAGAAAGCTTGAAGAGTGAAGATC 554
DB 481 CAGAGGAATGTGCAAAAAGCTGAAGACACAGTGAAGAAAGCTTGAAGAGTGAAGATC 540
QY 555 AAAGCAATGAGAACTGATTTGCTGTTATGCTCTGAGAAATGCCCTGCATTTGACCA 614
DB 541 AAAGCAATGAGAACTGATTTGCTGTTATGCTCTGAGAAATGCCCTGCATTTGACCA 600
QY 615 GAGCAAGCTGAAAAATGATACTAACCCCTTCCCTGCTAGAAATTAACAATTAGATG 674
DB 601 GAGCAAGCTGAAAAATGATACTAACCCCTTCCCTGCTAGAAATTAACAATTAGATG 660

QY 675 CCCCAAGCGATTTT 690
DB 661 CCCCAAGCGATTTT 676
RESULT 9
ABL88248
ID ABL88248 strand; cDNA; 1152 BP.
XX ABL88248;
AC 16-MAY-2002 (first entry)
XX
XX
DE Human PRO10096 cDNA sequence SEQ ID NO:353.
XX
XX Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endochelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200200690-A2.
PN
XX
XX 03-JAN-2002.
PD
XX
XX 20-JUN-2001; 2001WO-US19692.
PF
XX
XX 23-JUN-2000; 2000US-213637P.
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854280.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Fan J, Paoni NF;

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-090516/12.
DR P-PSDB; ABB84993.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT interaction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 2; Fig 353; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84917 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytoskeletal,
CC angiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC degeneration, atherosclerosis, hypertension, arterial restenosis,
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC carcinoma) and wound healing. The PRO polynucleotides have applications
CC in molecular biology, including use as hybridization probes, and in
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC probes used in the exemplification of the present invention.
XX
SQ Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;
Query Match 98.0%; Score 676; DB 24; Length 1152;
Best Local Similarity 100.0%; Pred. No. 3.1e-189;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CTTGAGAACAGAGTTCTCTCCAGTACAGAGTTCTCTGAGTGAATGTTCTGCAATG 74
DB 1 CTTGAGAACAGAGTTCTCTCCAGTACAGAGTTCTCTGAGTGAATGTTCTGCAATG 60
QY 75 GCGCGCCCTGCAAGAAATCTGTAGAGCTTTCTTCTTATGGGGAACCTTGGCCACGCTGCGCTC 134
DB 61 GCGCGCCCTGCAAGAAATCTGTAGAGCTTTCTTCTTATGGGGAACCTTGGCCACGCTGCGCTC 120
QY 135 CTTGCTTGGGCGCTCTGTATACAGGAGAGAGAGCTGCGCCCATGCTCCCATGCAAG 194
DB 121 CTTGCTTGGGCGCTCTGTATACAGGAGAGAGAGCTGCGCCCATGCTCCCATGCAAG 180
QY 195 CTTGACAAAGTCCAACTTCACAGAGCTTATATACCAACGCACTTATGCTGCTAAG 254
DB 181 CTTGACAAAGTCCAACTTCACAGAGCTTATATACCAACGCACTTATGCTGCTAAG 240
QY 255 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTCTTATTTGGGGAAGAACTGTTCCAC 314
DB 241 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTCTTATTTGGGGAAGAACTGTTCCAC 300
QY 315 GGAGTCAGATAGAGAGAGAGCTGATCTGATGAAGAGAGAGCTGTAACCTTGA 374
DB 301 GGAGTCAGATAGAGAGAGAGCTGATCTGATGAAGAGAGAGCTGTAACCTTGA 360
QY 375 GAAAGTGTCTTCCCTCAATCTGATAGTTCCAGCTTATATACAGAGAGTGTGCGCTTC 434
DB 361 GAAAGTGTCTTCCCTCAATCTGATAGTTCCAGCTTATATACAGAGAGTGTGCGCTTC 420
QY 435 CTGGCCAGGCTTACAGCAAGGCTTAAGACATGTCATATTGAAGGTATGACCTGCTATTC 494
DB 421 CTGGCCAGGCTTACAGCAAGGCTTAAAGCATATGTAAGGTATGACCTGCTATTC 480
QY 495 CAGAGAAATGTGCAAAAGCTGAAGGACAGAGTGAAGAACTTGGAGAGAGTGGAGATC 554
DB 481 CAGAGAAATGTGCAAAAGCTGAAGGACAGAGTGAAGAACTTGGAGAGAGTGGAGATC 540
QY 555 AAAGCAATTGGAAGAGCTGATTTGCTTTATGCTCTTGAGAAATGCTGCAATTGACCA 614
DB 541 AAAGCAATTGGAAGAGCTGATTTGCTTTATGCTCTTGAGAAATGCTGCAATTGACCA 600
QY 615 GAGCAAAAGCTGAAATGAATACTAACCCCTTCCCTGCTAGAAATAACAATTGATG 674

DB 601 GAGCAAAAGCTGAAATGAATACTAACCCCTTCCCTGCTAGAAATAACAATTGATG 660
QY 675 CCCCCAAGCGATTTT 690
DB 661 CCCCCAAGCGATTTT 676
RESULT 10.
ID ABR33657 standard; cDNA; 1152 BP.
XX ABR33657;
AC ABR33657;
XX 08-MAY-2002 (first entry)
DT
XX
DE cDNA encoding human PRO protein, Seq ID No 243.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.
OS
XX Homo sapiens.
XX
XX WO200208288-A2.
XX
XX 31-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US21066.
XX
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220585P.
XX 25-JUL-2000; 2000US-220605P.
XX 25-JUL-2000; 2000US-220607P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220638P.
XX 25-JUL-2000; 2000US-220664P.
XX 25-JUL-2000; 2000US-220666P.
XX 26-JUL-2000; 2000US-220893P.
XX 28-JUL-2000; 2000WO-US20710.
XX 28-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 15-SEP-2000; 2000US-000000P.
XX 10-NOV-2000; 2000WO-US30873.
XX 28-NOV-2000; 2000US-253646P.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 28-FEB-2001; 2001WO-US06520.
XX 10-MAY-2001; 2001US-0854280.
XX 25-MAY-2001; 2001WO-US17092.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-172001/22.
XX P-PSDB; AAB83713.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for treating a PRO related disorder and for diagnosing tumours
XX as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
XX tumour or liver tumour -
XX
XX Claim 2; Figure 243; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumours, especially lung

CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABR3356-ABR3365 represent human
 CC PRO protein coding sequences of the invention.

XX Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;

Query Match 98.0%; Score 676; DB 24; Length 1152;

Best Local Similarity 100.0%; Pred. No. 3.1e-189;

Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAAAGGTTCTCTCCAGTCACAGTTGCTGAGTTAGTAATTGCTGCAATG 74
 DB 1 CTTGAGAAAGGTTCTCTCCAGTCACAGTTGCTGAGTTAGTAATTGCTGCAATG 60
 QY 75 GCCGCCCTGCAAAATCTGTGAGCTTTCTTATGGGAGCCCTGGCCACAGCTGCTC 134
 DB 61 GCCGCCCTGCAAAATCTGTGAGCTTTCTTATGGGAGCCCTGGCCACAGCTGCTC 120
 QY 135 CTTCTTGGGCTCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
 DB 121 CTTCTTGGGCTCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 QY 195 CTTGACAAAGTCCAACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254
 DB 181 CTTGACAAAGTCCAACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 QY 255 GAGGCTAGCTTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAG 314
 DB 241 GAGGCTAGCTTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 QY 315 GGAGTCAGTATGAG 374
 DB 301 GGAGTCAGTATGAG 360
 QY 375 GAAAGTCTGTTCCCTCAATCTGATGAGTCCAGAGAGAGAGAGAGAGAGAGAGAG 434
 DB 361 GAAAGTCTGTTCCCTCAATCTGATGAGTCCAGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 435 CTGGCCAGGCTCAGCAACAGGCTAAGCATGTCAATTTGAAGGTGATGACCTGCATATC 494
 DB 421 CTGGCCAGGCTCAGCAACAGGCTAAGCATGTCAATTTGAAGGTGATGACCTGCATATC 480
 QY 495 CAGAGAGATGTCAGCAAAAGCTGAAGAGACAGTGAAGAAAGCTTGGAGAGGTGAGAGATC 554
 DB 481 CAGAGAGATGTCAGCAAAAGCTGAAGAGACAGTGAAGAAAGCTTGGAGAGGTGAGAGATC 540
 QY 555 AAGCAATTTGAGAACTGGATTGCTTTATGCTCTGAGAAAGAGCCGCAATTGACCA 614
 DB 541 AAGCAATTTGAGAACTGGATTGCTTTATGCTCTGAGAAAGAGCCGCAATTGACCA 600
 QY 615 GAGCAAGCTGAAAAATGATTAATTAACCTCCCTTCTGCTAGAAATTAACATTTAGATG 674
 DB 601 GAGCAAGCTGAAAAATGATTAATTAACCTCCCTTCTGCTAGAAATTAACATTTAGATG 660
 QY 675 CCCCAAGGAGTTT 690
 DB 661 CCCCAAGGAGTTT 676

RESULT 11
 ID AAF28841
 AC AAF28841 standard; DNA; 1139 BP.
 XX
 XX AAF28841;

DT 25-APR-2001 (first entry)
 XX Human interleukin-10 homologue IL-D110 DNA sequence.
 XX Anti-inflammatory; immunosuppressive; cytostatic; antirheumatic; human;
 DE interleukin-10 homologue; IL-D110; IL-D210; cytokine; tumour therapy;
 XX interleukin 10 homologue; IL-D110; IL-D210; cytokine; tumour therapy;
 KW haematopoietic cell; probe; immunogen; systemic lupus erythematosus;
 KW rheumatoid arthritis; Hashimoto's autoimmune response; ss.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT CDS 59..598
 FT /tag= a
 FT /product= "IL-D110"
 FT /transl_except= (pos:245..247,aa:Xaa)
 FT /note= "Xaa=unknown"
 FT sig_peptide 59..157
 FT /tag= b
 FT mat_peptide 158..595
 FT /tag= c
 PN MO200073457-A1.
 PD 07-DEC-2000.
 PF 26-MAY-2000; 2000WO-US14729.
 PR 27-MAY-1999; 99US-0322806.
 PA (SCHE) SCHERING CORP.
 PI Parham CL, De Waal Malefyt R, Marshalls NL;
 DR WPT: 2001-061539/07.
 DR P-PSDB; AAB371122.
 XX
 PT New interleukin-D110 genes and polypeptides useful for treating
 PT conditions associated with abnormal physiology, particularly e.g.
 PT inflammatory or autoimmune disorders -
 XX
 PS Claim 3; Page 51-52; 62pp; English.
 CC This sequence represents the gene sequence for a human interleukin 10
 CC homologue IL-D110. The invention also relates to another IL-10 homologue
 CC ID-210 (AAF28842). The IL-D110 is useful for treating conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions, either acute or chronic. The new cytokine
 CC also plays a role in the regulation or development of haematopoietic
 CC cells, e.g. lymphoid or myeloid cells, which affect immunological
 CC responses, such as inflammation and/or autoimmune disorders. These may
 CC also be used in drug screening to identify compounds having binding
 CC affinity to or other relevant biological effects on IL-D110 functions.
 CC in anti-tumour therapy, as probes for detecting IL-D110 levels in samples
 CC from patients suspected of having an abnormal condition, e.g. autoimmune
 CC or inflammatory, in raising or screen antibodies, as immunogen, in
 CC diagnostic assays, and in detecting, isolating or identifying a DNA clone
 CC encoding IL-D110 or IL-D210 from a natural source. IL-D110 antagonists
 CC may be used to block immune responses, e.g. in situations as inflammatory
 CC or autoimmune responses, including rheumatoid arthritis, systemic lupus
 CC erythematosus, or Hashimoto's autoimmune responses.
 XX
 XX Sequence 1139 BP; 337 A; 238 C; 227 G; 333 T; 4 other;

Query Match 97.2%; Score 671; DB 22; Length 1139;

Best Local Similarity 99.9%; Pred. No. 9.2e-158;

Matches 671; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 AGAAGAGTTCTCTCTCCAGTCACAGTTGCTGAGTTAGTAATTGCTGCAATGCGG 78
 DB 6 AGAAGAGTTCTCTCTCTCCAGTCACAGTTGCTGAGTTAGTAATTGCTGCAATGCGG 65

QY 79 CCTGAGAAATCTGTAGCTCTTCTTATAGGGAGACCTGGCCACAGCTGCTCTTC 138
 DB 66 CCTGAGAAATCTGTAGCTCTTCTTATAGGGAGACCTGGCCACAGCTGCTCTTC 125
 QY 139 TCTTGGCCCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 198
 DB 126 TCTTGGCCCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 185
 QY 199 ACAAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 258
 DB 186 ACAAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 245
 QY 259 CTACTGCTGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 318
 DB 246 NTAGCTTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 305
 QY 319 TCAATATAG 378
 DB 306 TCAATATAG 365
 QY 379 TGCTGCTTCCCTCAATCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 438
 DB 366 TGCTGCTTCCCTCAATCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 425
 QY 439 CCAAGGCTAGCAACAGAGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 498
 DB 426 CCAAGGCTAGCAACAGAGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 485
 QY 499 GGAATGTGCAAAAGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 558
 DB 486 GGAATGTGCAAAAGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 545
 QY 559 CAATTGAG 618
 DB 546 CAATTGAG 605
 QY 619 AAAGTGAATAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 678
 DB 606 AAAGTGAATAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 665
 QY 679 AAAGGATTTT 690
 DB 666 AAAGGATTTT 677
 RESULT 12
 AAC84310
 ID AAC84310 standard; cDNA, 1132 BP.
 AC AAC84310;
 AC 19-MAR-2001 (first entry)
 DT 19-MAR-2001 (first entry)
 XX Human EXCS encoding cDNA (clone ID 5571181CB1).
 DE Extracellular signaling molecule; EXCS; anti-inflammatory; human;
 KW immunosuppressive; cytotoxic; neuroprotective; gastroenteric; anti-
 KW virus; anti-bacterial; anti-HIV; human immunodeficiency virus;
 KW anti-infective; cerebroprotective; neurotropic; anti-leukemia; anti-fungal;
 KW anti-cancer; anti-infective; neuroleptic; vasodilator; gynecological;
 KW keratolytic; protozoicide; gene therapy; ss.
 OS Homo sapiens.
 OS WO200070049-A2.
 PN 23-NOV-2000.
 PD 19-MAY-2000; 2000WO-US13975.
 PF 19-MAY-2000; 2000WO-US13975.
 PR 15-JUL-1999; 99US-0134949.
 PR 15-JUL-1999; 99US-0144270.
 PR 30-JUL-1999; 99US-0146700.

PR 04-OCT-1999; 99US-0157508.
 XX (INCY-) INCYTE GENOMICS INC.
 PA Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;
 PI Azimzai Y, Lu DM, Patterson C;
 XX WPI: 2001-025021/03.
 DR P-PSDB: AAB48074.
 DR New human extracellular signaling nucleic acids and polypeptides useful
 PT for diagnosing, treating and preventing infections and
 PT gastrointestinal, neurological, reproductive, and
 PT autoimmune/inflammatory disorders -
 PT
 XX
 XX Claim 4; Page 108; 114pp; English.
 PS
 XX The invention provides human extracellular signaling molecules (EXCS)
 CC and polynucleotides which identify and encode EXCS. EXCS can be
 CC expressed by standard recombinant methodology. The amino acid and nucleic
 CC acid sequences of EXCS are useful for diagnosing, treating and
 CC preventing infections and gastrointestinal (peptic ulcer, dysphagia,
 CC pancreatitis), neurological (e.g. epilepsy, ischemic cerebrovascular
 CC disease, stroke), reproductive (infertility, ovulatory defects,
 CC endometriosis), autoimmune/inflammatory (actinic keratosis, acquired
 CC immunodeficiency syndrome (AIDS), Addison's disease), and cell
 CC proliferative disorders including cancers (of the breast, adrenal gland,
 CC bone). They may also be used to treat fatal familial insomnia,
 CC nutritional and metabolic diseases of the nervous system, myopathies,
 CC mental disorders (anxiety, schizophrenia, mood), as well as infections
 CC caused by parasites (malaria, leishmania, trypanosoma), viral
 CC (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus,
 CC staphylococcus, bacillus), and fungal (aspergillus, blastomycetes,
 CC dermatophytes) agents. The nucleic acids, polypeptides, and antibodies used
 CC as agonists, pharmaceutical compositions, and antibodies may also be used
 CC for treating or preventing disorders associated with increased or
 CC decreased expression or activity of EXCS. EXCS polynucleotides may also
 CC be used to detect and quantify gene expression in biopsied tissues in
 CC which expression of EXCS may be correlated with the disease, to determine
 CC presence or excess expression of EXCS, to monitor regulation of EXCS
 CC levels during therapeutic intervention, to detect the presence of EXCS
 CC associated disorders, as targets in microarray, to generate hybridization
 CC probes, and to detect differences in gene sequences among normal, carrier
 CC or affected individuals. Antibodies may also be used in diagnosing
 CC disorders, in monitoring patients being treated with EXCS agonists,
 CC antagonists or inhibitors. Sequences AAC84293-084318 represent nucleic
 CC acid molecules encoding the EXCS of the invention.
 XX
 XX Sequence 1132 BP; 333 A; 240 C; 226 G; 333 T; 0 other;
 SQ
 Query Match 97.0%; Score 669; DB 22; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 3; Ee-187;
 Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 ACAAGTTCCTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 81
 DB 1 ACAAGTTCCTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
 QY 82 TGCAAAATCTGTAG 141
 DB 61 TGCAAAATCTGTAG 120
 QY 142 TGGCCCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 201
 DB 121 TGGCCCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 QY 202 AGTCAACTTCCAG 261
 DB 181 AGTCAACTTCCAG 240
 QY 262 GCTTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 321
 DB 241 GCTTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

QY 322 GTATGAGTGAAGCGCTGCTATCTGATGAAGAGAGTGTGAACCTTACCCCTGAAAGAGTGC 381
 Db 301 GTATGAGTGAAGCGCTGCTATCTGATGAAGAGAGTGTGAACCTTACCCCTGAAAGAGTGC 360
 QY 382 TGTTCCTCAATCTGATGAGTTCAGAGCTTATATGACAGAGAGTGTGCTCCCTGAGGCA 441
 Db 361 TGTTCCTCAATCTGATGAGTTCAGAGCTTATATGACAGAGAGTGTGCTCCCTGAGGCA 420
 QY 442 GGCCTCAGCAACAGGCTTAAGCAATGTCATATTAAGGTGATGACCTGCAATATCCAGAGGA 501
 Db 421 GGCCTCAGCAACAGGCTTAAGCAATGTCATATTAAGGTGATGACCTGCAATATCCAGAGGA 480
 QY 502 ATGTGCAAAAGCTGAAGGACACAGTGAATAAGCTTGGAGAGAGTGAAGATCAAAAGCA 561
 Db 481 ATGTGCAAAAGCTGAAGGACACAGTGAATAAGCTTGGAGAGAGTGAAGATCAAAAGCA 540
 QY 562 TTGAGAACTGATGATTTGCTGTTATGCTCTGAGAAATGCTGCAATTTGACAGAGCAAA 621
 Db 541 TTGAGAACTGATGATTTGCTGTTATGCTCTGAGAAATGCTGCAATTTGACAGAGCAAA 600
 QY 622 GCTGAAAAATGAATTAACCTAACCCCTTTCTGCTGAGAAATTAACAAATTGATGCCCCAA 681
 Db 601 GCTGAAAAATGAATTAACCTAACCCCTTTCTGCTGAGAAATTAACAAATTGATGCCCCAA 660
 QY 682 GCGATTTT 690
 Db 661 GCGATTTT 669

RESULT 13

AAC81773
 ID AAC81773 standard; cDNA, 1177 BP.

AAC81773;

23-FEB-2001 (first entry)

Human GIL-19/AE289 protein coding sequence.

Human; GIL-19/AE289; IL-10; interleukin-10; nutrition;
 cell proliferation; immune stimulation; immune suppression;
 haematopoiesis regulation; tissue growth; inflammation; cancer; ss.

Homo sapiens.

WO200065027-A2.

02-NOV-2000.

28-APR-2000; 2000WO-US11479.

28-APR-1999; 99US-0131473.

(GENY) GENETICS INST INC.

Jacobs K, Fouser L, Spaulding V, Xuan D;

WPI; 2000-687325/67.

P-PsDB; AAB36292.

Human GIL-19 protein that shows a high degree of homology to IL
 (interleukin)-10, useful in upregulation of humoral immune responses,
 as an antiinflammatory agent and as a modulator of immune responses
 associated with injury.

Claim 1; Page 59; 60pp; English.

The present invention provides the protein and coding sequences for the
 novel human GIL-19/AE289 protein. The protein shows homology to
 interleukin-10 (IL-10) and is assumed to be a cytokine. It can be used
 in the regulation of cell proliferation and differentiation.
 haematopoiesis, immune stimulation or suppression, tissue growth and

CC tumour inhibition. In addition, it also has uses in the treatment of
 CC inflammation and in nutrition.
 XX Sequence 1177 BP; 362 A; 245 C; 232 G; 338 T; 0 other;

Query Match 97.0%; Score 669; DB 21; Length 1177;
 Best Local Similarity 100.0%; Pred. No. 3.7e-187;
 Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ACAGGTTCCCTTCCCAAGCAGTGTGCTGAGTGAATGTGTGCAATGCGCCGCC 81.
 Db 15 ACAGGTTCCCTTCCCAAGCAGTGTGCTGAGTGAATGTGTGCAATGCGCCGCC 74
 QY 82 TGCAGAAATCTGTAGCTCTTTCTTATGAGGACCTGCGCAACAGCTCCTCTCT 141
 Db 75 TGCAGAAATCTGTAGCTCTTTCTTATGAGGACCTGCGCAACAGCTCCTCTCT 134
 QY 142 TGGCCCTCTTGGTACAGGAGAGAGAGCTGCGCCCAATGCTCCCACTGAGGCTTGACA 201
 Db 135 TGGCCCTCTTGGTACAGGAGAGAGAGCTGCGCCCAATGCTCCCACTGAGGCTTGACA 194
 QY 202 AGTCCCACTTCAGAGAGCCCTATATCACCAACGACCTTCAATGCTGCTGAAGAGGCTA 261
 Db 195 AGTCCCACTTCAGAGAGCCCTATATCACCAACGACCTTCAATGCTGCTGAAGAGGCTA 254
 QY 262 GCTTGCTGATTAACAACAGACAGTTCGCTCATTTGGGAGAACTGTTCCACGAGATCA 321
 Db 255 GCTTGCTGATTAACAACAGACAGTTCGCTCATTTGGGAGAACTGTTCCACGAGATCA 314
 QY 322 GTATGAGTGAAGCGCTGCTATCTGATGAAGAGAGTGTGAACCTTGAAGAGTGC 381
 Db 315 GTATGAGTGAAGCGCTGCTATCTGATGAAGAGAGTGTGAACCTTGAAGAGTGC 374
 QY 382 TGTTCCTCAATCTGATGAGTTCAGAGCTTATGCTGAGAAATGCTGCAATTTGACAGAGCA 441
 Db 375 TGTTCCTCAATCTGATGAGTTCAGAGCTTATGCTGAGAAATGCTGCAATTTGACAGAGCA 434
 QY 442 GGCCTCAGCAACAGGCTTAAGCAATGTCATATTAAGGTGATGACCTGCAATATCCAGAGGA 501
 Db 435 GGCCTCAGCAACAGGCTTAAGCAATGTCATATTAAGGTGATGACCTGCAATATCCAGAGGA 494
 QY 502 ATGTGCAAAAGCTGAAGGACACAGTGAATAAGCTTGGAGAGAGTGAAGATCAAAAGCA 561
 Db 495 ATGTGCAAAAGCTGAAGGACACAGTGAATAAGCTTGGAGAGAGTGAAGATCAAAAGCA 554
 QY 562 TTGAGAACTGATGATTTGCTGTTATGCTCTGAGAAATGCTGCAATTTGACAGAGCAAA 621
 Db 555 TTGAGAACTGATGATTTGCTGTTATGCTCTGAGAAATGCTGCAATTTGACAGAGCAAA 614
 QY 622 GCTGAAAAATGAATTAACCTAACCCCTTTCTGCTGAGAAATTAACAAATTGATGCCCCAA 681
 Db 615 GCTGAAAAATGAATTAACCTAACCCCTTTCTGCTGAGAAATTAACAAATTGATGCCCCAA 674
 QY 682 GCGATTTT 690
 Db 675 GCGATTTT 683

RESULT 14

AAD09719
 ID AAD09719 standard; cDNA; 1116 BP.

AAD09719;

10-SEP-2001 (first entry)

Human cytokine, ZCYTO18 cDNA.

Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;
 cancer; inflammation; gene therapy; chromosome 12; ss.
 Homo sapiens.


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FH Key Location/Qualifiers
FT CDS 21..560
FT /tag= a
FT /product= "Human ZCYTO18 protein #1"
FT sig_peptide 21..119
FT /tag= b
FT /product= "Human mature ZCYTO18 protein #1"
FT mat_peptide 120..557
FT /tag= c
FT /product= "Human mature ZCYTO18 protein #1"
FT CDS 57..560
FT /tag= d
FT /product= "Human ZCYTO18 protein #2"
FT sig_peptide 57..119
FT /tag= e
FT /product= "Human mature ZCYTO18 protein #2"
FT mat_peptide 120..557
FT /tag= f
FT /product= "Human mature ZCYTO18 protein #2"

XX WO200146422-A1.
XX
XX
XX 28-JUN-2001.
XX
XX PF 22-DEC-2000; 2000WO-US35308.
XX
XX PR 23-DEC-1999; 99US-0471767.
XX
XX PR 01-DEC-2000; 2000US-0250841.
XX
XX PA (ZYMO ) ZYMOGENETICS INC.
XX
XX FI Presnell SR, Kindsvogel W,
XX
XX DR WPI; 2001-408648/43.
XX
XX DR P-PSDB; AAB04538, AAB04539.
XX
XX
XX PT Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer -
XX
XX PS Claim 2; Page 140-142; 167pp; English.
XX
XX CC The patent discloses novel human cytokine, ZCYTO18 protein and its
XX corresponding DNA. ZCYTO18 protein induces proliferation of cells
XX expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity
XX in K562 cells. ZCYTO18 DNA is useful for detecting a genetic
XX abnormality in a patient. ZCYTO18 DNA and its antibodies are useful
XX for detecting cancer and inflammation. ZCYTO18 protein is useful for
XX killing cancer cells. It is useful for increasing platelets in a
XX patient or injured tissue. It is also used in gene therapy.
XX CC The present sequence is a cDNA encoding novel human cytokine, ZCYTO18
XX protein. ZCYTO18 DNA is located at the 12q15 region of chromosome 12.
XX
XX SQ Sequence 1116 BP; 336 A; 229 C; 222 G; 329 T; 0 other;

Query Match 92.6%; Score 639; DB 22; Length 1116;
Best Local Similarity 100.0%; Pred. No. 2.6e-178;
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 TCGAGTTAAGATGTGTGCAATGCGCGCCCTGCAGAAATCTGTAGCTCTTCTTATGG 111
DB 1 TCGAGTTAAGATGTGTGCAATGCGCGCCCTGCAGAAATCTGTAGCTCTTCTTATGG 60
QY 112 GGAACCTGGCCACAGCTGCTCTTCTTGTGGCCCTTGTGACAGGAGAGACAGCTG 171
DB 61 GGAACCTGGCCACAGCTGCTCTTCTTGTGGCCCTTGTGACAGGAGAGAGACAGCTG 120
QY 172 CGGCCATCAGCTCCCACTGAGGCTTGACAAGTCCAACTTCCAGACGCCCTATATACCA 231
DB 121 CGGCCATCAGCTCCCACTGAGGCTTGACAAGTCCAACTTCCAGACGCCCTATATACCA 180
QY 232 ACCGACCTTCAGCTGAGGCTAAGAGGCTAGCTTGCTGATTAACAACAGACAGCTGCTC 291
DB 181 ACCGACCTTCAGCTGAGGCTAAGAGGCTAGCTTGCTGATTAACAACAGACAGCTGCTC 240
QY 292 TCATTGGGAGAAACTGTTCACAGGAGTCAAGTGAAGTGAAGCGCTGATCTGATGAAGC 351

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DB 241 TCATTGGGAGAAACTGTTCACAGGAGTCAAGTGAAGTGAAGCGCTGATCTGATGAAGC 300
QY 352 AGTGCTGAACCTTCAACCTTGAAGAAGTGTTCCTCCATCTGATAGTTCAGCCTT 411
DB 301 AGTGCTGAACCTTCAACCTTGAAGAAGTGTTCCTCCATCTGATAGTTCAGCCTT 360
QY 412 ATATGACAGAGGTGGTGGCCCTTCCCTGGCCAGGCTCAGCAAGGCTAAGACATGTCTA 471
DB 361 ATATGACAGAGGTGGTGGCCCTTCCCTGGCCAGGCTCAGCAAGGCTAAGACATGTCTA 420
QY 472 TTGAAGTGAATGACCTGATATCCAGAGAAATGTGCAAAAGCTGAAGACACAGTGA 531
DB 421 TTGAAGTGAATGACCTGATATCCAGAGAAATGTGCAAAAGCTGAAGACACAGTGA 480
QY 532 AGCTTGAAGAGAGTGAAGATCAAAAGCAATTTGAGAACTGATTTGCTTTATGCTC 591
DB 481 AGCTTGAAGAGAGTGAAGATCAAAAGCAATTTGAGAACTGATTTGCTTTATGCTC 540
QY 592 TGAGAAATGCTGCACTTTGACCCAGAGCAAGCTGAAAATGATTAACCTAACCCCTTCC 651
DB 541 TGAGAAATGCTGCACTTTGACCCAGAGCAAGCTGAAAATGATTAACCTAACCCCTTCC 600
QY 652 CTGCTAGAAATPACAAATTGATGCCCCCAAGCGATTTT 690
DB 601 CTGCTAGAAATPACAAATTGATGCCCCCAAGCGATTTT 639

RESULT 15
ID AAF83741 standard; cDNA; 1116 BP.
XX
XX AAF83741;
XX
XX AC 23-JUL-2001 (first entry)
XX
XX DR
XX
XX DE Human IL-TIF polypeptide encoding cDNA.
XX
XX KW Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cyostatic;
XX antirheumatic; antiallergic; antiaschmatic; antialtherosclerotic;
XX immunosuppressive; chromosome 6q24.1-25.2; human; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT CDS 21..560
FT /tag= a
FT /product= "IL-TIF"

XX
XX WO200140467-A1.
XX
XX PN 07-JUN-2001.
XX
XX PD 01-DEC-2000; 2000WO-US32703.
XX
XX PF 03-DEC-1999; 99US-0169049.
XX
XX PR 13-SEP-2000; 2000US-0232219.
XX
XX PR 31-OCT-2000; 2000US-0244610.
XX
XX PA (ZYMO ) ZYMOGENETICS INC.
XX
XX PI Presnell SR, Xu W, Kindsvogel W, Chen Z;
XX
XX DR WPI; 2001-356158/37.
XX
XX DR P-PSDB; AAB62664.
XX
XX PT New soluble cytokine receptor polypeptides and polynucleotides, useful
XX for diagnosing and treating cancer and inflammatory conditions -
XX
XX PS Example 17; Page 193-195; 210pp; English.
XX
XX CC The invention relates to a human cytokine receptor polypeptide,
XX designated zcytor16. The zcytor16 polypeptide can be expressed by
XX standard recombinant methodology and can bind to IL-TIF (undefined). The

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CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
CC or differentiation of hemopoietic cell(s) (progenitors); reducing
CC IL-TIF induced or IL-9 induced inflammation; and suppressing an
CC inflammatory response in a mammal with inflammation. Heteromeric/
CC multimeric receptor polypeptides such as soluble zcytor16/CRP2-4 can be
CC used to reduce progression and symptoms of cancer. Zcytor16 polypeptides
CC can also be used to detect IL-TIF levels which is indicative of
CC pathological conditions including inflammatory states (e.g. rheumatoid
CC arthritis) and cancer. Antibodies that bind zcytor16 polypeptides and the
CC polypeptides themselves are useful for the treatment of inflammation,
CC inflammatory diseases (e.g. infection, asthma, inflammatory bowel
CC disease, rheumatoid arthritis and atherosclerosis) and autoimmune
CC diseases. The antibodies and zcytor16 polynucleotides are also useful
CC for detecting cancer. The present sequence represents a cDNA encoding
CC the human IL-TIF protein.
XX

SO Sequence 1116 BP; 336 A; 229 C; 222 G; 329 T; 0 other;

Query Match 92.6%; Score 639; DB 22; Length 1116;
Best Local Similarity 100.0%; Pred. No. 2.6e-178;
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 TCAGATTAGATTGTCTGCATATGCGCCCTGCAGAAATCTGAGCTCTTCTTATGG 111
DB 1 TCAGATTAGATTGTCTGCATATGCGCCCTGCAGAAATCTGAGCTCTTCTTATGG 60
QY 112 GGACCCCTGGCCACACAGCTGCTCTTCTTCTTGGCCCTCTTGTACAGGAGAGCAGCTG 171
DB 61 GGACCCCTGGCCACACAGCTGCTCTTCTTCTTGGCCCTCTTGTACAGGAGAGCAGCTG 120
QY 172 CGCCCATCAGCTCCCACTGAGGCTTGACAGATCCAACTTCCAGCAGCCCTATATACCA 231
DB 121 CGCCCATCAGCTCCCACTGAGGCTTGACAGATCCAACTTCCAGCAGCCCTATATACCA 180
QY 232 ATCGACCTTCACTGCTGCTTAAGAGGCTAGCTTGGCTGATTAACAACAGAGCTTCGTC 291
DB 181 ACCGACCTTCACTGCTGCTTAAGAGGCTAGCTTGGCTGATTAACAACAGAGCTTCGTC 240
QY 292 TCATTGGGAGAACTGTTCCAGGAGTCAATGATGAGGCGCTGCTATCTGATGAAGC 351
DB 241 TCATTGGGAGAACTGTTCCAGGAGTCAATGATGAGGCGCTGCTATCTGATGAAGC 300
QY 352 AGGTGCTGAATCTCAACCCCTGAAGAGTGTCTTCCCTCAATCTGATAGTTCCAGCTT 411
DB 301 AGGTGCTGAATCTCAACCCCTGAAGAGTGTCTTCCCTCAATCTGATAGTTCCAGCTT 360
QY 412 ATATGACAGAGGTGTGCTCTCTGCGCAGGCTCAGCAACAGGCTAAGCATGTGCATA 471
DB 361 ATATGACAGAGGTGTGCTCTCTGCGCAGGCTCAGCAACAGGCTAAGCATGTGCATA 420
QY 472 TTGAAGGTGATGACTGCATATCCAGAGAAATGTCAAAAAGCTGAAGACACAGTGAATA 531
DB 421 TTGAAGGTGATGACTGCATATCCAGAGAAATGTCAAAAAGCTGAAGACACAGTGAATA 480
QY 532 AGCTTGAAGAGTGAAGATCAAAAGCAATTTGAGAACTGGATTGGCTTTATGTCTC 591
DB 481 AGCTTGAAGAGTGAAGATCAAAAGCAATTTGAGAACTGGATTGGCTTTATGTCTC 540
QY 592 TGAGAAATGCTGCTGATTTGACAGAGCAAAAGCTGAATAATGAATACTAACCCCTTCC 651
DB 541 TGAGAAATGCTGCTGATTTGACAGAGCAAAAGCTGAATAATGAATACTAACCCCTTCC 600
QY 652 CTGCTAGAAATTAACATTTAGATGCCCAAGGATTTT 690
DB 601 CTGCTAGAAATTAACATTTAGATGCCCAAGGATTTT 639

Search completed: July 19, 2003, 09:43:09
Job time : 96.6289 secs

Qy	13	CTTCAGAAAGGTTCTCTCTCCAGTACCAAGTTGCTCGAGTTAAGAAATGTCTGCATG	74
Db	1	CTTCAGAAAGGTTCTCTCTCCAGTACCAAGTTGCTCGAGTTAAGAAATGTCTGCATG	60
Qy	75	GGCGCCCTCAGAAATCTGTAGACCTTCTCTAATGGGGACCCGGCCACAGCTGCTC	134
Db	61	GGCGCCCTCAGAAATCTGTAGACCTTCTCTAATGGGGACCCGGCCACAGCTGCTC	120
Qy	135	CTTCTCTTGAGCCCTCTTGGTACAGGAGAGACAGCTGGCCCATCAGCTCCCATGCAAG	194
Db	121	CTTCTCTTGAGCCCTCTTGGTACAGGAGAGACAGCTGGCCCATCAGCTCCCATGCAAG	180
Qy	195	CTTGACAACTCCAACTTCCAGCAGCCCTAATACAAACGACACTTCATGCTGGCTAAG	254
Db	181	CTTGACAACTCCAACTTCCAGCAGCCCTAATACAAACGACACTTCATGCTGGCTAAG	240
Qy	255	GAGGCTAGCTTGGCTGATTAACAACAACAGCTTGGTCTCATTTGGGGAGAAACTGTTCCAC	314
Db	241	GAGGCTAGCTTGGCTGATTAACAACAACAGCTTGGTCTCATTTGGGGAGAAACTGTTCCAC	300
Qy	315	GGAGTCAGTATAGTAGAGCGCTGCATGTGATGGAAGCAGGTCGAACTTCACCCTTGAA	374
Db	301	GGAGTCAGTATAGTAGAGCGCTGCATGTGATGGAAGCAGGTCGAACTTCACCCTTGAA	360
Qy	375	GAAGTGCTTTTCCCTCAATCTGATAGTGTCCAGCCTTAATATGACAGAGTGTCCTTC	434
Db	361	GAAGTGCTTTTCCCTCAATCTGATAGTGTCCAGCCTTAATATGACAGAGTGTCCTTC	420
Qy	435	CTGGCCAGGCTCAGCAACAGCGTAAAGCATGTCAATTTGAAGGTGATGACTGCAATATC	494
Db	421	CTGGCCAGGCTCAGCAACAGCGTAAAGCATGTCAATTTGAAGGTGATGACTGCAATATC	480
Qy	495	CAGAGGAATGTGCCAAAACCTGAAGACACATGTGAAAAAAGCTTGGAGAGAGTGGAGATC	555
Db	481	CAGAGGAATGTGCCAAAACCTGAAGACACATGTGAAAAAAGCTTGGAGAGAGTGGAGATC	540
Qy	555	AAAGCAATTTGAGAACTGGATTTTGGTTATGTCTCGAAGAAATGCGCTGCATTTGACCA	614
Db	541	AAAGCAATTTGAGAACTGGATTTTGGTTATGTCTCGAAGAAATGCGCTGCATTTGACCA	600
Qy	615	GAGCAAAAGCTGAAAAATGATTACTAACCCCTTTTCCCTGCTAGAAATTAACAATTAGATG	674
Db	601	GAGCAAAAGCTGAAAAATGATTACTAACCCCTTTTCCCTGCTAGAAATTAACAATTAGATG	660
Qy	675	CCCAAAAGGATTTT 690	
Db	661	CCCAAAAGGATTTT 676	

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RESULT 3
US-10-063-588-153
; Sequence 153, Application US/10063588
; Publication No. US20030130483A1
GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,588
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 153
; LENGTH: 1152
; TYPE: DNA

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ORGANISM: Homo Sapien
US-10-063-588-153

Query Match 98.0%; Score 676; DB 14; Length 1152;
Best Local Similarity 100.0%; Pred. No. 9.1e-206;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 CTTCAAGACAGGTTCTCTCCCTCCAGTCAACAGTTCTGAGTTAGAAATTGTGCAATG 74
1 CTTCAAGACAGGTTCTCTCCCTCCAGTCAACAGTTCTGAGTTAGAAATTGTGCAATG 60
75 GCGGCGCTTCAAGAAATCTGAGCTTTTCTTATGAGGAGCCCTGGCCACCGAGTCCCTC 134
61 GCGGCGCTTCAAGAAATCTGAGCTTTTCTTATGAGGAGCCCTGGCCACCGAGTCCCTC 120
135 CTTCTCTTGGCCCTCTTGTATACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
121 CTTCTCTTGGCCCTCTTGTATACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
195 CTTGACAACTCCAACTTCCAGCAGCCCTTATATCACCACCGACCTTCAATGCTGCTAAG 254
181 CTTGACAACTCCAACTTCCAGCAGCCCTTATATCACCACCGACCTTCAATGCTGCTAAG 240
255 GAGGCTAGCTTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 314
241 GAGGCTAGCTTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
315 GAGGCTAGCTTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 374
301 GAGGCTAGCTTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
375 GAGGCTAGCTTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 434
361 GAGGCTAGCTTGGCTGATTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
435 CTTGCGCAGGCTCAGCAACAGGCTTACACATGCTATTAAGAGAGAGAGAGAGAGAGAG 494
421 CTTGCGCAGGCTCAGCAACAGGCTTACACATGCTATTAAGAGAGAGAGAGAGAGAGAG 480
495 CAGAGAAATGTGCAAAAGCTGAAGACACAGTGAAGAAAGCTTGGAGAGAGAGAGAGAG 554
481 CAGAGAAATGTGCAAAAGCTGAAGACACAGTGAAGAAAGCTTGGAGAGAGAGAGAGAG 540
555 AAAGCAATGTGAAGAACTGATTTGCTGTTATGCTCTGAGAAATGCTGCAATTTGACCA 614
541 AAAGCAATGTGAAGAACTGATTTGCTGTTATGCTCTGAGAAATGCTGCAATTTGACCA 600
615 GAGCAAAAGCTGAAGAAATGAAATACTAACCCCTTCTGCTGGAATAAATGATGATG 674
601 GAGCAAAAGCTGAAGAAATGAAATACTAACCCCTTCTGCTGGAATAAATGATGATG 660
675 CCCCCAAGGATTTT 690
661 CCCCCAAGGATTTT 676.

RESULT 4

US-10-006-867-153
Sequence 153, Application US/10006867
Publication No. US20020119130A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Geriltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1

CURRENT APPLICATION NUMBER: US/10/006.867
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/063435
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/064215
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/087759
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PRIOR APPLICATION NUMBER: 60/088021
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PRIOR APPLICATION NUMBER: 60/088734
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5	PRIOR FILING DATE: 1998-09-10
6	PRIOR APPLICATION NUMBER: 60/100627
7	PRIOR FILING DATE: 1998-09-16
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14	PRIOR APPLICATION NUMBER: 60/101279
15	PRIOR FILING DATE: 1998-09-22
16	PRIOR APPLICATION NUMBER: 60/101475
17	PRIOR FILING DATE: 1998-09-23
18	PRIOR APPLICATION NUMBER: 60/101758
19	PRIOR FILING DATE: 1998-09-24
20	PRIOR APPLICATION NUMBER: 60/101783
21	PRIOR FILING DATE: 1998-09-24
22	PRIOR APPLICATION NUMBER: 60/101916
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25	PRIOR FILING DATE: 1998-09-30
26	PRIOR APPLICATION NUMBER: 60/103449
27	PRIOR FILING DATE: 1998-10-06
28	PRIOR APPLICATION NUMBER: 60/103678
29	PRIOR FILING DATE: 1998-10-08
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38	PRIOR APPLICATION NUMBER: 60/105881
39	PRIOR FILING DATE: 1998-10-27
40	PRIOR APPLICATION NUMBER: 60/106030
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49	PRIOR FILING DATE: 1998-12-15
50	PRIOR APPLICATION NUMBER: 60/112422
51	PRIOR FILING DATE: 1998-12-15
52	PRIOR APPLICATION NUMBER: 60/112853
53	PRIOR FILING DATE: 1998-12-16
54	PRIOR APPLICATION NUMBER: 60/113011
55	PRIOR FILING DATE: 1998-12-16
56	PRIOR APPLICATION NUMBER: 60/112854
57	PRIOR FILING DATE: 1998-12-16
58	PRIOR APPLICATION NUMBER: 60/113300
59	PRIOR FILING DATE: 1998-12-22
60	PRIOR APPLICATION NUMBER: 60/113408
61	PRIOR FILING DATE: 1998-12-22
62	PRIOR APPLICATION NUMBER: 60/113430
63	PRIOR FILING DATE: 1998-12-23
64	PRIOR APPLICATION NUMBER: 60/113621
65	PRIOR FILING DATE: 1998-12-23
66	PRIOR APPLICATION NUMBER: 60/114223
67	PRIOR FILING DATE: 1998-12-30
68	PRIOR APPLICATION NUMBER: 60/115614
69	PRIOR FILING DATE: 1999-01-12
70	PRIOR APPLICATION NUMBER: 60/116537
71	PRIOR FILING DATE: 1999-01-20

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1 PRIOR APPLICATION NUMBER: 60/116843
2 PRIOR FILING DATE: 1999-01-22
3 PRIOR APPLICATION NUMBER: 60/119285
4 PRIOR FILING DATE: 1999-02-09
5 PRIOR APPLICATION NUMBER: 60/119287
6 PRIOR FILING DATE: 1999-02-09
7 PRIOR APPLICATION NUMBER: 60/119525
8 PRIOR FILING DATE: 1999-02-10
9 PRIOR APPLICATION NUMBER: 60/119549
10 PRIOR FILING DATE: 1999-02-10
11 PRIOR APPLICATION NUMBER: 60/120014
12 PRIOR FILING DATE: 1999-02-11
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16 PRIOR FILING DATE: 1999-04-16
17 PRIOR APPLICATION NUMBER: 60/131291
18 PRIOR FILING DATE: 1999-04-27
19 PRIOR APPLICATION NUMBER: 60/138387
20 PRIOR FILING DATE: 1999-06-09
21 PRIOR APPLICATION NUMBER: 60/144791
22 PRIOR FILING DATE: 1999-07-20
23 PRIOR APPLICATION NUMBER: 60/169495
24 PRIOR FILING DATE: 1999-12-07
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26 PRIOR FILING DATE: 2000-01-11
27 PRIOR APPLICATION NUMBER: 60/191007
28 PRIOR FILING DATE: 2000-03-21
29 PRIOR APPLICATION NUMBER: 60/199397
30 PRIOR FILING DATE: 2000-04-25
31 PRIOR APPLICATION NUMBER: 09/380139
32 PRIOR FILING DATE: 1998-08-25
33 PRIOR APPLICATION NUMBER: 09/311832
34 PRIOR FILING DATE: 1999-05-14
35 PRIOR APPLICATION NUMBER: 09/380137
36 PRIOR FILING DATE: 1999-08-25
37 PRIOR APPLICATION NUMBER: 09/380138
38 PRIOR FILING DATE: 1999-08-25
39 PRIOR APPLICATION NUMBER: 09/380142

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Query Match	Similarity	98.0%: Score	676: DB 15: Length	1152:
Matches	676: Conservative	100.0%: Pident	NO. 9.1e-206: Indels	0: Gaps
Qy	15	CTTCAGAACAGAGTTCCTCCCTCCAGTCACCAAGTGTCTCGATTAGATTGCTGCAGT	74	
Db	1	CTTCAGAAACAGAGTTCCTCCCTCCAGTCACCAAGTGTCTCGATTAGATTGCTGCAGT	60	
Qy	75	GCCTGCTGCAGAAATCTGTAGCTCTTTCTTATGGGAACTTGGCCACCAAGCTGCTC	134	
Db	61	GCCTGCTGCAGAAATCTGTAGCTCTTTCTTATGGGAACTTGGCCACCAAGCTGCTC	120	
Qy	135	CTTCTCTTTGGCCCTCTTGGTACAGAGGAGACACTGGCCATCAGCTCCCACTGCAGG	194	
Db	121	CTTCTCTTTGGCCCTCTTGGTACAGAGGAGACACTGGCCATCAGTCCCACTGCAGG	180	
Qy	195	CTTACCAAGTCCAACTTCAGAGCCCTATATACCAACCGACCTTATGCTGCTAAG	254	
Db	181	CTTACCAAGTCCAACTTCAGAGCCCTATATACCAACCGACCTTATGCTGCTAAG	240	
Qy	255	GAGGCTAGCTGGCTGGATTAACAACAAGACCTTGCTCATTTGGGAGAAACTGTTCCAC	314	
Db	241	GAGGCTAGCTGGCTGGATTAACAACAAGACCTTGCTCATTTGGGAGAAACTGTTCCAC	300	
Qy	315	GGAGTCAGTATGAGTGAGCGCTGTATCTGATGGAAGCAGGTGCTGAACCTTCAACCTTGA	374	
Db	301	GGAGTCAGTATGAGTGAGCGCTGTATCTGATGGAAGCAGGTGCTGAACCTTCAACCTTGA	360	
Qy	375	GAAGTGCATGTCCTTCATCTGATAGGTTCCAGGCTTATATGCAAGGAGTGTGCTCTTC	434	
Db	361	GAAGTGCATGTCCTTCATCTGATAGGTTCCAGGCTTATATGCAAGGAGTGTGCTCTTC	420	
Qy	435	GTGGCCAGGCTACGACCAACAGGCTAAGCACATGTATGATTAAGAGTGATGACTGTGATTC	494	

Db 421 CTGGCCAGGCTACGCAACGGCTTAAGCATCTATTTGAAGTGATGACCTGCAATTC 480
 QY 495 CAGAGAAATGTCCAAAGCTGGAAGACACAGTGAAGAAAGCTTGAAGAGTGAAGATC 554
 Db 481 CAGAGAAATGTCCAAAGCTGGAAGACACAGTGAAGAAAGCTTGAAGAGTGAAGATC 540
 QY 555 AAAGCAATTTGGAAGAACTGGATTGCTGTTTATGTCTCTGAGAAATGCTGCAATTTGACCA 614
 Db 541 AAAGCAATTTGGAAGAACTGGATTGCTGTTTATGTCTCTGAGAAATGCTGCAATTTGACCA 600
 QY 615 GAGCAAAAGTGAAGAAATGTAATCAACCCCTTCCCTGAGAAATGCAATTAAGATG 674
 Db 601 GAGCAAAAGTGAAGAAATGTAATCAACCCCTTCCCTGAGAAATGCAATTAAGATG 660
 QY 675 CCCCAAGCGATTTT 690
 Db 661 CCCCAAGCGATTTT 676

RESULT 5
 US-10-066-500-125
 Sequence 125, Application US/10066500
 Publication No. US2002017165A1
 GENERAL INFORMATION:
 APPLICANT: Avi J. Ashkenazi
 APPLICANT: Kevin P. Baker
 APPLICANT: David A. Botstein
 APPLICANT: Luc Desnoyers
 APPLICANT: Dan L. Eaton
 APPLICANT: Napoleone Ferrara
 APPLICANT: Sherman Fong
 APPLICANT: Wei-Qiang Gao
 APPLICANT: Hanspeter Gerber
 APPLICANT: Mary E. Gerltsen
 APPLICANT: Audrey Goddard
 APPLICANT: Paul J. Godowski
 APPLICANT: Austin L. Gurney
 APPLICANT: Ivar J. Kljavin
 APPLICANT: Jennie P. Mather
 APPLICANT: Mary A. Napier
 APPLICANT: James Pan
 APPLICANT: Nicholas F. Paoni
 APPLICANT: Margaret Ann Roy
 APPLICANT: Timothy A. Stewart
 APPLICANT: Daniel Tumas
 APPLICANT: Colin K. Watanabe
 APPLICANT: P. Mickey Williams
 APPLICANT: William I. Wood
 APPLICANT: Zemin Zang
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P130R1C7
 CURRENT APPLICATION NUMBER: US/10/066,500
 PRIOR FILING DATE: 2002-02-01
 PRIOR APPLICATION NUMBER: 10/002,796
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: 60/056974
 PRIOR FILING DATE: 1997-08-26
 PRIOR APPLICATION NUMBER: 60/059115
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059263
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/059588
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 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/062816
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 PRIOR APPLICATION NUMBER: 60/063082
 PRIOR FILING DATE: 1997-10-31
 PRIOR APPLICATION NUMBER: 60/063329
 PRIOR FILING DATE: 1997-10-27

PRIOR APPLICATION NUMBER: 60/063733
 PRIOR FILING DATE: 1997-10-29
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/066840
 PRIOR FILING DATE: 1997-11-25
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 PRIOR FILING DATE: 1998-12-08
 PRIOR APPLICATION NUMBER: 09/254311
 PRIOR FILING DATE: 1999-03-03
 PRIOR APPLICATION NUMBER: 09/254460
 PRIOR FILING DATE: 1999-03-09
 PRIOR APPLICATION NUMBER: 09/254465


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1  PRIOR APPLICATION NUMBER: PCT/US99/21090
2  PRIOR FILING DATE: 1999-09-15
3  PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match      98.0%: Score 676; DB 15; Length 1152;
Best Local Similarity 100.0%: Pred. No. 9,1e-206;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      15  CTTGAGAAACAGGTTCTCTCTCCAGTCACAGTCAGTTCGAGTTAGATTGTCTGCATG 74
DB      1  CTTGAGAAACAGGTTCTCTCTCCAGTCACAGTCAGTTCGAGTTAGATTGTCTGCATG 60
OY      75  GCGGCCCTGCGAGAAATCTGTGAGGCTCTTCCCTTAATGSGGAGCCCTGGGACACAGCTGCTC 134
DB      61  GCGGCCCTGCGAGAAATCTGTGAGGCTCTTCCCTTAATGSGGAGCCCTGGGACACAGCTGCTC 120
OY      135  CTTCTCTTTGGCCCTCTTGATACAGGAGAGAGAGCTGCGCCATCAGCTCCCATCTGCAGG 194
DB      121  CTTCTCTTTGGCCCTCTTGATACAGGAGAGAGAGCTGCGCCATCAGCTCCCATCTGCAGG 180
OY      195  CTTGACAAAGTCCAACTTCCAGCAGCCTTATATACCAACCGCACCTTCAATGCTGGCTAAG 254
DB      181  CTTGACAAAGTCCAACTTCCAGCAGCCTTATATACCAACCGCACCTTCAATGCTGGCTAAG 240
OY      255  GAGGCTAGCTGGCTGATTAACAACACAGAGCTTGCTCATTTGGGGAGAACTGTTCCAC 314
DB      241  GAGGCTAGCTGGCTGATTAACAACACAGAGCTTGCTCATTTGGGGAGAACTGTTCCAC 300
OY      315  GGAAGTCAGTATGATGATGAGCGCTGCTATCTGATGAAAGAGAGTGTGAACCTTACCCCTTGA 374
DB      301  GGAAGTCAGTATGATGATGAGCGCTGCTATCTGATGAAAGAGAGTGTGAACCTTACCCCTTGA 360
OY      375  GAAATGCTGTTCCCTCATCTGATAGGTTCCAGCTTATATGACAGAGAGTGAGGCCCTTC 434
DB      361  GAAATGCTGTTCCCTCATCTGATAGGTTCCAGCTTATATGACAGAGAGTGAGGCCCTTC 420
OY      435  CTGGCCAGAGCTCAGCAACAGGCTAAGACATGTCATATTGAAGTGTATGACCTGCATATC 494
DB      421  CTGGCCAGAGCTCAGCAACAGGCTAAGACATGTCATATTGAAGTGTATGACCTGCATATC 480
OY      495  CAGAGGAATGTGCAAAAGCTGAAAGACACAGTGAATAAGCTTGGAGAGAGTGGAGATATC 554
DB      481  CAGAGGAATGTGCAAAAGCTGAAAGACACAGTGAATAAGCTTGGAGAGAGTGGAGATATC 540
OY      555  AAACCAATTGGAGAACTGATTTGCTTTATGCTCTGTGAATAAGCTTCATTTGACCA 614
DB      541  AAACCAATTGGAGAACTGATTTGCTTTATGCTCTGTGAATAAGCTTCATTTGACCA 600
OY      615  GAGCAAAAGCTGAAATAAGTAATACTAACCCCCCTTCCCTGCTAGAAATTAACAATTAGATG 674
DB      601  GAGCAAAAGCTGAAATAAGTAATACTAACCCCCCTTCCCTGCTAGAAATAACAATTAGATG 660
OY      675  CCCCCAAGCGATTTT 690
DB      661  CCCCCAAGCGATTTT 676

RESULT 6
US-10-063-547-153
1 Sequence 153, Application US/10063547
2 Publication No. US20020182638A1
3 GENERAL INFORMATION:
4 APPLICANT: Eaton, Dan L.
5 APPLICANT: Filvaroff, Ellen
6 APPLICANT: Gerritsen, Mary E.
7 APPLICANT: Goddard, Audrey
8 APPLICANT: Godowski, Paul J.
9 APPLICANT: Grimaldi, Christopher J.
10 APPLICANT: Guiney, Austin L.
11 APPLICANT: Macanabe, Colin K.
12 APPLICANT: Wood, William I.
13 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
14 TITLE OF INVENTION: ACIDS ENCODING THE SAME

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FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-10
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 153
LENGTH: 1152
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-547-153

Query Match 98.0%; Score 676; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 9.1e-206; Indels 0; Gaps 0;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 15 CTTGAGAACAGGTTCTCTCCCTCCAGTCACAGTTGCTGAGTTAGATTGCTGCAATG 74
DB 1 CTTGAGAACAGGTTCTCTCCCTCCAGTCACAGTTGCTGAGTTAGATTGCTGCAATG 60
QY 75 GCCGCCCTGACAGAAATCTGTAGCTCTTTCTTATGGGAAACCTGGCCACAGCTGCTC 134
DB 61 GCCGCCCTGACAGAAATCTGTAGCTCTTTCTTATGGGAAACCTGGCCACAGCTGCTC 120
QY 135 CTTCTCTGGCCCTCTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
DB 121 CTTCTCTGGCCCTCTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 195 CTTGACAAAGTCCCACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254
DB 181 CTTGACAAAGTCCCACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 255 GAGGCTAGCTGTGCTGATTAACAACAACAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 314
DB 241 GAGGCTAGCTGTGCTGATTAACAACAACAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 315 GAGTCAAGTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 374
DB 301 GAGTCAAGTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 375 GAGGCTAGCTGTGCTGATTAACAACAACAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
DB 361 GAGGCTAGCTGTGCTGATTAACAACAACAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 435 CTTGCGCAGGCTCAGCAACAAGGCTTAAGCAATGCTATTTGAAGTATGACCTGCAATC 494
DB 421 CTTGCGCAGGCTCAGCAACAAGGCTTAAGCAATGCTATTTGAAGTATGACCTGCAATC 480
QY 495 CAGAGAAATGTGCAAAAAGCTGAAGAGACAGAGTGAAGAAAGCTTGGAGAGAGAGATC 554
DB 481 CAGAGAAATGTGCAAAAAGCTGAAGAGACAGAGTGAAGAAAGCTTGGAGAGAGAGATC 540
QY 555 AAAGCAATTGGAAGAACTGGAATTGCTGTTATGCTCTGAGAAATCCGCAATTGACCA 614
DB 541 AAAGCAATTGGAAGAACTGGAATTGCTGTTATGCTCTGAGAAATCCGCAATTGACCA 600
QY 615 GAGCAAAAGCTGAATAATGATACTAACCCCTTTCCCTGCTAGAATAACAATTAGATG 674
DB 601 GAGCAAAAGCTGAATAATGATACTAACCCCTTTCCCTGCTAGAATAACAATTAGATG 660
QY 675 CCCCAAAAGGATTTT 690
DB 661 CCCCAAAAGGATTTT 676
```

RESULT 7
US-10-063-616-153
Sequence 153, Application US/10063616
Publication No. US2003013855A1
GENERAL INFORMATION:
APPLICANT: Baton, Dan L.
APPLICANT: Rilyarov, Elen
APPLICANT: Geritlsen, Mary E.
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,616
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 153
LENGTH: 1152
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-616-153

Query Match 98.0%; Score 676; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 9.1e-206; Indels 0; Gaps 0;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 15 CTTGAGAACAGGTTCTCTCCCTCCAGTCACAGTTGCTGAGTTAGATTGCTGCAATG 74
DB 1 CTTGAGAACAGGTTCTCTCCCTCCAGTCACAGTTGCTGAGTTAGATTGCTGCAATG 60
QY 75 GCCGCCCTGACAGAAATCTGTAGCTCTTTCTTATGGGAAACCTGGCCACAGCTGCTC 134
DB 61 GCCGCCCTGACAGAAATCTGTAGCTCTTTCTTATGGGAAACCTGGCCACAGCTGCTC 120
QY 135 CTTCTCTGGCCCTCTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
DB 121 CTTCTCTGGCCCTCTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 195 CTTGACAAAGTCCCACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254
DB 181 CTTGACAAAGTCCCACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 255 GAGGCTAGCTGTGCTGATTAACAACAACAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 314
DB 241 GAGGCTAGCTGTGCTGATTAACAACAACAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 315 GAGTCAAGTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 374
DB 301 GAGTCAAGTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 375 GAGGCTAGCTGTGCTGATTAACAACAACAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
DB 361 GAGGCTAGCTGTGCTGATTAACAACAACAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 435 CTTGCGCAGGCTCAGCAACAAGGCTTAAGCAATGCTATTTGAAGTATGACCTGCAATC 494
DB 421 CTTGCGCAGGCTCAGCAACAAGGCTTAAGCAATGCTATTTGAAGTATGACCTGCAATC 480
QY 495 CAGAGAAATGTGCAAAAAGCTGAAGAGACAGAGTGAAGAAAGCTTGGAGAGAGAGATC 554
DB 481 CAGAGAAATGTGCAAAAAGCTGAAGAGACAGAGTGAAGAAAGCTTGGAGAGAGAGATC 540
QY 555 AAAGCAATTGGAAGAACTGGAATTGCTGTTATGCTCTGAGAAATCCGCAATTGACCA 614
DB 541 AAAGCAATTGGAAGAACTGGAATTGCTGTTATGCTCTGAGAAATCCGCAATTGACCA 600
QY 615 GAGCAAAAGCTGAATAATGATACTAACCCCTTTCCCTGCTAGAATAACAATTAGATG 674
DB 601 GAGCAAAAGCTGAATAATGATACTAACCCCTTTCCCTGCTAGAATAACAATTAGATG 660
QY 675 CCCCAAAAGGATTTT 690
DB 661 CCCCAAAAGGATTTT 676
```

RESULT 8
US-10-063-502-153

Sequence 153, Application US/10063502
Publication No. US20030023042A1
GENERAL INFORMATION:
APPLICANT: Eacra, Dan L.
APPLICANT: Filveroff, Ellen
APPLICANT: Geriltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,502
PRIORITY FILING DATE: 2002-05-01
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 153
LENGTH: 1152
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-502-153

Query Match 98.0%; Score 676; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred No. 9.1e-206; Indels 0; Gaps 0;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 CTTGAGACAGGTTCTCTCCAGTCAAGTCTGAGTTAGATTGCTGCATG 74
1 CTTGAGACAGGTTCTCTCCAGTCAAGTCTGAGTTAGATTGCTGCATG 60
75 GCGCCCTGCAAAAATCTGTGAGCTTTTCTTATGGGACCTGSCCAACAGTCTC 134
61 GCGCCCTGCAAAAATCTGTGAGCTTTTCTTATGGGACCTGSCCAACAGTCTC 120
135 CTTCTTTGGCCCTCTTGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 194
121 CTTCTTTGGCCCTCTTGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
195 CTTGACAGTCCAACTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 254
181 CTTGACAGTCCAACTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
255 GAGGCTAGCTTGGCTATTAACAACAACAAGCTTCTGATGGGAGAACTGTTCCAC 314
241 GAGGCTAGCTTGGCTATTAACAACAACAAGCTTCTGATGGGAGAACTGTTCCAC 300
315 GGAGTCAGTATGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 374
301 GGAGTCAGTATGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
375 GAAGTCTGTTCCCTCAATCTGATAGTTCCAGCCTTATATGAGAGGAGGAGGAGG 434
361 GAAGTCTGTTCCCTCAATCTGATAGTTCCAGCCTTATATGAGAGGAGGAGGAGG 420
435 CTGGCCAGGCTCAGCAACAGGCTTAAGCATGTCAATATGAAAGTATGACCTGATATC 494
421 CTGGCCAGGCTCAGCAACAGGCTTAAGCATGTCAATATGAAAGTATGACCTGATATC 480
495 CAGAGGAATGTGCAAAAAGTGAAGACACAGTGAAGAAAGCTTGGAGAGGAGTGAAGATC 554
481 CAGAGGAATGTGCAAAAAGTGAAGACACAGTGAAGAAAGCTTGGAGAGGAGTGAAGATC 540
555 AAAGCAATTTGAGAACTGATTTGCTGTTATGCTCTGAGAAATGCTGCAATTGACCA 614
541 AAAGCAATTTGAGAACTGATTTGCTGTTATGCTCTGAGAAATGCTGCAATTGACCA 600
615 GAGCAAAAGTGAATAAATGATTAATCAATCAATCAATCAATCAATCAATCAATGATG 674
601 GAGCAAAAGTGAATAAATGATTAATCAATCAATCAATCAATCAATCAATGATG 660

QY 675 CCCCCAAGGATTTT 690
DB 661 CCCCCAAGGATTTT 676
RESULT 9
US-10-227-884-243
Sequence 243, Application US/10227884
Publication No. US20030027988A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Geriltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C79
CURRENT APPLICATION NUMBER: US/10/227,884
PRIORITY FILING DATE: 2002-08-26
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 10/119,480
SEQ ID NO 119
LENGTH: 1152
TYPE: DNA
ORGANISM: Homo Sapien
US-10-227-884-243

PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/095302
 PRIOR FILING DATE: 1998-08-04
 PRIOR APPLICATION NUMBER: 60/095318
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 PRIOR APPLICATION NUMBER: 60/095916
 PRIOR FILING DATE: 1998-08-10
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 PRIOR FILING DATE: 1999-11-16
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 PRIOR FILING DATE: 1999-12-07
 PRIOR APPLICATION NUMBER: 60/169495
 PRIOR FILING DATE: 1999-12-07
 PRIOR APPLICATION NUMBER: 60/169835

Query Match 98.0%; Score 676; DB 15; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 9.1e-206;
 Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGACAGATTCTCTCCGACGACAGGTCCTCGAGTATGATGCTGCAATG 74
 DB 1 CTTGAGACAGATTCTCTCCGACGACAGGTCCTCGAGTATGATGCTGCAATG 60
 QY 75 GCCGCCCTGCAGAAATGTGTAGGCTCTTCTTATGAGGACCTGGCCACGAGCTGCTC 134
 DB 61 GCCGCCCTGCAGAAATGTGTAGGCTCTTCTTATGAGGACCTGGCCACGAGCTGCTC 120

PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 09/114844
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: 09/136801
PRIOR FILING DATE: 1998-08-19
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PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/202088
PRIOR FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: 09/254311
PRIOR FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: 09/254460
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PRIOR APPLICATION NUMBER: 09/254465
PRIOR FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: 09/284663
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 09/332928
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PRIOR APPLICATION NUMBER: 09/548815
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 09/664610
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PRIOR APPLICATION NUMBER: 09/665350
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PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/767609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/808689
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/866028
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PRIOR FILING DATE: 2001-06-01
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PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: PCT/US98/14552
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: PCT/US98/18824
PRIOR FILING DATE: 1998-09-10

PRIOR APPLICATION NUMBER: PCT/US98/19093
PRIOR FILING DATE: 1998-09-14
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PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR FILING DATE: 1998-09-17
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PRIOR FILING DATE: 1998-12-01
PRIOR APPLICATION NUMBER: PCT/US98/25190
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28301

Query Match 98.0%; Score 676; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 9, 1e-206;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 CTTGAGAAACAGGTTCTTCTCCCACTGACCAAGTCTGAGTAAATTTGTGAATG 74
1 CTTGAGAAACAGGTTCTTCTCCCACTGACCAAGTCTGAGTAAATTTGTGAATG 60
75 GCGGCGCTGAGAAATCTGAGACTTTTCTTATGAGGACCTTGCCACCACTGCTC 134
61 GCGGCGCTGAGAAATCTGAGACTTTTCTTATGAGGACCTTGCCACCACTGCTC 120
135 CTTCTCTTGCCCTCTTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 194
121 CTTCTCTTGCCCTCTTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
195 CTTGAGCAAGTCCCACTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 254
181 CTTGAGCAAGTCCCACTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
255 GAGGCTAGCTTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 314
241 GAGGCTAGCTTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
315 GAGGCTAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 374
301 GAGGCTAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
375 GAGGCTAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 434
361 GAGGCTAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
435 CTTGCGCAGGCTGAGCAACAGGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 494
421 CTTGCGCAGGCTGAGCAACAGGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
495 CAGAGGATGTGCAAAAGCTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 554
481 CAGAGGATGTGCAAAAGCTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
555 AAAGCAATTGAGAACTGAGATTGCTTTATGCTTGAATGCTGCAATTTTGCA 614
541 AAAGCAATTGAGAACTGAGATTGCTTTATGCTTGAATGCTGCAATTTTGCA 600
615 GAGCAAGCTGAGAAATGAACTAATCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 674
601 GAGCAAGCTGAGAAATGAACTAATCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660

OY 675 CCCCAAGCATTTT 690
Db 661 CCCCAAGCATTTT 676
RESULT 11
US-10-066-273-125
Sequence 125, Application US/10066273
Publication No. US20030032062A1
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerltsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kljavin
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3130R1C2
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
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PRIOR APPLICATION NUMBER: 60/062885
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
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PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066840
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PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25

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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/095998
PRIOR FILING DATE: 1998-08-10
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 PRIOR APPLICATION NUMBER: PCT/US99/20594
 PRIOR FILING DATE: 1999-09-08
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 98.0%; Score 676; DB 15; Length 1152;

Best Local Similarity 100.0%; Pred. No. 9,1e-206; Indels 0; Gaps 0;

Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 75 GCCGCCCTGCGAAGATCTGTAGAGTCTTTCTTATGGGACCCGCGCCAGCTGCTC 134

DB 61 GCCGCCCTGCGAAGATCTGTAGAGTCTTTCTTATGGGACCCGCGCCAGCTGCTC 120
 QY 135 CTTCTCTTGGCCCTCTTGTGTAACAGGAGAGAGCTGCGCCATCACTCTCCACTGCAAG 194
 DB 121 CTTCTCTTGGCCCTCTTGTGTAACAGGAGAGAGCTGCGCCATCACTCTCCACTGCAAG 180
 QY 195 CTTGACAGTCACCTTCCAGGAGCCCTATATACCAACCGGACCTTCATGCTGGGCTAAG 254
 DB 181 CTTGACAGTCACCTTCCAGGAGCCCTATATACCAACCGGACCTTCATGCTGGGCTAAG 240
 QY 255 GAGGCTAGCTTGGCTGATATAACACAGACGTTGCTCTCATTTGGGAGAACTGTTCCAC 314
 DB 241 GAGGCTAGCTTGGCTGATATAACACAGACGTTGCTCTCATTTGGGAGAACTGTTCCAC 300
 QY 315 GAGTCAGTATGAGTAGAGCGCTGCTATCTGATGAGCAGGCTGTAACCTTCACTTGA 374
 DB 301 GAGTCAGTATGAGTAGAGCGCTGCTATCTGATGAGCAGGCTGTAACCTTCACTTGA 360
 QY 375 GAGTCGCTGTTCCCTCAATCTGATAGTTCACCTTATATGAGAGGCTGTCCTTC 434
 DB 361 GAGTCGCTGTTCCCTCAATCTGATAGTTCACCTTATATGAGAGGCTGTCCTTC 420
 QY 435 CTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCATATTGAAGTATGATGATCATATC 494
 DB 421 CTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCATATTGAAGTATGATGATCATATC 480
 QY 495 CAGAGGATGTGCAAAAGCTGAAAGACACAGTGAAGAAAGCTTGAAGAGTGAAGATC 554
 DB 481 CAGAGGATGTGCAAAAGCTGAAAGACACAGTGAAGAAAGCTTGAAGAGTGAAGATC 540
 QY 555 AAGCAATTGGAACATGATTTGCTGTTTATATGCTCTGAGAAATGCTTCGATTTGACCA 614
 DB 541 AAGCAATTGGAACATGATTTGCTGTTTATATGCTCTGAGAAATGCTTCGATTTGACCA 600
 QY 615 GAGCAAGCTGAAGAAATGAATACTAACCCCTTCCCTGCTGAATAATCAATTAGATG 674
 DB 601 GAGCAAGCTGAAGAAATGAATACTAACCCCTTCCCTGCTGAATAATCAATTAGATG 660
 QY 675 CCCCAGGCGATTTT 690
 DB 661 CCCCAGGCGATTTT 676

RESULT 12
 US-10-066-494-125
 Sequence 125, Application US/1006494
 Publication No. US20030032063A1
 GENERAL INFORMATION:
 APPLICANT: Avi J. Ashkenazi
 APPLICANT: Kevin P. Baker
 APPLICANT: David A. Boerslein
 APPLICANT: Luc Desnoyers
 APPLICANT: Dan L. Eaton
 APPLICANT: Napoleone Ferrara
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 APPLICANT: Ivar J. Kljavin
 APPLICANT: Jennie P. Mather
 APPLICANT: Mary A. Napier
 APPLICANT: James Pan
 APPLICANT: Nicholas F. Paoni
 APPLICANT: Margaret Ann Roy
 APPLICANT: Timothy A. Stewart
 APPLICANT: Daniel Tumas
 APPLICANT: Colin K. Watanabe
 APPLICANT: P. Mickey Williams
 APPLICANT: William I. Wood
 APPLICANT: Zemin Zhang

* TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 * TITLE OF INVENTION: ACIDS ENCODING THE SAME
 * FILE REFERENCE: P3130RIC9
 * CURRENT APPLICATION NUMBER: US/10/066,494
 * CURRENT FILING DATE: 2002-02-01
 * PRIOR APPLICATION NUMBER: 10/002,796
 * PRIOR FILING DATE: 2001-11-15
 * PRIOR APPLICATION NUMBER: 60/056974
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63	PRIOR APPLICATION NUMBER: 60/169835

Query Match	98.0%;	Score 676;	DB 15;	length 1152;
Best Local Similarity	100.0%;	Pred. No. 9.1e-206;		
Matches 676;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 13 CTTGAGAAAGGTTCTCTCTTCCCAAGTCACCAAGTTGCTCGAGTTAGAAATGTCTGCATG 74
DB 1 CTTGACAAAGGTTCTCTCTTCCCAAGTCACCAAGTTGCTCGAGTTAGAAATGTCTGCATG 60
QY 75 GCCGACCTGCACAAATCTGTAGAGCTCTTCTTATGGGGAACCTGGGCACACAGCTGCCTC 134

Db 61 |CCCCCCTGCGAAGATCTGTAGCTCTTCTTATGGGAGCCCTGGCCACGAGCTGCTC 120
Qy 135 |CTTCTCTTGGCCCTCTTGGTACAGGAGAGAGAGCTGGCCATCAGTCTCCATCGCAGG 194
Db 121 |CTTCTCTTGGCCCTCTTGGTACAGGAGAGAGAGCTGGCCATCAGTCTCCATCGCAGG 180
Qy 195 |CTTACAGTCCACTTCCAGCAGCCCTATATCAACACCCGACCTTATAGTGGCTAG 254
Db 181 |CTTACAGTCCACTTCCAGCAGCCCTATATCAACACCCGACCTTATAGTGGCTAG 240
Qy 255 |GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTGGCTTGGGAGAACTGTTCCAC 314
Db 241 |GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTGGCTTGGGAGAACTGTTCCAC 300
Qy 315 |GAGCTAGTATAGTAGAGCGCTGTATCTGATGAAGCAGTGTGAACCTTGAAC 374
Db 301 |GAGCTAGTATAGTAGAGCGCTGTATCTGATGAAGCAGTGTGAACCTTGAAC 360
Qy 375 |GAGTGTCTTCTCTCTCAATCTGATAGTTCAGGCTTATATGACAGAGTGTGCTTC 434
Db 361 |GAGTGTCTTCTCTCTCAATCTGATAGTTCAGGCTTATATGACAGAGTGTGCTTC 420
Qy 435 |CTGGCCAGGCTCAGCAAGAGCTAAGCAATGTCAATTTGAAGTGAAGTGTGATATC 494
Db 421 |CTGGCCAGGCTCAGCAAGAGCTAAGCAATGTCAATTTGAAGTGTGATATC 480
Qy 495 |CAGAGGAATGTGCAAAAGCTGAGAGACAGTGAAGAAAGCTTGGAGAGTGAAGATC 554
Db 481 |CAGAGGAATGTGCAAAAGCTGAGAGACAGTGAAGAAAGCTTGGAGAGTGAAGATC 540
Qy 555 |AAAGCAATTTGAGAACTGATTTGTGTTATGTCTCTGAGAAATGCTGTGATTTGACA 614
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Qy 675 |CCCCAAGCGATTTT 690
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RESULT 14

US-10-066-269-125

Sequence 125, Application US/10066269

Publication No. US20030040014A1

GENERAL INFORMATION:

APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
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APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kjaerav
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood

APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3130R1C4
CURRENT APPLICATION NUMBER: US/10/066,269
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
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Query Match 98.0%; Score 676; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 9; le-206;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GCGGCGTCGAGAAATCTGTAGCTTTTCTTATAGGGGACCTTGCCACCGCTGCTTC 120
QY 135 CTTCTTTGGCCCTCTTGTATACAGGAGAGAGAGCTGGCCATCAGCTCCCACTGCAGG 194
DB 121 CTTCTTTGGCCCTCTTGTATACAGGAGAGAGAGCTGGCCATCAGCTCCCACTGCAGG 180
QY 195 CTTGACAAAGTCACTTCCAGCAGCTTATATACAAACCGACCTTCACTGCTGAAG 254
DB 181 CTTGACAAAGTCACTTCCAGCAGCTTATATACAAACCGACCTTCACTGCTGAAG 240
QY 255 GAGGCTAGCTTGGCTGATTAACAACAACAGCTTCTCATTTGGGAGAAATGTTTCCAC 314
DB 241 GAGGCTAGCTTGGCTGATTAACAACAACAGCTTCTCATTTGGGAGAAATGTTTCCAC 300
QY 315 GGAGTCAGTATAGAGAGAGAGAGCTGATATGATGAAGAGAGTGTCAACTTCACTTGA 374
DB 301 GGAGTCAGTATAGAGAGAGAGAGCTGATATGATGAAGAGAGTGTCAACTTCACTTGA 360
QY 375 GAAGTGTCTTCCCTCAATCTGATAGTTTCCAGCTTATATGACAGAGGTGTCCTTC 434
DB 361 GAAGTGTCTTCCCTCAATCTGATAGTTTCCAGCTTATATGACAGAGGTGTCCTTC 420
QY 435 CTGGCCAGGCTCAGCAACAGGCTAAGCAATGTCATATTGAAGGTGATGACTGATATC 494
DB 421 CTGGCCAGGCTCAGCAACAGGCTAAGCAATGTCATATTGAAGGTGATGACTGATATC 480
QY 495 CAGAGGAATGTCAGAAAGCTGAAGAGACAGTGAAGAAAGCTTGGAGAGTGAAGATC 554
DB 481 CAGAGGAATGTCAGAAAGCTGAAGAGACAGTGAAGAAAGCTTGGAGAGTGAAGATC 540
QY 555 AAAGCAATTGAGAACTGATTTGCTTTATATGCTCTGAGAAATGCTGCAATTGACCA 614
DB 541 AAAGCAATTGAGAACTGATTTGCTTTATATGCTCTGAGAAATGCTGCAATTGACCA 600
QY 615 GAGCAAGCTGAAAAATGAAATTAAGTAAAGCCCTTCTGCTAGAAATTAAGTATG 674

Db 601 GAGCAAGCTGTAATACTAACCCCTTCCCTGCTGATAATTAAGATG 660
QY 675 CCCCCAAGCATTTT 690
Db 661 CCCCCAAGCATTTT 676

RESULT 15

US-10-066-211-125

Sequence 125, Application US/10066211

Publication No. US20030044844A1

GENERAL INFORMATION:

APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerltsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kjaev
APPLICANT: Jennie P. Mather
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APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P130R1C8
CURRENT APPLICATION NUMBER: US/10/066,211
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
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Query March 98.0%; Score 676; DB 15; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 9.1e-206; Indels 0; Gaps 0;
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 QY 135 CTTCTCTGAGCCCTCTGTGTAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
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 Db 181 CTTGACAACTGCACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
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 QY 315 GAGGCTAGTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 374
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 QY 375 GAGGCTGCTGCTCTCAATCTGATGATGATGATGATGATGATGATGATGATG 434
 Db 361 GAGGCTGCTGCTCTCAATCTGATGATGATGATGATGATGATGATGATGATG 420
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 QY 495 CAGAGAAATGTGCAAAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 554
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 Db 661 CCCCAGGAGATTTT 676

Search completed: July 20, 2003, 03:46:02
 Job time: 99.6244 secs

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Qy 361 ACTTCACCCCTTGAAGAAGTGTCTTCTCCATCTGATAGGTTCCAGGCTTAATATGCAGG 4200

Dp 361 ACTTCACCCCTTGAAGAAGTGTCTTCTCCATCTGATAGGTTCCAGGCTTAATATGCAGG 4200

Qy 421 AGGTGTGTCCTTCTCTGGCCAGGCTTCAGCAAGGCTAAGACATATCATATTAATGAAGTG 4800

Dp 421 AGGTGTGTCCTTCTCTGGCCAGGCTTCAGCAAGGCTAAGACATATCATATTAATGAAGTG 4800

Qy 481 ATGACTCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGACACAGTGAAGAAAGCTTGGAG 5400

Dp 481 ATGACTCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGACACAGTGAAGAAAGCTTGGAG 5400

Qy 541 AGAGTGGAGAGATCCAAAGCAATTGGAGAACTGGAATTTCTGTTATGTCTCTGAGAAATG 6000

Dp 541 AGAGTGGAGAGATCCAAAGCAATTGGAGAACTGGAATTTCTGTTATGTCTCTGAGAAATG 6000

Qy 601 CCTGCATTTGACCCAGAGCAAACTGTGAATAATGAATTAACCCCTTTTCCCTGCTAGAA 6600

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RESULT 2
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; Sequence 24, Application US/09354243B
Date: 09/01/2012

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GENERAL INFORMATION:
APPLICANT: Dumontier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides
TITLE OF INVENTION: (Tifs)
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 28
LENGTH: 690
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
IS-09-354-243B-24

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QY	61	AATTGCTGCAATGGCGCGCCCTGCGAATCTGAGACTCTTTTCCTTATGGGAGCCTGAG	120
Db	61	AATTGCTGCAATGGCGCGCCCTGCGAATCTGAGACTCTTTTCCTTATGGGAGCCTGAG	120
QY	121	CCACCAAGCTGCTCTCTTTCTTTGGCCCTCTTGGTACAGGAGGAGCAGCTGCGCCCATCA	180
Db	121	CCACCAAGCTGCTCTCTTTCTTTGGCCCTCTTGGTACAGGAGGAGCAGCTGCGCCCATCA	180
QY	121	GCATCCACTGACGGCTTGACAAAGTCCAACTTCACGACGCGCTTATTCACCAACCGGACT	240
Db	181	GCTCCCACTGACGGCTTGACAAAGTCCAACTTCACGACGCGCTTATTCACCAACCGGACT	240
QY	241	TATAGCTGAGCTAAGGAGGCTAGCTTGGCTGTATTAACAACAGAGCTTTGCTCTATTGGGG	300

Db 241 TCATGCTGGCTAAGGAGGCTAGCTTGGCTGATTAACAACACACAGCGTTCCGTCATTGGGG 3000

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Db 481 ATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAGAAAGCTTGGAG 540

Qy 541 AGAGTGAAGAGATCAAGCAATGTGAGAACTGATTTGGCTGTTATGTCTCGAGAAATG 600

Db 541 AGAGTGAAGAGATCAAGCAATGTGAGAACTGATTTGGCTGTTATGTCTCGAGAAATG 600

Qy 601 CCTGCATTTGACCAAGCAAAAGCTGAAAAATGAATTAACCTACCCCTTCCCTGCTAGAA 660

Db 601 CCTGCATTTGACCAAGCAAAAGCTGAAAAATGAATTAACCTACCCCTTCCCTGCTAGAA 660

Qy 661 ATTAACAATTAGATGCCCAAAAGCAATTTT 690

Db 661 ATTAACAATTAGATGCCCAAAAGCAATTTT 690

RESULT 3
US-09-178-973B-7
Sequence 7 Analysis: no/00170073B

```

: Sequence 7, Application US/09178973B
: Patent No. 6274710
: GENERAL INFORMATION:
: APPLICANT: Dumontier, Laure
: APPLICANT: Louned, Yamila
: TITLE OF INVENTION: Retnaud, Jean-Christophe
: TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
: TITLE OF INVENTION: (Tifs)
: TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
: FILE REFERENCE: LUD 5543
: CURRENT APPLICATION NUMBER: US/09/178,973B
: CURRENT FILING DATE: 1998-10-26
: NUMBER OF SEQ ID NOS: 17
: SEQ ID NO 7
: LENGTH: 1119
: TYPE: DNA
: ORGANISM: Mus musculus
: US-09-178-973B-7

```

Query Match	59.3%	Score	409.2	DB	4	Length	1119
Best Local Similarity	76.1%	Pred. No.	7.5e-113				
Matches	504	Conservative	0	Mismatches	158	Indels	0
						Gaps	0

Qy	29	CTCTTCCCCAGTCAACAGTTGCTCTGAGTAATGTCTGCAATGGCCGCCCTGCAGAA	88
Db	9	CTCTCTCTCACTTATCAACTGTTGACACTTGTGGAGATCTGTATGGCTGTCTGCAGAA	68
Qy	89	ATTCTGAGACTCTTTTCTTATATGGGAGACCTTGGCCACCAAGTGTCTCTTCTTTGGCCCT	148
Db	69	ATCTAAGATTTTTCCTTATATGGGAGACTTTGGCCGCGCAGCTGCTGTCTTCATGTCCCT	128
Qy	149	CTTGTATACGGGAGAGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGCAAGTCCAA	208
Db	129	GTGGGCGCCAGAGGCAATATGCCCTGCCCTCAACCCGGGTGCAAGCTTATAGTGTCCAA	188
Qy	209	CTTCCAGACGCCCTTATATCAACCAACCGCACTTATATGTGTGCTAAGAGGCTAGCTTGGC	268
Db	189	CTTCCAGACGCCGTCATATCTCAACCGCACTTTATATGTGGCCCAAGAGGCTCAGCTTGC	248

QY 2,9 TGATACACACAGAGCTTCTCTCTATTTGGGAGAAAGCTTCCAGAGAGTCAGTATGAG 328
DB 249 AGATACACACAGAGCTTCTCTCTATTTGGGAGAAAGCTTCCAGAGAGTCAGTATGAG 308
QY 329 TGAGGCTGCTATCTGATGAGAGAGAGTGTGAACTTCAACCTTGAAGAAGTCTGCTCC 388
DB 309 AGATCAGTCTACCTGATGAGAGAGTGTGAACTTCAACCTTGAAGAAGTCTGCTCC 368
QY 389 TCAATCTGATAGTGTCCAGAGCTTATATGAGAGAGTGTGCTTCTCTGAGAGTCTGAG 448
DB 369 CCAGTCAGACAGAGTGTCCAGAGCTTATGAGAGAGTGTGCTTCTCTGAGAGAGTCTGAG 428
QY 449 CAACAGGCTAAGCAGATGATGATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 508
DB 429 CAATCAGCTCAGCTCTCTGATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 488
QY 509 AAAGCTGAGAGACAGAGTGTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 568
DB 489 AAAGCTGAGAGAGAGAGTGTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 548
QY 569 ACTGATTTGCTGTTTATGTCCTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 628
DB 549 ACTGACCTGCTGTTTATGTCCTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 608
QY 629 AATGATTAAGTAAACCCCTTCCCTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 688
DB 609 AAGGAGAGAGTGTCT 668
QY 689 TT 690
DB 669 TT 670

RESULT 4
US-09-419-568F-7

Sequence 7, Application US/09419568F
Patent No. 6331613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
TITLE OF INVENTION: (Tifs) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 7
LENGTH: 1119
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-419-568F-7

Query Match 59.3%; Score 409.2; DB 4; Length 1119;
Best Local Similarity 76.1%; Pred. No. 7.5e-113;
Matches 504; Conservative 0; Mismatches 158; Indels 0; Gaps 0;
QY 29 CTCCTTCCCACTACAGAGTGTCTGAGATTGATGCAATGAGCCGCCCTGAGAA 88
DB 9 CTCCTCTCACTATCAACTGTGACACTGTGACATCTGATGAGTGTGCTGCTGAGAA 68
QY 89 ACTGTGAGCTCTTTCTTATGAGGAGCCCTGAGCCAGCACTGCTCTCTCTGAGCCCT 148
DB 69 ATCTAAGAGTTTTCCTTATGAGGAGCTTTGAGCCGCACTGCTCTCTCTCTCTCTCT 128
QY 149 CTGTGAGAGAGGAGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 208
DB 129 GTGGAGCCAGAGAGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 188

QY 209 CTCACAGAGCCCTATATCAACCAACGACCTTATGCTGCTTAAGAGAGTCTGAGC 268
DB 189 CTCACAGAGCCCTATATCAACCAACGACCTTATGCTGCTTAAGAGAGTCTGAGC 248
QY 269 TGATACACACAGAGCTTCTCTCTATTTGGGAGAAAGCTTCCAGAGAGTCAGTATGAG 328
DB 249 AGATACACACAGAGCTTCTCTCTATTTGGGAGAAAGCTTCCAGAGAGTCAGTATGAG 308
QY 329 TGAGGCTGCTATCTGATGAGAGAGTGTGAACTTCAACCTTGAAGAAGTCTGCTCC 388
DB 309 AGATCAGTCTACCTGATGAGAGAGTGTGAACTTCAACCTTGAAGAAGTCTGCTCC 368
QY 389 TCAATCTGATAGTGTCCAGAGCTTATATGAGAGAGTGTGCTTCTCTGAGAGTCTGAG 448
DB 369 CCAGTCAGACAGAGTGTCCAGAGCTTATGAGAGAGTGTGCTTCTCTGAGAGAGTCTGAG 428
QY 449 CAACAGGCTAAGCAGATGATGATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 508
DB 429 CAATCAGCTCAGCTCTCTGATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 488
QY 509 AAAGCTGAGAGACAGAGTGTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 568
DB 489 AAAGCTGAGAGAGAGAGTGTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 548
QY 569 ACTGATTTGCTGTTTATGTCCTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 628
DB 549 ACTGACCTGCTGTTTATGTCCTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 608
QY 629 AATGATTAAGTAAACCCCTTCCCTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 688
DB 609 AAGGAGAGAGTGTCT 668
QY 689 TT 690
DB 669 TT 670

RESULT 5
US-09-354-243B-7

Sequence 7, Application US/09354243B
Patent No. 6359117
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
TITLE OF INVENTION: (Tifs) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 7
LENGTH: 1119
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-354-243B-7

Query Match 59.3%; Score 409.2; DB 4; Length 1119;
Best Local Similarity 76.1%; Pred. No. 7.5e-113;
Matches 504; Conservative 0; Mismatches 158; Indels 0; Gaps 0;
QY 29 CTCCTTCCCACTACAGAGTGTCTGAGATTGATGCAATGAGCCGCCCTGAGAA 88
DB 9 CTCCTCTCACTATCAACTGTGACACTGTGACATCTGATGAGTGTGCTGCTGAGAA 68
QY 89 ACTGTGAGCTCTTTCTTATGAGGAGCCCTGAGCCAGCACTGCTCTCTCTGAGCCCT 148
DB 69 ATCTAAGAGTTTTCCTTATGAGGAGCTTTGAGCCGCACTGCTCTCTCTCTCTCTCT 128

Oy	149	CTTGGTAA	CAGGGAGAG	CAGCTGCGCCCA	TCAGCTCCCA	CTGGAGGCTTGA	CAAAAGTCAA	208
Db	129	GTGGGCCCA	GAGGCGAA	ATGCGCTGCCCGCTCA	CAACCCGGGTCA	AGCTTTGAGGTGCCAA	188	
Oy	209	CTTCAGACAG	CCCTTATATACCA	CAACCCGCA	CTTCATGCTAGCTAGGAGGCTA	GCTTGTGC	268	
Db	189	CTTCAGACAG	CCGTCATGTC	CAACCGGCA	CTTTATGTGTGGCCAA	GAGGCCAGCCCTTGC	248	
Oy	269	TGATTAACA	CACAGACGTT	CGTCTCATTTGGGGAGAA	CTGTTCACAGGAGTCA	GTATGAG	328	
Db	249	AGATTAACA	CACAGACGTC	CGGCTCATTCGGGGAGAA	CTGTTCAGGAGTCA	GTCTAA	308	
Oy	329	TGAGGCGTGC	TCATTCGATAGACAGG	TGCTGAACCTCACCCCTTGA	AGAAAGTGTGTTCCC	388		
Db	309	AGATAGTGCTCA	TCGTGATAGACAGG	TGCTCAACCTTCAGGAGAC	CTTTGCTCCC	368		
Oy	389	TCAATCTGAT	AGGTTCCACGCTTATAT	TGACAGAGGTGTGTGCCCTTC	CTGGCCAGGCTCAG	448		
Db	369	CCAGTCAGAC	AGGTTCCAGCCCTA	CATGACAGAGGTGTGTACCTTCT	CTGACCAAACTCAG	428		
Oy	449	CACACGGCTA	AGCAGTCATATTTGAA	GGTGATGACTTCGATATTC	CAAGAGATGTCA	508		
Db	429	CAATCAGCTCA	GCCTCTGTCACATCAG	CGGGTGCACAGAACATCCAGAA	GAATGTCA	488		
Oy	509	AAAGCTGAAG	GCACAGTGA	AAAGCTTGGAGAGATGAGATCA	AAAGCAATTTGAGA	568		
Db	489	AAAGCTGAAG	GCAGACGTGA	AAAGCTTGGAGAGATGAGATCA	AAAGCGATTTGGGA	548		
Oy	569	ACTGATTTG	CTGTTATGTCTCTG	GAATAGTGCCTCATTTGAC	CGAGCAAAAGCTGAAA	628		
Db	549	ACTGACCTG	CTGTTATGTCTCTG	GAATATGCTTGCCTCTGAG	CGAAGAAAGCTTGA	608		
Oy	629	AATGAATA	CTAACCCCTTTCC	TGCTAGAAATACAAATT	AGATCCCCCAAGCAYTT	688		
Db	609	AACGAAGA	ACTCTCTCTCTCTCT	CTTA	AAAAAGACAAAT	AGATCCCTGAATGAC	668	
Oy	689	TT	690					
Db	669	TT	670					

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RESULT 6
US-09-178-973B-9
: Sequence 9, Application US/09178973B
: Patent No. 6274710
:
: GENERAL INFORMATION:
: APPLICANT: Dumoutier, Laure
: APPLICANT: Louhed, Jamila
: TITLE OF INVENTION: Renaud, Jean-Christophe
: TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factors
: TITLE OF INVENTION: (Tifs)
: FILE REFERENCE: LUD 5543
: CURRENT APPLICATION NUMBER: US/09/178, 973B
: CURRENT FILING DATE: 1998-10-26
: NUMBER OF SEQ ID NOS: 17
: SEQ ID NO 9
: LENGTH: 1111
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-178-973B-9

```

Query Match	59.1%	Score 407.6	DB 4	Length 1111
Best Local Similarity	76.0%	Pred. No. 2.2e-112		
Matches 503	Conservative 0	Mismatches 159	Indels 0	Gaps 0

QY	29	CTCCTCCCAAGTCAACAGTTGCTGAGTTAGATTGTCTGCATAGGCCGCCCTGCACAA	88
DB	7	CTCTCCTCTCAGTATCAACTTTGACACTGTGGAGTCGGATGGCTGCTCTCAGAA	66
QY	89	ATTGTGATGCTTTTCTTATGGGACCCCTGGCCACGACGTCCTCTTCTTGGCCTT	148

Db	67	ATCATATGAGTTTTCCTTATGAGGAACTTGGGCCCGCCAGCTCCTGCTTCAATGACCTT	126
OY	149	CTTGATACAGGAGAGAGACGCTGGGCCCATACAGCTCCACTGACAGGCTTGACAAATGCCAA	208
Db	127	GTTGGGCCAGAGAGGAAATATGCGCTGCCCATCAACCCGGTGTCAAGCTTGAGGTGTCCAA	186
OY	209	CTTCAGCAGAGCCCTATATCACCACCCGACCTTCATGCTGCTGAAGAGGCTAGTTGGC	268
Db	187	CTTCAGAGAGCCGTACATGTGTCAACCGACCTTTATGTGTGGCCAGAGAGCCAGCCTTGC	246
OY	269	TGATPACAAACAAGCGTTCCGTCTCATTTGGGGGAAACTGTTCCACGAGTCAGTATGAG	328
Db	247	AGATPACAAACAAGCGTCCGGCTCATCGGGGAAACTGTTCCGAGGAGTCAGTCTAA	306
OY	329	TGAGGGCGCATCTGATGAAAGAGAGTGTGAACCTTCAACCTGSAAGAAGTGTGTTCCC	388
Db	307	GGATCAGTGTCACTCGATGAAAGCAGAGTGTCACTTCACTTCGAGAAACATTTGCTCCC	366
OY	389	TCAATCTGATAGTTCCAGCCTTATATGACAGAGGTGTGTGCCCTTCCTGGCCAGGCTCAG	448
Db	367	CCAGTCAGACAGGTTCCGGGCCCTAATCAGAGAGGTGTGTGCCCTTCTTACCAAATCCAG	426
OY	449	CAACAGGCTAAGCACATGTCAATTGAAAGTGTACCTGCATATCCAGAGGATGTGCA	508
Db	427	CAATCAGTCAAGCTCTCTCTCAATCAGTGTGTACCAACAGCAATCCACAAAGATGTCA	486
OY	509	AAAGCTGAAGACACAGTGAAGAAAGCTGTGAGAGGTGTGAGAGATCAAGCAATTGGAG	568
Db	487	AAGCTGAAGAGACAGTGAAGAAAGCTGTGAGAGGCGAGAGATCAAGGCAATCCGGGA	546
OY	569	ACTGGATTGTGCTTTATGTCTGTGAGAAATGCTGCATTTTACCAGAGCAAGCTGA	628
Db	547	ACTGGACCTGTGTTTATGTCTGTGAGAAATGCTTGGCTGTGAGGAGAAAGAGCTAGAA	606
OY	629	AATGATATACATACCCCTTTCCCTGCTAGAAATACAAATTGATGCCCAAGCATTT	688
Db	607	AACGAGAACTGTCTCTCTGCTCTTAAAAAGAAACAATAGATCCCTGAAATGACATT	666
OY	689	TT 690	
Db	667	TT 668	

```

RESULT 7
US-09-419-568F-9
: Sequence 9, Application US/09419568F
: Patent No. 6331613
: GENERAL INFORMATION:
: APPLICANT: Dumoutier, Laure
: APPLICANT: Louhed, Jamila
: APPLICANT: Renaud, Jean-Christophe
: TITLE OR INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
: TITLE OR INVENTION: (Tfirs) The Proteins Encoded, and Uses Thereof
: FILE REFERENCE: LUD 5543.2
: CURRENT APPLICATION NUMBER: US/09/419,568F
: CURRENT FILING DATE: 1999-10-18
: PRIOR APPLICATION NUMBER: US09/354,243
: PRIOR FILING DATE: 1999-07-16
: PRIOR APPLICATION NUMBER: US09/178,973
: PRIOR FILING DATE: 1998-10-26
: NUMBER OF SEQ ID NOS: 29
: SEQ ID NO 9
: LENGTH: 1111
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
US-09-419-568F-9

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	Query Match	Score	407.6	DB	4	Length	1111
	Best Local Similarity	76.0%	Pred.	No. 2.2e-112			
	Matches	503	Conservative	0	Mismatches	159	Indels
						0	Gaps
							0
29	CTCTCTTCCCGAGTCACCAAGTTGCTCGAGTAGAATTCTTCGCAATGCGCGCCCTTCGACAA	88					

Db 7 CTCCTCCTCAAGTATCAACTTTTGACACTTGTGGCATGGTGATGAGCTGTCTCTGAGAA 66
QY 89 ATCTGTAGAGCTTTTCTTATGAGGACCTGTGGCAACAGACTGTCTCTCTGTGGCCCT 148
Db 67 ATCTATGAGTTTTCCTTATGAGGACCTTGTGGCCGACAGCTGTCTCTCTGTGGCCCT 126
QY 149 CTTGTGACAGGAG 208
Db 127 GTGGGCCCCAG 186
QY 209 CTTGAG 268
Db 187 CTTGAG 246
QY 269 TGATTAACAACAACAAG 328
Db 247 AGATTAACAACAACAAG 306
QY 329 TGAGGAG 388
Db 307 GATCAG 366
QY 389 TCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 448
Db 367 CAGTACAG 426
QY 449 CAACAG 508
Db 427 CAATCAG 486
QY 509 AAAGCTGAAG 568
Db 487 AAGGCTGAAG 546
QY 569 ACTGATTTGCTGTTATGCTGTTATGCTGTTATGCTGTTATGCTGTTATGCTGTTATGCT 628
Db 547 ACTGATTTGCTGTTATGCTGTTATGCTGTTATGCTGTTATGCTGTTATGCTGTTATGCT 606
QY 629 AATGAATACTAACCCCTTTCTCTGCTAGAAATAACAATTAGATCCCAAGCATTT 688
Db 607 AACGAAGAAGCTGCT 666
QY 689 TT 690
Db 667 TT 668
RESULT 8
US-09-354-243B-9
Sequence 9, Application US/09354243B
Patent No. 6359117
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louned, Jamila
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
TITLE OF INVENTION: (Tifs)
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-354-243B-9
Query Match 59.1%; Score 407.6; DB 4; Length 1111;

Best Local Similarity 76.0%; Pred. No. 2,2e-112;
Matches 503; Conservative 0; Mismatches 159; Indels 0; Gaps 0;
QY 29 CTCCTCCCAAGTATCAACTTTTGACACTTGTGGCATGGTGATGAGCTGTCTCTGAGAA 88
Db 7 CTCCTCCTCAAGTATCAACTTTTGACACTTGTGGCATGGTGATGAGCTGTCTCTGAGAA 66
QY 89 ATCTGTAGAGCTTTTCTTATGAGGACCTGTGGCAACAGACTGTCTCTCTGTGGCCCT 148
Db 67 ATCTATGAGTTTTCCTTATGAGGACCTTGTGGCCGACAGCTGTCTCTCTGTGGCCCT 126
QY 149 CTTGTGACAGGAG 208
Db 127 GTGGGCCCCAG 186
QY 209 CTTGAG 268
Db 187 CTTGAG 246
QY 269 TGATTAACAACAACAAG 328
Db 247 AGATTAACAACAACAAG 306
QY 329 TGAGGAG 388
Db 307 GATCAG 366
QY 389 TCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 448
Db 367 CAGTACAG 426
QY 449 CAACAG 508
Db 427 CAATCAG 486
QY 509 AAAGCTGAAG 568
Db 487 AAGGCTGAAG 546
QY 569 ACTGATTTGCTGTTATGCTGTTATGCTGTTATGCTGTTATGCTGTTATGCTGTTATGCT 628
Db 547 ACTGATTTGCTGTTATGCTGTTATGCTGTTATGCTGTTATGCTGTTATGCTGTTATGCT 606
QY 629 AATGAATACTAACCCCTTTCTCTGCTAGAAATAACAATTAGATCCCAAGCATTT 688
Db 607 AACGAAGAAGCTGCT 666
QY 689 TT 690
Db 667 TT 668
RESULT 9
US-09-419-568F-25
Sequence 25, Application US/09419568F
Patent No. 6331613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louned, Jamila
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
TITLE OF INVENTION: (Tifs) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 25
LENGTH: 4797
TYPE: DNA


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; ORGANISM: Homo sapiens
; FEATURE:
US-09-419-568F-25

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Query Match	37.4%	Score 258	DB 4	Length 4797
Best Local Similarity	100.0%	Pred. No. 2.6e-67		
Matches 258; Conservative	0	Mismatches	0	Indels 0
		Gaps	0	

[illegible]

RESULT 10
US-09-354-243B-25

Query Match	37.4%	Score 258;	DB 4;	Length 4797;
Best Local Similarity	100.0%	Pred. No. 2.6e-67;		
Matches 258; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	GGCAAGGAGAAATCTTCAGAAACAGTCTCTCCCTCCAGATCACAGATTGCTCCAGTTAG	60
Dp	1	TGCAGACGCAAACTTTCAGAACAGTCTCTCTCCCAAGTACACAGTTGCTCGAGTTAG	60
QY	61	AATTGTCTGAATGGCGCCCTGCGAAATCTGTAGCTCTTCTTATGGGAGCCCTGG	120
Dp	61	AATGTCTGCAATGGCGCCCTGCGAAATCTGTAGCTCTTCTTATGGGAGCCCTGG	120
QY	121	CCACAGCTGCTCTCTTCTTTGGCCCTTGGTACAGGGAGAGCAAGCTGCGCCATCA	180
Dp	121	CCACAGCTGCTCTCTTCTTTGGCCCTTGGTACAGGGAGAGCAAGCTGCGCCATCA	180
QY	181	GCTCCCACTGAGGCTTGACAAGTCCAACTTCACAGACCCCTATTCACCAACCGGCACT	240
Dp	181	GCTCCCACTGAGGCTTGACAAGTCCAACTTCACAGACCCCTATTCACCAACCGGCACT	240

Oy	241	TCATGCTGGCTAAGGAGG	258
Ub	241	TCATGCTGGCTAAGGAGG	258

RESULT 11
 US-09-178-973B-17
 : Sequence 17, Application US/09178973B
 : Patent No. 6274710
 : GENERAL INFORMATION:
 : APPLICANT: Dumoutier, Laure
 : APPLICANT: Louhed, Jamila
 : APPLICANT: Renaud, Jean-Christophe
 : TITLE OF INVENTION: 'Isolated Nucleic Acid Molecules which Encode T Cell Inducible
 : TITLE OF INVENTION: (Tlrs)
 : FILE REFERENCE: LUD 5543
 : CURRENT APPLICATION NUMBER: US/09/178, 973B
 : CURRENT FILING DATE: 1998-10-26
 : NUMBER OF SEQ ID NOS: 17
 :

Query Match	18.5%	Score 127.6;	DB 4;	Length 5935;
Best Local Similarity	72.2%;	Pred. No. 3e-28;		
Matches 166;	Conservative 0;	Mismatches 64;	Indels 0;	Gaps 0;

QY	22	CTCCCTCCCACTGACAGAGTTGCTGCAGTTGAAATGTCTTGCACAATGGCCGCCCTGCAGAA	88
Db	356	CTCTCCTCTCACTTATCAACTTTTGTACACTTGTGCCATCGGTGATGGCTGTCTTCAGAA	415
QY	89	ATCTGTGAGCTTTTCTTATGTGGGACCCCTGGCCACAGAGTGCTCCTCTTCTTGGGCCCT	148
Db	416	ATCTATGAGTTTTCCTTATGGGGAATTGGCCGACAGTGCTGCTTCTTCAATTGGCCT	475
QY	149	CTTGGTACAGSAGSAGSAGAGCTGGGCCCATGACTGCCACTGCAGGCTTGACAATTCAA	208
Db	476	GTGGGCCCAAGSAGSAGAAATGGCGTGCCTATCAACCCGGTGCAGAGTTGATGGTTCAA	535
QY	209	CTTCCAGAGGCCCTTATACCAACCGACCTTCATCTGGCTTAAGSAGG	258
Db	536	CTTCCAGAGCCCGTACATGTCAACCGACCTTATATCTGGCCCAAGSAGG	585

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; LENGTH: 4797
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-354-243B-25

RESULT 12
US-09-419-568F-29
; Sequence 29, Application US/09419568F
; Patent No. 6331613
; GENERAL INFORMATION:

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Query Match 18.5%; Score 127.6; DB 4; Length 5935;

Best Local Similarity 72.2%; Pred. No. 3e-28;
Matches 166; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 29 CTCCTTCCCAATGACAGTTGCTCGAGTTAGAAATGTCTGCATATGGCCGCCCTGCAGAA 88
Db 356 CTCCTCTCTAGTATATCACTTTTGACACTTGTCCGATCGGTGTGCTGTCTGCAGAA 415
QY 89 ATCTGTAGCTCTTCTCTTAATGGGGACCTGGCCACAGCTGCTCTCTCTTGGGCCCT 148
Db 416 ATCTATAGATTTTTCCTTAATGGGACTTTGGCCGCACTGCTCTCTCTCTATGGCCT 475
QY 149 CTGTGTACAGGAGAGACAGCTGCGCCCATCAGCTCCCATCTGACAGCTTGACAAATCCAA 208
Db 476 GTGGGCCCCAGAGCAATATGCGTCCCATCAACACCCGGTGCAAGCTTGAGGTGTCCAA 535
QY 209 CTTCACAGACCCCTATATCAACCAACCGACCTTCATCTGTGCTTAAGAGG 258
Db 536 CTTCACAGACCCGTAATCGTCAACCGACCTTATGTGTGCCAAGAGG 585

RESULT 13

US-09-354-243B-29
Sequence 29, Application US/09354243B
Patent No. 6359117

GENERAL INFORMATION:

APPLICANT: Dumoutier, Laure

APPLICANT: Louhed, Jamila

APPLICANT: Renaud, Jean-Christophe

TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible P

TITLE OF INVENTION: (TIIFS) The Proteins Encoded, and Uses Thereof

FILE REFERENCE: LUD 5543.1

CURRENT APPLICATION NUMBER: US/09/354,243B

CURRENT FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US09/178,973

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 29

LENGTH: 5935

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

US-09-354-243B-29

Query Match

Best Local Similarity 18.5%; Score 127.6; DB 4; Length 5935;

Matches 166; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 29 CTCCTTCCCAATGACAGTTGCTCGAGTTAGAAATGTCTGCATATGGCCGCCCTGCAGAA 88

Db 356 CTCCTCTCTAGTATATCACTTTTGACACTTGTCCGATCGGTGTGCTGTCTGCAGAA 415

QY 89 ATCTGTAGCTCTTCTCTTAATGGGGACCTGGCCACAGCTGCTCTCTCTTGGGCCCT 148

Db 416 ATCTATAGATTTTTCCTTAATGGGACTTTGGCCGCACTGCTCTCTCTCTATGGCCT 475

QY 149 CTGTGTACAGGAGAGACAGCTGCGCCCATCAGCTCCCATCTGACAGCTTGACAAATCCAA 208

Db 476 GTGGGCCCCAGAGCAATATGCGTCCCATCAACACCCGGTGCAAGCTTGAGGTGTCCAA 535

QY 209 CTTCACAGACCCCTATATCAACCAACCGACCTTCATCTGTGCTTAAGAGG 258

Db 536 CTTCACAGACCCGTAATCGTCAACCGACCTTATGTGTGCCAAGAGG 585

RESULT 14

US-09-178-973B-8

Sequence 8, Application US/09178973B

Patent No. 6274710

GENERAL INFORMATION:

APPLICANT: Dumoutier, Laure

APPLICANT: Louhed, Jamila

APPLICANT: Renaud, Jean-Christophe

TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible

TITLE OF INVENTION: (TIIFS) The Proteins Encoded, and Uses Thereof

FILE REFERENCE: LUD 5543

CURRENT APPLICATION NUMBER: US/09/178,973B

CURRENT FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 8

LENGTH: 7445

TYPE: DNA

ORGANISM: Mus musculus

US-09-178-973B-8

Query Match

Best Local Similarity 18.3%; Score 126; DB 4; Length 7445;

Matches 165; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 29 CTCCTTCCCAATGACAGTTGCTCGAGTTAGAAATGTCTGCATATGGCCGCCCTGCAGAA 88

Db 2034 CTCCTCTCTAGTATATCACTTTTGACACTTGTCCGATCGGTGTGCTGTCTGCAGAA 2093

QY 89 ATCTGTAGCTCTTCTCTTAATGGGGACCTGGCCACAGCTGCTCTCTTGGGCCCT 148

Db 2094 ATCTATAGATTTTTCCTTAATGGGACTTTGGCCGCACTGCTCTCTCTATGGCCT 2153

QY 149 CTGTGTACAGGAGAGACAGCTGCGCCCATCAGCTCCCATCTGACAGCTTGACAAATCCAA 208

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QY 209 CTTCACAGACCCCTATATCAACCAACCGACCTTCATCTGTGCTTAAGAGG 258

Db 2214 CTTCACAGACCCGTAATCGTCAACCGACCTTATGTGTGCCAAGAGG 2263

RESULT 15

US-09-419-568F-8

Sequence 8, Application US/09419568F

Patent No. 6331613

GENERAL INFORMATION:

APPLICANT: Dumoutier, Laure

APPLICANT: Louhed, Jamila

APPLICANT: Renaud, Jean-Christophe

TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible

TITLE OF INVENTION: (TIIFS) The Proteins Encoded, and Uses thereof

FILE REFERENCE: LUD 5543.2

CURRENT APPLICATION NUMBER: US/09/419,568F

CURRENT FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: US09/354,243

PRIOR FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US09/178,973

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 8

LENGTH: 7445

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

US-09-419-568F-8

Query Match

Best Local Similarity 18.3%; Score 126; DB 4; Length 7445;

Matches 165; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 29 CTCCTTCCCAATGACAGTTGCTCGAGTTAGAAATGTCTGCATATGGCCGCCCTGCAGAA 88

Db 2034 CTCCTCTCTAGTATATCACTTTTGACACTTGTCCGATCGGTGTGCTGTCTGCAGAA 2093

QY 89 ATCTGTAGCTCTTCTCTTAATGGGGACCTGGCCACAGCTGCTCTCTTGGGCCCT 148

Db 2094 ATCTATAGATTTTTCCTTAATGGGACTTTGGCCGCACTGCTCTCTCTATGGCCT 2153

QY 149 CTGTGTACAGGAGAGACAGCTGCGCCCATCAGCTCCCATCTGACAGCTTGACAAATCCAA 208

Db 2154 GTGGGCCAGAGGCAATGGCTGCCCCGTCAACACCCGGTGCAAGCTTGAGGTGTCCA 2213
Qy 209 CTTCCAGCAGCCCCCTATATCAACCAACGCGACCTTCATGCTGCTTAAGGAGG 258
Db 2214 CTTCCAGCAGCCGCTACATCGTCAACCGCACCTTTATGCTGGCCAAGGAGG 2263

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Job time : 27.7543 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:03:00 ; Search time 8036.2 Seconds

(without alignments)
17372.171 Million cell updates/sec

Title: US-09-751-797-25

Perfect score: 4797

Sequence: 1 tgcacacagcagaatcttcag.....gatgcacacagcagattttc 4797

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pac:*

7: gb_ph:*

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12: gb_sy:*

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16: em_fun:*

17: em_hum:*

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21: em_or:*

22: em_ov:*

23: em_pac:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_scs:*

28: em_sy:*

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31: em_hcg_hum:*

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34: em_hcg_mus:*

35: em_hcg_pin:*

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39: em_hcg_hum:*

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41: em_hcg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	4740.2	98.8	8393	AF387519	AF387519 Homo sapi
5	4735.4	98.7	133350	AC022511	AC022511 Homo sapi
6	3353.2	69.9	135146	AC087562	AC087562 Pan trogl
7	3023.8	63.0	191111	AC007458	AC007458 Homo sapi
8	686	14.3	7445	AR165227	AR165227 Sequence
9	686	14.3	7445	AR201398	AR201398 Sequence
10	686	14.3	8270	MMU294727	AX459954 Sequence
11	686	14.3	8270	AR165224	AJ294727 Mus muscu
12	650	13.6	5935	AR201417	AR165234 Sequence
13	650	13.6	5935	AX459988	AR201417 Sequence
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ALIGNMENTS

RESULT 1
LOCUS AR201415
DEFINITION Sequence 25 from patent US 6359117.
ACCESSION AR201415
VERSION AR201415.1 GI:20252303
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4797)
AUTHORS Dumoutier,L., Louhed,J. and Renaud,J.-C.
TITLE Isolated nucleic acid molecules which encode T cell inducible factors (TIFs), the proteins encoded, and uses therefor
JOURNAL Patent: US 6359117-A 25 19-MAR-2002;

FEATURES Location/Qualifiers
 source 1..4797 /organism="unknown"
 BASE COUNT 1339 a 910 c 1063 g 1485 t
 ORIGIN
 Query Match 100.0%; Score 4797; DB 6; Length 4797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 TGACACAGCAGATCTTCAGAACAGGTTCTCTCCCACTACACAGTTCCTGAGTTAG 60
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 DB 61 AATTGCTGCAATGCGCCGCTTCAGAAATCTGTAGCTTTCTTATGGGACCTGG 120
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 DB 841 TGACCTTTCTGTTTCCCTTCCACCTGACATGAGAGCGCTGCTATCTGATGAAGCAG 900
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 QY 1321 GCTTGGAATGATTCATTGCTAAGTGTGAGGGAGGAGGATGAGAGAGA 1380
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 DB 1381 ATTGAAGAGAAAGGGAATGGGAAGCTTAAAGTGGTGGGAGGAGACTGT 1440
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 DB 1441 GCCCTGTTGATGATGAGGAGCAACAAATCGAGGCTGTGAACCTTGACCTGTA 1500
 QY 1501 CATTTGAACTATGAAAAAAGTTGAGTGGAGTGGCCCAATTAAGGCTTGAAGACTT 1560
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 QY 1681 GTCTTTCACAAATGCAAACTCAGTAGATTTCCCAAGATGAGAGAGTCTCTGTA 1740
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 QY 1801 TGTGAAATCTAGTCAATGTTGGGCAAAATTAAGAGCTTTAAATCCAGGTAATGT 1860
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 QY 1861 ACTGTAACCTTCATGGGTGAGGATTCATTAAGTTTCAGACAACTTAAGATGTTATG 1920
 DB 1861 ACTGTAACCTTCATGGGTGAGGATTCATTAAGTTTCAGACAACTTAAGATGTTATG 1920
 QY 1921 CTTGTTATGTTTATAGATATTAAGATGAGTGAACCTGCAATCCAGGAAATGGCA 1980
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 QY 1981 AAGCTGAAGACACAGTGAAGAAAGTGAAGTGAATCACTGCAATCTAAGTCAAT 2040
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QY	2161	TATCTAGATGTCAGTTTCCAAATCTTGCAATTGTAGAAATCTAGAACTGGTGGGACT	2220
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DEFINITION AX459972
ACCESSION AX459972
VERSION AX459972.1 GI:21725708
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Dumoutier, L. and Renaud, V.C.
Isolated nucleic acid molecules which encode a cell inducible
factors, or interleukin-21, the proteins encoded, and uses thereof
Patent: WO 0210393-A 26-07-FEB-2002;
JOURNAL LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
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 AUTHORS Dimouliet, L., Van Roost, E., Amez, G., Michaux, L. and Renaud, J.C.
 TITLE IL-1f/IL-22: genomic organization and mapping of the human and mouse genes
 JOURNAL Genes Immun. 1 (8), 488-494 (2000)
 MEDLINE 21069354
 PUBMED 11197690
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 AUTHORS Renaud, J.C.
 TITLE Direct Submission
 JOURNAL Submitted (10-APR-2000) Renaud J.C., UCL 74.59, Ludwig Institute for Cancer Research, Avenue Hippocrate, 74, B-1200 Brussels, BELGIUM
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Query Match	Best Local Similarity	98.8%;	Score 4740.2;	DB 9;	Length 8393;
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Qy 3317 TTTAATCATTTTAAAGAAATCAATTTTCAATTTTGAATGGGTTCCATGTGAAGAGTG 3376
Db 5361 TTTAATCATTTTAAAGAAATCAATTTTCAATTTTGAATGGGTTCCATGTGAAGAGTG 5420
Qy 3377 ATTATGCTTTTCTGTAGCTTCAAGAAAGCAGAGAGGAGAGCAATGTTTCAAGAG 3436
Db 5421 ATTATGCTTTTCTGTAGCTTCAAGAAAGCAGAGAGGAGAGCAATGTTTCAAGAG 5480
Qy 3437 AAGATCAACAGAGAGAACTGTCAAGAGCTGTCTGAATAGAGGTTTGGAGAGCA 3496
Db 5481 AAGATCAACAGAGAGAACTGTCAAGAGCTGTCTGAATAGAGGTTTGGAGAGCA 5540

Qy 3497 TTAATTCCTCTCGTGGGGGTAAAGAGAGAACCGAGGTGGTACTATAATCATGACAG 3556
Db 5541 TTAATTCCTCTCGTGGGGGTAAAGAGAGAACCGAGGTGGTACTATAATCATGACAG 5600
Qy 3557 ACAGTAGGAGACGATTAACCTTTAAATTTCTTTATAGTCTTGGAGCTTTGAGATGAAA 3616
Db 5601 ACAGTAGGAGACGATTAACCTTTAAATTTCTTTATAGTCTTGGAGCTTTGAGATGAAA 5660
Qy 3617 GAATATCTTTTGGGCTTATGTCAAAAGAGATGGAAGGAAAGGCGGAAGAAAGC 3676
Db 5661 GAATATCTTTTGGGCTTATGTCAAAAGAGATGGAAGGAAAGGCGGAAGAAAGC 5720
Qy 3677 AGAAAAAGAAAGAACATGATTAATATAGAGACAAATGATGACAAAGTTTTTCTGAAT 3736
Db 5721 AGAAAAAGAAAGAACATGATTAATATAGAGACAAATGATGACAAAGTTTTTCTGAAT 5780
Qy 3737 AATGCAATATAGATAGATTAGAGAAATTTCTGTAAGGAATGCTTTTCACTGAATGGG 3796
Db 5781 AATGCAATATAGATAGATTAGAGAAATTTCTGTAAGGAATGCTTTTCACTGAATGGG 5840
Qy 3797 TTTCTCTTGATTAAGTTGGAGATCCATCTGATCTGATTTGACTTGGAGAGAGAAAGATG 3856
Db 5841 TTTCTCTTGATTAAGTTGGAGATCCATCTGATCTGATTTGACTTGGAGAGAGAAAGATG 5900
Qy 3857 AATGTAGACCTATATCTGTTTCTATTAATTAAGCAAGTGAAGAAAGCTTATTTGG 3916
Db 5901 AATGTAGACCTATATCTGTTTCTATTAATTAAGCAAGTGAAGAAAGCTTATTTGG 5960
Qy 3917 TATTTTCCCAAAAGTGAAGAACTTTTCTTTTACTGTTTGTCAAAAAGGTGAATAAGA 3976
Db 5961 TATTTTCCCAAAAGTGAAGAACTTTTCTTTTACTGTTTGTCAAAAAGGTGAATAAGA 6020
Qy 3977 AAAAGCCTTATATGATGATGGAATACATGCTCAAAATCTATTAAGTATGATGATTTAA 4036
Db 6021 AAAAGCCTTATATGATGATGGAATACATGCTCAAAATCTATTAAGTATGATGATTTAA 6080
Qy 4037 ATCAGAGTGTCCATCATTTTGGCTTCCCTGAGCAACCTTGAAGAAATGCTTGGTACA 4096
Db 6081 ATCAGAGTGTCCATCATTTTGGCTTCCCTGAGCAACCTTGAAGAAATGCTTGGTACA 6140
Qy 4097 CACATTAATTAACAAAGCAATAGCTGATGAGCTTAAAAAAGTCCATGATTAATCTCATAC 4156
Db 6141 CACATTAATTAACAAAGCAATAGCTGATGAGCTTAAAAAAGTCCATGATTAATCTCATAC 6200
Qy 4157 TGTTTTAAAGAAAGTTTAAATTTCTGTTAGGGTGACTTAAAGCTGCTCGGCCCATGT 4216
Db 6201 TGTTTTAAAGAAAGTTTAAATTTCTGTTAGGGTGACTTAAAGCTGCTCGGCCCATGT 6260
Qy 4217 GCGGCTGTGGGCTGACAGTTGGAACAAGCTCTTATTAAGTATCTGTATAGATGTTT 4276
Db 6261 GCGGCTGTGGGCTGACAGTTGGAACAAGCTCTTATTAAGTATCTGTATAGATGTTT 6320
Qy 4277 GAGGCTGCAAAACAGGCAAGGATATAGGGTGCACTCGGGAATCCCCAGATCCAGACC 4336
Db 6321 GAGGCTGCAAAACAGGCAAGGATATAGGGTGCACTCGGGAATCCCCAGATCCAGACC 6380
Qy 4337 TCACTTCAGTCTCTGCTCTGTGTTAAAGAGGGGTGTCACTCTGCCCCAGCTTTTAA 4396
Db 6381 TCACTTCAGTCTCTGCTCTGTGTTAAAGAGGGGTGTCACTCTGCCCCAGCTTTTAA 6440
Qy 4397 ACAGCTTCATTAAGTGTAGAGTGACCTGAAATATGATGCGGTGGGCTCTCAGGCCA 4456
Db 6441 ACAGCTTCATTAAGTGTAGAGTGACCTGAAATATGATGCGGTGGGCTCTCAGGCCA 6500
Qy 4457 GAGAGCGGTCAATTTAAGCTCTTTGGCAATCAATCAATATCTTAAGGATATTACTATGA 4516
Db 6501 GAGAGCGGTCAATTTAAGCTCTTTGGCAATCAATCAATATCTTAAGGATATTACTATGA 6560
Qy 4517 ATGTTTAACAATATGCTTAAACCTCGGTTCTGTCTCCATCAACCTTAATCTTGAATTTCT 4576
Db 6561 ATGTTTAACAATATGCTTAAACCTCGGTTCTGTCTCCATCAACCTTAATCTTGAATTTCT 6620
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Qy	4577	AATTGTCACATTGAGAAAACATGGCATAAATGCGCAATATCTTTGGATCTTAATTC	4636
Dd	6621	AATTGTCACATTGAGAAAACATGGCATAAATGCGCAATATCTTTGGATCTTAATTC	6686
Qy	4637	ACAGCTTGAGAGAGATGAGAGATCAAGACATTTGGAGAACTGATTTGCTGTTATGTC	4693
Dd	6681	ACAGCTTGAGAGAGATGAGAGATCAAGACATTTGGAGAACTGATTTGCTGTTATGTC	6740
Qy	4697	TCTGAGAAATGCTTGACATTTTGAACAGAGCAAAAGCTGAAAAATGAATTAACAAACCCCTTT	4756
Dd	6741	TCTGAGAAATGCTTGACATTTTGAACAGAGCAAAAGCTGAAAAATGAATTAACAAACCCCTTT	6800
Qy	4757	CCCTGCTGGAATAATCAATTTAGATGCCCAAGACGATTTT	4797
Dd	6801	CCCTGCTGGAATAATCAATTTAGATGCCCAAGACGATTTT	6841
RESULT 5			
AC022511/c			
LOCUS	AC022511	133350 bp	DNA linear PRI 11-JUL-2001
DEFINITION	Human sapiens 12 BAC RP11-71J4 (Roswell Park Cancer Institute Human		
ACCESSION	AC022511		
VERSION	AC022511.22	GI:14665924	
KEYWORDS	HTG.		
ORGANISM	Homo sapiens.		
SOURCE	Homo sapiens		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
AUTHORS	1 (bases 1 to 133350)		
	Muzny,D.M., Adams,C., Adio-Obiola,B., Ali-osman,F.R., Allen,C.,		
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	Zorilla,S., Kuchelapatti,R. and Gibbs,R.		
TITLE	Direct Submission		
JOURNAL	Unpublished		

REFERENCE	2 (bases 1 to 133350)
AUTHORS	Worley, K.C.
TITLE	Direct Submission
JOURNAL	Submitted (05-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	3 (bases 1 to 133350)
AUTHORS	Worley, K.C.
TITLE	Direct Submission
JOURNAL	Submitted (11-JUL-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT	On Jul 11, 2001 this sequence version replaced gi:12656660. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, CDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished) for Human and Mouse sequences. Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES. This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8086/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

```
----- Summary Statistics -----
Config length: 150667
Phrap values in estimate: 149705
Average error rate (BCM-Phrap estimate): 1.52949e-05
Fraction of Phrap values less than 40 : 0.0163588
Number of N's in consensus : 83
0
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Position	Consensus	changing	edit	Edited-Context
7824	catatcatat (n) nmgatcact		catatcatat (g) cgtgatacact	
7825	attatcatatn (n) nmgatcact		attatcatat (t) cgtgatacact	
7826	ttatatatnn (n) nmgatcact		ttatatatgt (g) cgtgatacact	
7827	ttatatatnn (n) gtaatacata		ttatatatgt (g) gtaatacata	
7855	atatataatgc (n) acatttata		atatataatgc (a) acatttata	
8162	agacacacatt (n) tgaagtatgca		agacacacatt (t) tgaagtatgca	
10049	tggagacatc (n) ccttgatgca		tggagacatc (t) ccttgatgca	
10051	ggacatcatc (n) nnnngnnnn		ggacatcatc (t) tgaagtcatg	
10052	ggacatcatcn (n) nnnngnnnn		ggacatcatc (t) tgaagtcatg	

QY	1038	CCGACCTAACCCCTCTCTCCCTCCCTTCCAGAGAGACCCCTTAACCCCAACTCTCTCTCTT	1097
Db	5895	CCGACCTAACCCCTCTCTCCCTCCCTTCCAGAGAGACCCCTTAACCCCAACTCTCTCTCTT	5776
QY	1098	CCCCCTACCCCTTAAGCTAGCAGAGAAAGGTCTCTTGGACGAGGTATATCAGAGTCAATT	1157
Db	5775	CCCCCTACCCCTTAAGCTAGCAGAGAAAGGTCTCTTGGACGAGGTATATCAGAGTCAATT	5716
QY	1158	TGGAGTCATAGAGTATTTGCTTTTGCTTTGACTGAGTCACATCTTGAATTATAGTGTG	1217
Db	5715	TGGAGTCATAGAGTATTTGCTTTTGCTTTGACTGAGTCACATCTTGAATTATAGTGTG	5656
QY	1218	AATGGGGCTCTGGAACCTTAAGTGTACAGAGCCGCAATGGTGTTCCTCGAAAAAGACA	1277
Db	5655	AATGGGGCTCTGGAACCTTAAGTGTACAGAGCCGCAATGGTGTTCCTCGAAAAAGACA	5596
QY	1278	ACTGAGGTGGCTGAAGATGAGAAAAGGTGGG-AAAACATCTGAGCTGGGAATGATC	1336
Db	5595	ACTGAGGTGGCTGAAGATGAGAAAAGGTGGGAAAACATCTGAGTGGAAAAATGATC	5536
QY	1337	CATTGAGCTTAAGTTGTTGAGGGGAGGGGATGCGATGGAGAGAAATTAGAAGAAAGT	1396
Db	5535	CATTGAGCTTAAGTTGTTGAGGGGAGGGGATGCGATGGAGAGAAATTAGAAGAAAGT	5476
QY	1397	GGAATAGGGAAGGCTTAAAGTGGGTGGTGGGTCGGACAGACTGTGCCCTGTGAT	1456
Db	5475	GGAATAGGGAAGGCTTAAAGTGGGTGGTGGGTCGGACAGACTGTGCCCTGTGATCAT	5416
QY	1457	GGGAAGCCACAATAATCGGAGGGCGGTGTACCTTGATGCCGCTGAACTTTGAAACTATGAA	1516
Db	5415	GGGAAGCCACAATAATCGGAGGGCGGTGTACCTTGATGCCGCTGAACTTTGAAACTATGAA	5356
QY	1517	AAAAAGTTTGAGTGAAGTGGGCCCCAGTAAAGAGCCCTTAGACCTACTAGAAGGGCTTAA	1576
Db	5355	AAAAAGTTTGAGTGAAGTGGGCCCCAGTAAAGAGCCCTTAGACCTACTAGAAGGGCTTAA	5296
QY	1577	TTTTCACATGAGATGTTTTATGTATCAATTTCTGTCTTAAGAGCAATTTTCTGGAATA	1636
Db	5295	TTTTCACATGAGATGTTTTATGTATCAATTTCTGTCTTAAGAGCAATTTTCTGGAATA	5236
QY	1637	CGATTGAGGTTTTATTCCTTACAAATTTTGATAACTACCTCGGCTCTTCCCAAAATGC	1696
Db	5235	CGATTGAGGTTTTATTCCTTACAAATTTTGATAACTACCTCGGCTCTTCCCAAAATGC	5176
QY	1697	AAACCTCAGTGAAGATTTCCCAAAATGAGAGAGTCTCTTGAAGGAGATGACTGGAT	1756
Db	5175	AAACCTCAGTGAAGATTTCCCAAAATGAGAGAGTCTCTTGAAGGAGATGACTGGAT	5116
QY	1757	TCTGGCGTCCAGGGAATTCAGAGCTCAGGAAATCTAGGCACTGTTGAATCTAGGTC	1816
Db	5115	TCTGGCGTCCAGGGAATTCAGAGCTCAGGAAATCTAGGCACTGTTGAATCTAGGTC	5056
QY	1817	ATTGTGGGCAAAATTTACTAGAGCTTTAATTCGAGGTAAATGTATCTGTACCTCATGGG	1876
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QY	1877	TGTGGAGGTTATTAAGTTTACAGACAACATTAAGATAGTAAAGCTGTTATGTTTTAT	1936
Db	4995	TGTGGAGGTTATTAAGTTTACAGACAACATTAAGATAGTAAAGCTGTTATGTTTTAT	4936
QY	1937	AGCATATTTGAAGGTATGACCTGCAATTCAGAGAAATGTGCAAAAGCTGAGAGACAG	1996
Db	4935	AGCATATTTGAAGGTATGACCTGCAATTCAGAGAAATGTGCAAAAGCTGAGAGACAG	4876
QY	1997	TGAAAAAGGTAGACTGATTAACCTGTCAATGCTTAAGTCAATGCAATAGAGAGACAAATGT	2056
Db	4875	TGAAAAAGGTAGACTGATTAACCTGTCAATGCTTAAGTCAATGCAATAGAGAGACAAATGT	4816
QY	2057	GTTTTTCTTCTCTTCTTCTTCCCATCACTTGATGATTTTCACTTGATCTCTCAACA	2116
Db	4815	GTTTTTCTTCTCTTCTTCTTCCCATCACTTGATGATTTTCACTTGATCTCTCAACA	4756
QY	2117	CCAGGCGCATTACTTTGGTGTCTGTGTATGTAGATATATCTATATCTAGATGTCAATT	2176

[illegible]

Db 3675 ACAGGATGCTTTACATCTTGTAAATAATTCATCTTCTGTTGTCT 3616
 Qy 3257 TTAGAAAAGTGAAGTGAAGAGAGAAATCTCATGATCTGTGTATTTTCAAGACC 3316
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 Qy 3737 AATGCAAAATGATATATATAGAGAAATTCAGTAAAGAAATCTTTTCACTGAAATTTGG 3796
 Db 3135 AATGCAAAATGATATATATAGAGAAATTCAGTAAAGAAATCTTTTCACTGAAATTTGG 3076
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 Qy 3977 AAAAGCTTATGTTTGGTGAATACATGTTCAAAAGTCAATTTGAGTAAAGTATTTAA 4036
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 Db 2775 CACATAAATATACAGAAATACATGATGAGCTTAAAGTCAATGATTAATCTATAC 2716
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 Db 2235 ACAGCTTGGAGAGAGTGGAGAGATCAAGCAATGAGAGATGAGATTTGCTTTATGTC 2176
 Qy 4697 TCTGAAATGCTGCTGATTTGACACAGCAAGCTGAAAAATGAATTAATCAACCCCTTT 4756
 Db 2175 TCTGAAATGCTGCTGATTTGACACAGCAAGCTGAAAAATGAATTAATCAACCCCTTT 2116
 Qy 4757 CCTGCTGAAATTAACATTAATGATGCCCCAAGCGATTTT 4797
 Db 2115 CCTGCTGAAATTAACATTAATGATGCCCCAAGCGATTTT 2075

RESULT 6

AC087562/c 135146 bp DNA linear HTG 19-OCT-2001
 AC087562 Pan troglodytes clone RP43-74117, WORKING DRAFT SEQUENCE, 31
 LOCUS unnumbered pieces.

ACCESSION AC087562
 VERSION AC087562.4 GI:14190648
 KEYWORDS HTG, HTGS, PHASE1, HTGS_DRAFT.
 SOURCE Pan troglodytes

ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.

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 Hollins, B., Homsi, F., Howard, S., Huber, J., Hui, S., Hume, J.,
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homimidae; Homo.
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 Gorrell, L.L., Hernandez, J., Issar, A., Jackson, L., Kneitz, S.,
 Kondeljewska, N., Lau, S., Leal, B., Lee, E., Lichtarge, O., Liu, W.,
 Logan, O., Lu, J., Matrondel, I., Martinez, C., Mercher, S., Miller, A.,
 Montgomery, K., Oswal, G., Pampell, L.R., Parish, B.J., Perez, L.,
 Rashid, N.D., Rives, C., Scherer, S.E., Shen, H., Shim, C., Simon, M.,
 Vo, O., Williamson, A., Worley, K.C., Xiang, A.M., Yang, R., Yu, W.,
 Zhou, X., Kuchnerlpati, R., Nelson, D., Nickerson, E. and Gibbs, R.A.
 Direct Submission
 Submitted (31-JUL-1999) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 4 (bases 1 to 191111)
 Worley, K.C.
 Direct Submission
 Submitted (03-AUG-1999) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 191111)
 Worley, K.C.
 Direct Submission
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 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 6 (bases 1 to 191111)
 Worley, K.C.
 Direct Submission
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 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 7 (bases 1 to 191111)
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 Direct Submission
 Submitted (16-MAY-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 COMMENT On Jul 31, 1999 this sequence version replaced gi:5230396.

INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES: SSRs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSSs, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, published) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-3) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

Summary Statistics

Contig length:	151624
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Average error rate (BCM-Phrap estimate):	0.000165522
Fraction of Phrap values less than 40 :	0.020725
Number of consensus changing edits:	5
Number of N's in consensus :	0

----- Consensus changing editors

Position	Original+Context	Edited+Context
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123710	tcttcataat (n) tggttatcag	tcttcataat (c) tggttatcag
127972	ttcttcctgg (n) gaatcctaac	ttcttcctgg (c) gaatcctaac

----- Distribution of Quality < 40 Bases

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Version: 1.01  qxfo.
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Db 189131 AGATTAG 189072
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Db 189071 AAGTTGGAG 189012
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Oy      4111 GAACAATAGCTGATGAGCTAAAAAAGTCATGATTAATTCATCTGTTTAAAGAAAGT 4170
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Oy      4231 GCAGGTGGACAGCTCTCTTATAGTAATCTGTCAATAGTAATGTTTGAAGCTGCAAAACA 4290
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Oy      4651 GTGAGAGATCAAAACCAATTGAGAACTGATTTGCTGTTTATGTCTGTGAGAAATGCTT 4710
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Db      188111 ACAATTAGATGCCCCCAAGCGATTTT 188085

RESULT 8
ARI65227 7445 bp DNA linear PAT 17-OCT-2001
LOCUS ARI65227
DEFINITION Sequence 8 from patent US 6274710.
ACCESSION ARI65227
VERSION ARI65227.1 GI:16238720
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7445)
AUTHORS Dumoulier L., Lohued J. and Renaud J.-C.
TITLE Antibodies which specifically bind T cell inducible factors (Tifs)

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JOURNAL Patent: US 6274710-A 8 14-AUG-2001;
FEATURES Location/Qualifiers
SOURCE 1..7445 /organism="unknown"
BASE COUNT 2058 a 1570 c 1597 g 2220 t
ORIGIN

Query Match 14.3%; Score 686; DB 6; Length 7445;
Best Local Similarity 53.8%; Pred. No. 8,16-148;
Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;

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Oy      89 ATCTGAGCTCTTCTCTTATAGGAGACCTTGCCACCAAGCTGCTCTCTCTTGGCCCT 148
Db      2094 ATCTATAGTCTTCTCTTATAGGAGACCTTGCCACCAAGCTGCTCTCTCTCTCATGCTT 2153
Oy      149 CTGTGTACAGGAGAGAGACAGCTGCGCCATAGCTCCCACTGACAGCTTGACAACTCCA 208
Db      2154 GTGGGCCAGAGAGCAATATGCGCTGCGCCGTCMAACCGGCTGCAAGCTTGAGTGTCCAA 2213
Oy      209 CTTCACAGAGCCCTATATACCAACCGACCTTATGCTGCTGCTAGAGATATACATCTC 268
Db      2214 CTTCACAGAGCCCTATATACCAACCGACCTTATGCTGCTGCTAGAGATATACATCTC 2273
Oy      269 AATCTGCTCTTCTCTGTTGATCTACTGTGAATCCAAATGTTCTTAACTTTCTTCA 328
Db      2274 TCTCTTCTCTCCATACCGCTTCCATTTCTCTGAAGCACTTGCAAACTTTAGGGG 2333
Oy      329 GAGCATCTTAAAGACTTTAGAAACCACTGTTTATCCCTGAGGATATTAATTTCTG 388
Db      2334 CGCTTATCTCCGAGGCTCTCACTACATGTTT-----TCTGTCTTTTAAAG 2382
Oy      389 TTTTTCAGAGACTTTTGGAAATCTGCTTTTCTTTTCTTGAATCTTCTCTCAT 448
Db      2383 ACTCTTAAAGACTGCGGCTTTTCTTATTTCTTATTTCAAGGCTCTCAGACCACTTTCTAT 2442
Oy      449 TTGGCCCTTATGATATATATGATGAAATTTTCCCAAGAGCGGCATCTAGTATCAT 508
Db      2443 CTGGCCCTTACGACACATATACGAAATTTATATACAGAGCGCATTT--AGAAAGCA 2500
Oy      509 CTGATGATTTTCTTCTTATGCTGTGCAATGTTCTTAACTCATGACACATCTG 568
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Oy      569 AATCTGCTTTAGCTTTATGATGTTGCTCTGGGGAGAGGGGATGGGGCATGCTAT 628
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Oy      629 GATTAATTTTCTTCTTATTTGCTCAATGTCAGACCTTATGCTTTCTTCTCTTCAG 688
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Oy      689 GCTAGCTTGTGATTAACACACAGAGCTTGTCTCATTTGGGAGAAACTGTTCCAGGA 748
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Oy      749 GTCAGTGAATCAAGTTGAGAGAGAGGCGGTGCGCTCATAGGATACTTGGGGT 808
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Oy      809 GGTGATGATGATGTTTATGCTTATCCCTTATAGACCTTTCTGTTTCCCTTCACTGC 868
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Oy      869 AGATGATGAGCGCTCTATCTGATGAAGAGGCTGTAATCTTCACTTGAAGAGTGC 928
Db      2818 AGGCTTAAGATCAGTCTACCTGATGAGAGGCTGTAATCTTCACTTGAAGAGTGC 2877
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Dh 2878 TGCTCCCAAGTACAGACAGGTTCCAGCCCTACATGACAGAGGTGTACTTTCCTGACCA 2937
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Dh 2938 AACTCAGAAATCAGCTGCTCTGTGTAGTGTGAGCTGCTGCTATGCTCTCTCT 2997
Qy 1049 CTCTTCCCTCTCTTCCACAGAGACCCCTTACCCCAATCTCTCTCTCTCTCTCTCT 1108
Dh 2998 CT 3057
Qy 1109 TAACTAGACAGAAAGAGTGTGTGACAGAGTGTATCAGAGTCA-----TTTGGG 1161
Dh 3058 GGAAGGCTCAGCACACCACTATGAGCCATTGAAATAGGTCAAAAGGCTTTGGC 3117
Qy 1162 ATCATAGATATTTGCTTTGCTTTGCTTGAAGTCAATCTTGAATTAAGTGTGAATG 1221
Dh 3118 TTCAATAGATATTTGCTTTGCTTTGCTTGAAGTCAATCTTGAATTAAGTGTGAATG 3177
Qy 1222 GGGTCTGGAATTAAGTGTACAGAAAGCCGCACTGGTTTGTCTTGGAAAAAGGCACTC 1281
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Qy 1282 A-----GGTTGCGTAAGTGAAGAGGCTTGG 1309
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Qy 1310 GAAACATCTAGCTGTGAAATGATCCATTGAGTCTAAGTTGTGAGAGGAGGGGATG 1369
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Qy 1370 CATGAGAGAAATTAAGAGAGAAAGTGGAAATGGAAAGCTTAA-----1415
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Qy 1416 -----GTGCTGTGTGGGCTGGCAGACTGTGCTTGTGATGCTATGGGA 1460
Dh 3418 AAGATGAGAGGCTCATGTGTGGGGGTGAAGGTGATCTCTTTCATGTGTAGTGAAG 3477
Qy 1461 AGCCCAAAATCGAGAGGCGTGTGAATCTGATGCGCTGAGATTTGAATGAAAAA 1520
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Qy 1521 AGTTGAGTGAAGTGGGCCAGTAAAGCCCTAGAGCTTACTGAAGAGGCTTAATTT 1580
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Qy 1821 TGGGCAAAATTAAGAGCTTTAATTCAGAGTGAATTTACTGACTCCATGAGTGTG 1880
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Qy 1881 GAGGTCTAAGATTTCAAGACACATTAAGTATGCTTGTATTTGTTATGACA 1940
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Qy 1941 TATTGAAGTATGACTGCAATTCAGAGAAATGTCAGAAAGCTGAAAGGAGACAGTGA 2000
Dh 3933 CATCAGCGTGAAGACAGAACATCCAGAAATGTCTAGAAAGCTGAAAGGAGACAGTGA 3992

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Dh 4753 TCAAGCACTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4812
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Qy 3006 GCTTAACCTTAATTTCCCTTTTCTCTGACTTTTAAAGGCTTTCTCTGAG 3065
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RESULT 9
 AR201398 7445 bp DNA linear PAT 20-Apr-2002
 LOCUS
 DEFINITION Sequence 8 from patent US 6359117.
 ACCESSION AR201398
 VERSION AR201398.1 GI:20252286
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 7445)
 AUTHORS Dumoutier,L., Loubet,J. and Renaud,J.-C.
 TITLE Isolated nucleic acid molecules which encode T cell inducible factors (Tifs), the proteins encoded, and uses therefor
 JOURNAL Patent: US 6359117-A 8 19-MAR-2002;
 FEATURES Location/Qualifiers
 source 1..7445
 BASE COUNT 2058 a 1570 c 1597 g 2220 t
 ORIGIN
 Query Match 14.3%; Score 686; DB 6; Length 7445;
 Best Local Similarity 53.8%; Pred. No. 8,1e-148;
 Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;

QY 29 CTCCTCCCGCAGTCAACCACTGTCGAGTTAGATTGTCTGCAATGCGCCCTTGAGAA 88
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 DB 3418 AAGATGAGAGAGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3477
 QY 1461 AGCCCAAAATGGAGAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1520
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Qy 4042 GAGTGTCAATTAATTTGT 4101
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Qy 4102 AAAATTAAG 4161
Db 6059 TACCTGTAG 6118
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Db 6119 TCTGT 6163
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	Db	4282	TGCAAAAAGGCGCAAGGCATTAATGGGTGGACCTGGGATCCCCAGATCCAGACTACT	4311
Oy	4342	TCAGTCTCCTTGCTCTGGTTAAGAAGGGGTGTCAACTCTGCCAGCTTTAAACAGC	4401	
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Db	6644	TGCTCTTCTCCGCTCTTCAAAAAGACAATAGATCCCTGATGATGACTTTT	6695	
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DEFINITION	Sequence 8 from Patent WO0210393.			
ACCESSION	AX459954			
VERSION	AX459954.1	GI:21725690		
KEYWORDS				
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
TITLE	1 Dunmoyer, L. and Renaud, J.C.			
JOURNAL	Isolated nucleic acid molecules which encode t cell inducible factors, or interleukin-2L, the proteins encoded, and uses thereof			
FEATURES	Patent: WO 0210393-A 8 07-FEB-2002;			
source	LUDWIG INSTITUTE FOR CANCER RESEARCH (US)			
	Location/Qualifiers			
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	/organism="Mus musculus"			
	/db_xref="taxon:10090"			
BASE COUNT	2059 a 1568 c 1597 g 2221 t			
ORIGIN				
	Query Match 14.3%; Score 686; DB 6; Length 7445;			
	Best Local Similarity 53.8%; Pred. No. 6,1e-148;			
	Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;			
Oy	29 CTCCTTCCCAGTCAACAGTTGCTGGAATTGATGAATGTCTGCATGTGGCCGCTTCAGAA	88		
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Oy	89 ATCTGTAGAGCTTTTCCCTTATGGGAGACCTGGCCACAGAGCTCCCTTCTTGGCCCT	148		
Db	2094 AATTAATGAGTTTTCCTTATGGGAGCTTTGGCCGCGCACGTGCTTCTCATATGGCT	2153		

OY	149	TTGGGTACAGAGGAGCAGCTGGGCCATCAGCTCCACGACGGCTTGACAAGTCCAA	208
Db	2154	GTGGGCCCAAGAGCAATGGCTGGCCCGTCAACCCGGGTGCAAGCTTGAGGTTCAA	2213
OY	209	CTTTCACAGACCCCATATATCAACCAACCGCACCTTCATGCTGGCTAAGAGGATATCATCTC	268
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OY	269	AATCTGCTCTTCTCTGTTGGATCTACTGGAAATCCAAATAGTTCCTTAACTTTTCTTCA	328
Db	2274	TCTCTTCTCTCCATACCGGCTTGGCCATTTTCTGTGAAGCACTTGCAAACTCTTTAGGGG	2333
OY	329	GAGATCTCTTAAGGCTTTAGAACCCACGTTTATCCCTGAGGGTGAATPAAATTTCTG	388
Db	2334	CGCTTATCTCCCGAGGTCTCACTCACTAATGTTT-----TCTGTCTTTTAGAG	2382
OY	389	TTTTTACAGACCTCTTGGGAATCTGAGCTTTTCTTTTCTTGAACCTTCTCTCCAT	448
Db	2383	ACTCTTTAAGACCTGGGTCTTTTCTATTTCTATTTCAAGTCTCAGACCATTTCCAT	2442
OY	449	TTTGGCCTTATATGATACATATGATGAATTTTTCCAAAGAGCGGCATTCAGTAATCAT	508
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OY	1049	CTCTTCTCTCTTCCACAAGACCCCTTACCCCACTCTCTCTCTTCTTCCCTTACCCC	1108
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 Qy 1310 GAAAACTAGCTGAGAAATGATTCATGAGTCTAGTGTGGAGGGGAGGGATG 1369
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 QY 4222 CTGTGGGCTGCAAGTTGACAAAGCTCTTATTAAGTATCTGTACATAGATTTTGGAGC 4281
 DB 6164 -----AACCCCACTAAATTTTATTTAGCAAAAGACGTGTAAATTTG 6205
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 DB 6344 GGATGATTTTAAAGCTTTGGCAATCATATATATACATGCTAAATATATATATGT 6403
 QY 4509 TACTATGAATGTTTTCAAATGCTTAAACTGGTCTGTCTCATCACTATCTTTG 4568
 DB 6404 GATTATTAATCTTTTGAAGAGGCTGATATCTGTTTGTGCTCAGAGAAATGTCA 6463
 QY 4569 CAATTTCT--AATTGTCACTTAGAAACATGAGCATTAATGCTCAATCTTTTGA 4625
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 QY 4626 TTCTTATTTTCAACAGCTTGGAGAGTGGAGATCAAGCAATTTGAGAACTGTATTTG 4685
 DB 6524 TTCTTATTTTCACTAGCTTGGAGAGTGGAGATCAAGGCAATTTGGGAACTGGACCTG 6583
 QY 4686 CTGTTATGTCTCTGAGAAATGCTGCAATTTGACCAAGACAAAGCTGAAATGAAATAC 4745
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 DB 6644 TGCTCTTCTCTGCTTTAAAGAAACATTAAGATCCGTAATGACATTTT 6695

RESULT 11
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 LOCUS Mus musculus ILT1fa gene for IL-TIF alpha protein (IL-22), exons
 DEFINITION 1a-5.
 ACCESSION AJ294727
 VERSION AJ294727.1 GI:11967892
 KEYWORDS IL-22 protein; IL-TIF alpha protein; ILT1fa gene; interleukin.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 8270)
 AUTHORS Dumoutier, L., Van Roost, E., Ameye, G., Michaux, L. and Renauld, J.C.
 TITLE IL-TIF/IL-22: genomic organization and mapping of the human and
 mouse genes
 JOURNAL Genes Immun. 1 (8), 488-494 (2000)
 MEDLINE 21069354
 PUBMED 11197690
 REFERENCE 2 (bases 1 to 8270)
 AUTHORS Renauld, J.C.
 TITLE Direct Submission
 JOURNAL Submitted (18-SEP-2000) Renauld J.C., UCL 74.59, Ludwig Institute
 for Cancer Research, Avenue Hippocrate, 74, B-1200 Brussels, BELGIUM

FEATURES
 source location/Qualifiers
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 /gene="ILT1fa"
 CAAT_signal 2673..2676
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 TATA_signal 2705..2709
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 exon /note="number 1a"

Query	Subject	Score	Expect	Ident	Length	Mismatches	Indels	Gaps
intron	2758..2857 /gene="ILTI1Fa" /note="number 1a"	14.3%	53.8%	88	8270	393	44	
exon	2858..3087 /gene="ILTI1Fa" /note="number 1b"			88				
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2979 GTGGGCCACAGAGGCAATGCGTGGCCGCTCAACACCCGGTGCAAGCTTGAGGTGCCAA	3038							
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3039 CTTCAGAGAGCCATATACCAACCGGACCTTCATGCTGGCTAAGAGGTATACATCTC	3098							
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3099 TCTCTTCTCTTCATACCGCCTGCGATTTTCTCGAAGCACTTGCAACTTTTGAAGG	3158							
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Db 4183 CACTGAGTACAGTACTTGTGGGGGAGGGAATGGCAGACAGAAAAGTTGAAGGAAAG 4242
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QY 1521 AGTTGAGTGAAGTGGGCGCCAGTAAAAAGCCCTAGACTTACTGAAAGAGGCTTAATTT 1580
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Db 4758 CATCAGCGGTGAGACCAAAATCCAGAAATGTCAAGAGCTGAAGAGACATGAA 4817
QY 2001 AAAGTGAAGTATGATCTGTCAATGTCAATGTCAATGAGAGACAAATGTTGTTT 2060
Db 4818 AAAGTACTATTTGGCAGCAACAATCTAAGCCATTCAGTAG--GAGAGTGGGGAATTC 4875
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Db	7409	CTGTTATATGTCTCTAGAGAAATGCTCGCATTTTGAACAGAGCAAAAGCTGAAATGAAATAC	7468
Qy	4746	TAAACCCCTTTCCCTGCTGTAAGAAATTAACATTAAGATGCCCCAAAGCATTTT	4797
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DEFINITION	Sequence 17 from patent US 6274710.		linear
ACCESSION	AR165234		
VERSION	AR165234.1	GI:16238731	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 5935)		
AUTHORS	Dumoulier, L., Lohmed, J. and Renaud, J.-C.		
TITLE	Antibodies which specifically bind T cell inducible factors (TIFs)		
JOURNAL	Patent: US 6274710-A 17 14-AUG-2001.		
FEATURES	Location/Qualifiers		
source	1..5935		
BASE COUNT	1732 a 1174 c 1346 g 1683 t		
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Db	476	GTGGGCCAGGAGGCAATGCGCTGCCATCAACACCCGGTGCAGCTTGAGGTTCCTCA	535
Qy	209	CTTCCAGAGCCCTAATCAACCAACGCGACCTTCATGCTGGCTTAAGAGGATTAACATCTC	268
Db	536	CTTCCAGAGCCGATCACTGTCAACCGCACCTTATGCTGGCCAGGAGGTACAGCTGCA	595
Qy	269	AATCTGCTCTTTCCTGTTGATGATCACTTGGAAATCCAAATAGTCTTAACTTTCTTCA	328
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Qy	329	GAGCATCTTAAGAGCTTTAGGAACCACTGTTATCCCTGAGGGATGAATAATTTCTG	388
Db	656	GCTTATCTCCGAGGCTCAGTACCTAATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	703
Qy	389	TTTTTTCAGAGACTCTTTGGAAATCTGGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT	448
Db	704	ACTCTTAAAGACTGATCTTTTCTTATTTCTAATTTCAATTTCAAGAGTCTCAGACCATTTCTAT	763
Qy	449	TTTGGGCTTATATATCATATGATGAAATTTTCCCAAGAGGCGCATTCAGTATTCAT	508
Db	764	CTTGGGCTTAAAGACATATCTGAAATTTTATCTCAAGAGGCGCTTTT--AGAAAGCCA	821
Qy	509	CTATGATATTTTCTTCTTATAGCTCTGCTGATGTTCTTAACTCATGACACACATCTG	568

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Qy	749	GTCAAGTAAAGCTACAGTTGTGACGAACAGGGCCGTGACGTCATGAGGACTTGGAGGT	808
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Qy	809	GGTGTGATGATGAGTTTAAAGTCTTATCCCTTATGACCCCTTCTGTCTTCCCTCACTGC	868
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Qy	1222	GGGTCTGAACTTAAGTATACAGAAAGCCGACATTGGTTGTCTTGGGAAAAAGGCAATC	1281
Db	1499	AGAAATCAATCAAAATTTCTGTAGATGAGAAAGATGTTGGGAGCAAAAGGCTGTAGT	1558
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					Dumontier,J., Louhed,J. and Renaud,J.-C.
					Isolated nucleic acid molecules which encode T cell inducible factors (TIFs), the proteins encoded, and uses therefor
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- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hlc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hlc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vit:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	457.4	9.5	534	17	AQ762065 HS_3136_B
2	373.8	7.8	377	17	AQ212781 HS_3118_B
3	267.4	5.6	389	17	AQ104025 HS_3108_B
4	140	2.9	1035	14	BQ436632 AGENCOURT
5	133.4	2.8	562	17	AZ449260 1M0247121
6	132.8	2.8	426	17	AQ012598 CIT-HSP-2

7	131.8	2.7	617	17	BH609959	BH609959 HIV2SH11
8	131	2.7	650	17	AG092864	AG092864 Pan troy1
9	129.2	2.6	423	17	AQ113016	AQ113016 CIT-HSP-2
10	127	2.6	680	17	AG093514	AG093514 Pan troy1
11	126.4	2.6	928	17	AQ0901154	AQ0901154 HS_3171_A
12	124	2.6	397	10	AM238510	AM238510 XP27a05_X
13	123.6	2.6	561	17	AO108812	AO108812 CIT-HSP-2
14	123.4	2.6	542	12	BG215075	BG215075 RST34733
15	122.6	2.6	383	17	AQ171322	AQ171322 HS_3071_B
16	122.4	2.6	414	14	BQ358580	BQ358580 PM3-H7090
17	122.4	2.6	820	17	AQ253316	AQ253316 HS_2046_B
18	122	2.5	609	17	AQ626984	AQ626984 CITBI-E1-
19	122	2.5	680	17	AQ625928	AQ625928 CITBI-E1-
20	122	2.5	715	17	AQ628187	AQ628187 CITBI-E1-
21	121.8	2.5	960	17	AQ747439	AQ747439 HS_5537_A
22	121.2	2.5	621	17	AQ241294	AQ241294 RPT11-69
23	121.2	2.5	924	9	AL571429	AL571429 AL571429
24	120.6	2.5	498	9	AL039515	AL039515 DXF2P43B
25	120	2.5	415	17	AQ076937	AQ076937 CIT-HSP-2
26	119.4	2.5	711	17	AG001875	AG001875 Homo sapi
27	119.2	2.5	942	13	BI831451	BI831451 603074554
28	118.8	2.5	527	17	AQ635346	AQ635346 RPT1-11-4
29	118.8	2.5	580	17	AQ628202	AQ628202 CITBI-E1-
30	117.6	2.5	709	17	AG001874	AG001874 Homo sapi
31	117.2	2.4	586	17	B57786	B57786 CIT-HSP-201
32	116.8	2.4	230	17	AQ133433	AQ133433 CIT-HSP-2
33	116.8	2.4	404	17	AQ129766	AQ129766 HS_2253_A
34	116.8	2.4	426	17	B54270	B54270 CIT-HSP-201
35	116.6	2.4	484	17	AQ144241	AQ144241 HS_3085_A
36	116.6	2.4	688	9	AL706925	AL706925 DXF2P686C
37	116.4	2.4	3238	17	AF101911	AF101911 AF101911
38	116	2.4	464	17	B71167	B71167 CIT-HSP-202
39	116	2.4	650	17	AQ108135	AQ108135 CIT-HSP-2
40	115.2	2.4	719	17	AG001829	AG001829 Homo sapi
41	115	2.4	362	17	AQ063248	AQ063248 CIT-HSP-2
42	114.6	2.4	474	17	AO833127	AO833127 HS_5484_A
43	114.4	2.4	396	17	B70199	B70199 CIT-HSP-202
44	114.2	2.4	414	17	AQ227236	AQ227236 HS_2017_B
45	114.2	2.4	455	17	AQ700916	AQ700916 HS_2116_A

ALIGNMENTS

RESULT 1
AQ762065
LOCUS
DEFINITION HS_3136_B1_H07_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=13 Row=P, DNA sequence.
ACCESSION AQ762065
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Mahairas G.G., Wallace J.C., Smith K., Swartzell S., Holzman T., Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and Hood L., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and

TITLE
JOURNAL
MEDLINE
COMMENT
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
Contact: Mahairas GG, Wallace JC, Hood L
University of Washington
High Throughput Sequencing Center
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end web server: http://www.htsc.washington.edu

Plate: 3136 row: P column: 13
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 534.
 Location/Qualifiers
 1..534
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Plate:3136 Col=13 Row=P"
 /sex="male"
 /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 171 a 84 c 104 g 170 t 5 others

ORIGIN

Query Match 9.5%; Score 457.4; DB 17; Length 534;
 Best Local Similarity 98.2%; Pred. No. 1.4e-90;
 Matches 483; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 2229 CTAGTCACATPACCTCAGATTCCTGGGATGTCAGTCAGACAGATAGGCTAGATGACAG 2288
 DB 44 CTAGTCACATPACCTCAGATTCCTGGGATGTCAGTCAGACAGATAGGCTAGATGACAT 102
 QY 2289 GTCTCCGATCCCAAGCCAGCACTTTCCGGGTGTCATACAGATTAGTTTGTGACCA 2348
 DB 103 GTCTCCGATCCCAAGCCAGCACTTTCCGGGTGTCATACAGATTAGTTTGTGACCA 162
 QY 2249 TTAATCTTGGGAAATTTGAGATTCCTATTTGACTCATGTATGTGAAGATCTTGT 2408
 DB 163 TTAATCTTGGGAAATTTGAGATTCCTATTTGACTCATGTATGTGAAGATCTTGT 222
 QY 2409 TAAACACAGAAAAATGCTTATGGCAATTTATTTGAAGTCATTTTGAAGTCATTATG 2468
 DB 223 TAAACACAGAAAAATGCTTATGGCAATTTATTTGAAGTCATTTTGAAGTCATTATG 282
 QY 2469 CATTCCTTTGAAATTTGAGAAATTAATCTGAGAAATGAGAAAGAGCTGAGATTCAT 2538
 DB 283 CATTCCTTTGAAATTTGAGAAATTAATCTGAGAAATGAGAAAGAGCTGAGATTCAT 342
 QY 2529 ATAGGGCTAATTTCTGGAGTATTAACACTATTTGAATATCATATATCTATCAT 2588
 DB 343 ATAGGGCTAATTTCTGGAGTATTAACACTATTTGAATATCATATATCTATCAT 402
 QY 2589 ATTGATTATAGTTTAAAGCAGACAGACACACCCCGATCTCTTTATACAGTTCAAT 2648
 DB 403 ATTGATTATAGTTTAAAGCAGACAGACACACCCCGATCTCTTTATACAGTTCAAT 462
 QY 2649 AGAGTAAATAATTTAGTAAGAGATTTATATGTTAATGGAATCTGAATTTGTAAGCT 2708
 DB 463 AGAGTAAATAATTTAGTAAGAGATTTATTAAG-TAAATGGAATCTGAATTTGTAAGCT 521
 QY 2709 TTTTTCCTCC 2720
 DB 522 TTTTTCCTCC 533

RESULT 2
 A0212781 377 bp DNA linear GSS 18-SEP-1998
 LOCUS
 DEFINITION HS_3118_B2_B08_MR_CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=3118 Col=16 Row=D, DNA sequence.
 ACCESSION A0212781
 VERSION A0212781.1 GI:3623982
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 377)
 AUTHORS Mahairas G.G., Wallace J.C., Smith K., Swartzell S., Holzman T.,
 Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and
 Hood L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas G.G., Wallace J.C., Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3118 row: D column: 16
 Class: BAC ends
 High quality sequence stop: 377.
 Location/Qualifiers
 1..377
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Plate=3118 Col=16 Row=D"
 /sex="male"
 /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 119 a 60 c 80 g 118 t

ORIGIN

Query Match 7.8%; Score 373.8; DB 17; Length 377;
 Best Local Similarity 99.5%; Pred. No. 4.5e-72;
 Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2203 TAGAAGTGTGGGATCTTATGCTGTCATACATPACCTCAGATTCGGGATGTC 2262
 DB 1 TAGAAGTGTGGGATCTTATGCTGTCATACATPACCTCAGATTCGGGATGTC 60
 QY 2263 GTGGCAGATAGGGGTAGAAATGACAGTCTCCGATCCCAAGCCAGCACTTTCCGGT 2322
 DB 61 GTGGCAGATAGGGGTAGAAATGACAGTCTCCGATCCCAAGCCAGCACTTTCCGGT 120
 QY 2323 GGTGATACAGATTAGTTTGTGACATTAATCTTGAAGAAATTCAGATTCTTATGAC 2382
 DB 121 GGTGATACAGATTAGTTTGTGACATTAATCTTGAAGAAATTCAGATTCTTATGAC 180
 QY 2383 TCATGTATCTGAGAGATCTTGTTTAAACAGAAAAATGCTTATGGCAATTTAT 2442
 DB 181 TCATGTATCTGAGAGATCTTGTTTAAACAGAAAAATGCTTATGGCAATTTAT 240
 QY 2443 TGAAGTCATTTTGAAGTCATTAATGCTTGTGAACCTTGAAGAAATTAACAGAA 2502
 DB 241 TGAAGTCATTTTGAAGTCATTAATGCTTGTGAACCTTGAAGAAATTAACAGAA 300
 QY 2503 CAATGAGAAAGAGCTGACCTGCATATAGGGCTAATTTCTGGAGTAATTAACACTTAT 2562
 DB 301 CAATGAGACAGAGCTGACCTGCATATAGGGCTAATTTCTGGAGTAATTAACACTTAT 360
 QY 2563 TTGAATTATCATTAAT 2579
 DB 361 TTGAATTATCATTAAT 377

RESULT 3
 A0104025/c 389 bp DNA linear GSS 28-AUG-1998
 LOCUS
 DEFINITION HS_3108_B1_C01_T7 CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=3108 Col=1 Row=F, DNA sequence.
 ACCESSION A0104025
 VERSION A0104025.1 GI:3478961
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 389)

AUTHOR	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A.,Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE	99380589
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Sequence Tagged Connector Plate: 3108 row: F column: 1 Class: BAC ends High quality sequence stop: 389.
FEATURES	Location/Qualifiers 1..389 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="plate=3108 COL=1 Row=F" /clone_1id="CIT Approved Human Genomic Sperm Library D" /sex="male" /note="Organ: sperm; Vector: pBelBAC11; BAC clones in E-Coli DH10B"
BASE COUNT	119 a 86 c 65 g 118 t 1 others
QUERY	Query Match 5.6%; Score 267.4; DB 17; Length 389; Best Local Similarity 92.8%; Pred. No. 1.6e-48; Matches 347; Conservative 0; Mismatches 17; Indels 10; Gaps 6;
QY	1709 GATTGCCAAGATTAAGAGAGCTCTCTTGAAGGAGAGTACGTGATTCGGCTCCAA 1768
DB	364 GATTTCCCAAGATTAAGAGAGCTCTCTGT---AAGAAAGTACGTGATTCGGG--TCNA 311
QY	1769 GCGAATTCAGAGCTCAGAGAAATCAGTGCACCTGTTGAATCTAGTCAATTGGGCGAAA 1828
DB	310 AGGAGTTCAAGGCTCA-GAATCTAGTCACTGTT-AAATCTAGTCAATTGT-GGCAA 254
QY	1829 ATTACTAAGAGCTTAATTCAGAGTGAATTGTACTGTAACCTTCATGGGTGTGAGGTTCA 1888
DB	253 ATTACTAAGAGCTTT-ATTCAGAGGGAATTGACTGTACCTCCAGGGGTGTGAGGTTCA 195
QY	1889 TAAAGTTCAGACACAATTAAGATAGTATAGCTGTAATGTTTATAGCAATTTAAG 1948
DB	194 TAAAGTTCAGACACAATTAAGATAGTATAGCTGTAATGTTTATAGCAATTTAAG 135
QY	1949 GTGATGACCTGCATATCCAGAGAGATGTGCAAAAGCTGAAGACACAGTGAAGAAAGTAG 2008
DB	134 GTGATGACCTGCATATCCAGAGAGATGTGCAAAAGCTGAAGACACAGTGAAGAAAGTAG 75
QY	2009 GACTGATTAAGCTGTAATCTTAAGTCAATGCAATAGAGAGACAAATGTTGTTTCTTCC 2068
DB	74 GACTGATTAAGCTGTAATCTTAAGTCAATGCAATAGAGAGACAAATGTTGTTTCTTCC 15
QY	2069 TTTCTTTCTTCCCA 2082
DB	14 TTTCTTTCTTCCCA 1
RESULT 4	
LOCUS	B0436632 1035 bp mRNA linear EST 24-MAY-2002
DEFINITION	AGENCYCOURT_7582829 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5045008
ACCESSION	B0436632
VERSION	B0436632.1 GI:21175708
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	Eukaryote, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	NIH-MGC http://mgc.nci.nih.gov/ .	National Institutes of Health, Mammalian Gene Collection (MGC)	unpublished (1999)
1	(bases 1 to 1035)			Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: LHAM13288 row: 1 column: 09 High quality sequence stop: 473.
FEATURES	SOURCE	LOCATION/Qualifiers		
	1..1035	/organism="Homo sapiens"		
		/db_xref="taxon:9606"		
		/clone="IMAGE:6045008"		
		/clone_lib="NIH MGC 92"		
		/tissue_type="embryonal carcinoma, cell line"		
		/lab_host="DH10B (phage-resistant)"		
		/site="Organ: testis; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; Oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."		
BASE COUNT	285 a	246 c	189 g	314 t
ORIGIN			1 others	
Query Match	2.9%	Score 140;	DB 14;	Length 1035;
Best Local Similarity	72.8%	Pred. No. 2.6e-20;		
Matches 195;	Conservative 0;	Mismatches 70;	Indels 3;	Gaps 1;
QY	4026	AGATGTTTAAATCAGAGTGTCCATCATTTGGCTTCCCTGACCACTTGA--AAGA	4083	
DB	270	AAATCATTTAAACCAAGGGGTGCCATCTCTTGGCTTCCCTGGGACACACTGAAAGA	211	
QY	4083	ATTGTCTTGGACACACTAAATACAAAGAACATAGCTATGAGCTTAAATAAGCCATG	4143	
DB	210	ATTGTTTGGAACCAACACTAAATACCTAACATAGCTGATGAACTTAAAAAATGTA	151	
QY	4143	CATTAATCTACTGTTTAAAGAAAGTTATGATTTCTGTAGGGTGCACTTCAAAGCT	4202	
DB	150	AAAAACAATCTAATGTTTAAAGAAAGTTATGATTTGTGTGGCGTCATTCAAAGCT	91	
QY	4203	GTCCCTGGCCATGTGCGGCGCTGTGGGCTGACAGTTGACAAAGCTCTTATAAGTAATCTG	4265	
DB	90	GTCCCTGGGCCACATGCGGCGCCATGCGGTGCTGAGCAAACTGATTTAAACATTTAA	31	
QY	4263	TCATATGATATGTTTGGAGCTGCCAAAAC	4290	
DB	30	ACTTTTCTCAATTTGACCAAGTAATAA	3	
RESULT 5				
LOCUS	AZ449260	562 bp	DNA	linear
DEFINITION	1M0247J21F Mouse 10kb plasmid UUCIM library Mus musculus genomic clone UUCIM0247J21 F, DNA sequence.			
ACCESSION	AZ449260			
VERSION	AZ449260.1	GI:10602872		
KEYWORDS	GSS.			
SOURCE	house mouse.			
ORGANISM	Mus musculus.			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly			

TITLE
JOURNAL
COMMENT

'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0247 row: J column: 21
Seq primer: CGTTGTAAACGACGCGCCACT
Class: plasmid ends
High quality sequence stop: 562.

FEATURES

source

1. 562
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGCM024721"
/clone_1lb="Mouse 10kb plasmid UUCGCM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (G14732114|BP|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 119 a 155 c 116 g 172 t

ORIGIN

Query Match 2.8%; Score 133.4; DB 17; Length 562;
Best Local Similarity 61.1%; Pred. No. 7.5e-19;
Matches 367; Conservative 0; Mismatches 176; Indels 58; Gaps 7;

QY 374 TACATAAATTTCTGTTTTCAGAGACTTTGGGAATGCGTTTCTTTTCTTGA 433
DB 8 TACCTATGTTTCTGCTCTTGAAGACTCTTTAAGACTGATCTTTTCAATTCA 67
QY 434 -----ACTCTTCCTTCATTTGGCCTTATGATCATATGATGATTTTC 481
DB 68 TTTCAGAGTCTAGGAACATTTCTATTTGGCTTCAGATACATATGATTTAT 127
QY 482 CCAAGAGCGGCATTCAGTATCATCTGATGATTTTTCCTTATGCTCTGTGC 541
DB 128 CTCAGAGCGGCATTTAG--AAAGCACCACAGCATGACATCTTCCATCTCTGTG 185
QY 542 ATGTTCTTAACATCAGACACATCTGAATTCGCTTTAGCTTATGATGCTGTG 601
DB 186 TCTCTCTGAATCACTCTCTGCTACTC-----CTG 220
QY 602 GGGAGACGGAGTGGGACATGCTATGATTAATTTTCTATTTGCTCAATGCCA 661
DB 221 AGACCACTGTGACATACATCTCTACTTACAGGCTTTTCTCATCTCTGTATCCA 280

QY 662 GACCCCTTACTTTTCTTCTTCCAGGCTTACTGCTGATPAACACAGACCTTGT 721
DB 281 GGCACCTTAGGTTTTC-TCTCTTCAAGGCGACCTTGACATPACACAGATGTCGG 339
QY 722 CTCATTGGGAGAAACTGTTCCAGGAGTCACTGATGATGATGATGATGATGAT 781
DB 340 CTCATGCGGAGAAATGTTCCAGAGAGTCACTGATGATGATGATGATGATGAT 399
QY 782 CCGTGCCTCCATGAGGACTTGGGCTGCTGATGATGATGATGATGATGATGAT 841
DB 400 -----TAGCTCGGAGAGCTGTGATGATGATGATGATGATGATGATGAT 442
QY 842 GACCCCTTCTTCTTCTTCCCTTCCAGCTGACATGATGATGATGATGATGATG 901
DB 443 GACCCCTGCTGCTTCTTCTTCCAGCTGACATGATGATGATGATGATGATGAT 502
QY 902 TGCTGAATCACTACCCCTTGAAGAGCTGCTTCCCTCAATGATGATGATGATG 961
DB 503 TGCTCAACTTC-CCCTGGAAGAGTTCCTGCTCCCGATGACAGGTTCCAGCC 561
QY 962 T 962
DB 562 T 562

RESULT 6

AQ012598/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

2.8%; Score 132.8; DB 17; Length 426;
77.9%; Pred. No. 1e-18;

1. 426
/organism="Homo sapiens"
/db_xref="GDB:7154145"
/db_xref="taxon:9606"
/clone="229915"
/clone_1lb="CIR-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
HindIII"

129 a 93 c 75 g 129 t

Matches 173; Conservative 0; Mismatches 47; Indels 2; Gaps 1;

QY 4027 GATGTTTAAATCAGAGTGTCCATCATTTGGCTTCCCTGACACACTTGAAGAATTG 4086
 DB 226 GATTTTCACTAGACCGGGGTGTCCAACTTTTGGCTTCCCTGGCCACACTGGAAGATTG 167
 QY 4087 TTTTGTACACATTAATAATACAGAACATAGCTATAGCTTAAATAAG--TCCATGCA 4144
 DB 166 TTTTGGGCGACAGTAAATCTTCAACATAGCTTAAATAAGAAATCGTACA 107
 QY 4145 TAAATCTCATCTGTTTAAAGAAAGTTTATGAATTTCTGTAGGGGTCATTCAAAGCTGT 4204
 DB 106 AAAATCTCATCTGTTTAAAGAAAGTTTATGAATTTCTGTAGGGGTCATTCAAAGCTGT 47

QY 4205 CCTGGGCCATGTGCGGCTGTGGCTGACAGTTGACAAAGCT 4246
 DB 46 CCTGGGACACATGTGGGCCCAAGGCTGCGAGTGACAAAGCT 5

RESULT 7
 LOCUS BH609959 617 bp DNA linear GSS 18-DEC-2001
 DEFINITION HIV2SH11 SupT1 HIV-1 in vitro integration lines Homo sapiens
 ACCESSION BH609959
 VERSION BH609959.1 GI:17922568
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 617)
 Schroder,A.R.W., Shinn,P., Chen,H., Berry, C., Ecker,J.R. and Bushman,F.
 Favored Sites for HIV-1 Integration in the Human Genome
 TITLE Unpublished (2002)
 JOURNAL Contact: Frederic Bushman
 COMMENT Salk Institute Infectious Disease Laboratory
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1630
 Fax: 858 554 0341
 Email: bushman@salk.edu
 Classes: PCR with specific primers.
 Location/Qualifiers
 1..617
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HIV2SH11"
 /clone_lib="SupT1 HIV-1 in vitro integration lines"
 /note="Integration sites were generated in vitro using naked SupT1 DNA as a target. HIV preintegration complexes (PICs) were used as a source of integration activity. DNA was cleaved with restriction enzymes, linkers were ligated onto the cleaved DNA and DNAs were amplified using one primer that bound to the linker DNA and one that bound to the HIV cDNA. Junctions between integrated HIV proviruses and cellular DNA were cloned and sequenced."

BASE COUNT 217 a 93 c 110 g 197 t

ORIGIN

Query Match 2.7%; Score 131.8; DB 17; Length 617;
 Best Local Similarity 78.0%; Pred. No. 1.7e-18;
 Matches 188; Conservative 0; Mismatches 42; Indels 11; Gaps 2;

QY 4032 TTTAAATCGAGTGTCCATCATTTGGCTTCCCTGACCACTTGA---AAATATTC 4088
 DB 319 TGTAAATCGAGGTTGTCCATCTTTGGTTCCCGACCACTGGAAGAAATTTGCC 378
 QY 4089 TTGGTACACATTAATAATACAGAACATAGCTGATGAGCTAA-----AAAGTCCA 4140
 DB 379 TTGGGCGACACATTAATAATACATTAATAGTATGCTGATGAGCTTAAATAAGTCCA 438

QY 4141 TGCATAAATTCATACCTGTTTAAAGAAAGTTTAAGATTTCGTAGGAGTCATCAAG 4200
 DB 439 TGCATAAATTCATATATTTTCAAGAAAGTTTATGAATTTGTTGGGCTGCATTCAG 498
 QY 4201 CTGTCTGGGCGCATGTGGCGGCTGTGGCTGACAGGTGAGCAAGCTTATTAAGTAA 4260
 DB 499 CCGTCTGGGCGCATGTGGCGGCTGTGGCGGCGACAGGTGAGCAAGCTTATTAAGTAA 558

QY 4261 T 4261
 DB 559 T 559

RESULT 8
 LOCUS AG092864 650 bp DNA linear GSS 03-NOV-2001
 DEFINITION Pan troglodytes DNA, clone: PTB-093C12.R, genomic survey sequence.
 ACCESSION AG092864
 VERSION AG092864.1 GI:16644666
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC library clone:PTB-093C12.R.
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 REFERENCE 1
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Matanabe,H. and Sakaki,Y.
 BAC end sequences of library PTB
 TITLE Unpublished
 JOURNAL 2 (bases 1 to 650)
 Direct Submission
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22, Suenitro-chou, Tsunumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the RAD process and may have higher chance of clone tracking errors.
 PRIMERS
 Sequencing: M13Rev
 LIBRARY
 Vector : PK5145
 R.Site 1 : SacI
 R.Site 2 : SacI.
 Location/Qualifiers
 1..650
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="PTB-093C12.R"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_lib="PTB Chimpanzee Male BAC library"

BASE COUNT 173 a 136 c 137 g 204 t

ORIGIN

Query Match 2.7%; Score 131; DB 17; Length 650;
 Best Local Similarity 69.5%; Pred. No. 2.5e-18;
 Matches 212; Conservative 0; Mismatches 80; Indels 13; Gaps 2;

QY 3967 TCGAATAGAAAAGCCTTATGTGTTGGTGAATACATGTCCTCAAGTCATTTGATGAG 4026
 DB 272 TCGAAGAAAGAAAGATGTTGTTGTTTAAAGTAAGCTAAGTAAAGCGTTAGGC 331
 QY 4027 GATGTTTAAATCGAGAGTGTCCATCATTTGGCTTCCCTGACCACTTGA-----AA 4080
 DB 332 TATGTCGCAAAATCAGGGGTGTCCAACTTTGGCTTCCCTGGCCACACTGGAAGAGA 391
 QY 4081 GAATGTCTGTGATACACATTAATAATACAGAACATAGCTGATGAGCTTAAATAAGTCCA 4140

Db 392 GAATTCCTGGCCGACACATAAATACACCAACATAGCTGATGACCTTTAAAAAATC 451
 QY 4141 TGCATAATCTCATACTGTTTAAAGAAATTTATGAATTTCTGTAGGCGCATTCAG 4200
 Db 452 GCAAAAAACCTCAATGTTTCAATAAAGTTTACGAATTTGTGTGGTTGCATTCAG 511
 QY 4201 CTGTCCCTGGGCGCATG-----TCGGCCCTGTGGGCTGCAGGTGGACAGCTCCTATA 4253
 Db 512 CCATCTGAGCCATGAGCCACATGTGGCTGTGGCGGAGGCTGCAAACTGTGTGTA 571
 QY 4254 AGTAA 4258
 Db 572 AATCA 576

RESULT 9
 AQL13016/c 423 bp DNA linear GSS 29-AUG-1998
 LOCUS CIT-HSP-2375K21.TR CIT-HSP Homo sapiens genomic clone 2375K21. DNA
 DEFINITION
 ACCESSION AQL13016
 VERSION AQL13016
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 423)
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Baas,S., Libher,K., Golden,K.,
 Berry,K., Granger,D., Sub,E., Wible,C., Shizuya,H., Simon,M. and
 Venter,M.C.
 TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1998)
 COMMENT Other GSSs: CIT-HSP-2375K21.TF
 CONTACT: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@igf.org
 Clones are available from Reseach Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1..423
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2375K21"
 /clone_lib="CIT-HSP"
 /sex="Male"
 /cell_type="Sperm"
 /note="Vector: pbeIOBAC11; Site_1: HindIII; Site_2:
 HindIII"

BASE COUNT 115 a 82 c 73 g 153 t

ORIGIN
 Query Match 2.7%; Score 129.2; DB 17; Length 423;
 Best Local Similarity 74.4%; Pred. No. 6.3e-18;
 Matches 177; Conservative 0; Mismatches 58; Indels 3; Gaps 1;

QY 4012 AGTCATTGAGTAGAGATGTTTAAATCAGAGTGCATTCATTTGGCTTCCCTGGACC 4071
 Db 247 AATTAATCTGAATATGAAATCCCTGCGAGAGGTGTCATCTTTGGCTTCCCTGGACC 188
 QY 4072 ACCTGAAAGAAATTTGTTGGTGAACACATTAATAATACAGAACATAGCTGATGAGT-- 4129
 Db 187 AATTTGGAAGAAATTTGTTGGGCGACACAAATAATACATTAATGATGCTGATGAGGCTTT 128
 QY 4130 -AAAAAGTCATGCAATTAATCTCATCTGTTTAAAGAAAGTTTAAATTTCTGTAGG 4188

Db 127 AAAAAAAAAATCAAAATATCATCTCATTAAGTTTAAAGAAAGTTTAAATTTGTGTGA 68
 QY 4189 GTGCATTCAAGCTGCTGCTGGCCATGTCGGGCTGTGGGCTGCAGTTGGACACT 4246
 Db 67 CCACATTCAAGGCTATCCAGGCTGCAATGGCCCATGGGCTGCGAGTTGGACAACT 10

RESULT 10
 AG093514/c 680 bp DNA linear GSS 03-NOV-2001
 LOCUS Pan troglodytes DNA, clone: PTB-094A01.R, genomic survey sequence.
 ACCESSION AG093514
 VERSION AG093514.1 GI:16645316
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
 BAC library clone:PTB-094A01.R.
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE 1
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 TITLE BAC end sequences of Library PTB
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 680)
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 TITLE Direct Submision
 JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chimbep@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
 was generated during the R&D process and may have higher chance of
 clone tracking errors.
 PRIMERS
 Sequencing: M13rev
 LIBRARY
 Vector : PK6145
 R.Site 1 : SacI
 R.Site 2 : SacI.
 Location/Qualifiers
 1..680
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="PTB-094A01.R"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 158 a 151 c 163 g 201 t 7 others

ORIGIN
 Query Match 2.6%; Score 127; DB 17; Length 680;
 Best Local Similarity 76.8%; Pred. No. 1.9e-17;
 Matches 182; Conservative 0; Mismatches 50; Indels 5; Gaps 2;

QY 4023 TAGAGATGTTTAAATCAGAGTGCATTCATTTGGCTTCCCTGGACCACTTG--AA 4079
 Db 633 TATCGCTGTTTAAAGCAACGTGTCATCTTTGGCTTCCCTGGACCGCACTGAAAA 574
 QY 4080 AGAATTTGTTGGTGCACACATTAATAACAAACATAGCTGATGAGCTAAAAAAATGCC 4139
 Db 573 AGAATTTGTTGGGCGACACATTAATATGCGAGCATGCTGATGAGCTTAAAAAANA 514
 QY 4140 ATGCA -TAAATCTCATCTGTTTAAAGAAAGTTTAAATTTCTGTAGGCTGATTA 4197
 Db 513 CTGCAACAAATTTCTAATCGTTTAAAGAAATTTAAGAAATTTGTGTGGCCCCCATTC 454
 QY 4198 AAGCTGCTGGGCGCATGTCGGGCTGTGGGCTGCAAGTTTGAAGAGCTCTTATA 4254
 Db 453 AAGCATCTGGGCGCATATGTGGCTGCGGCGCTGTGATGAGCAAGGCTTAATTAA 397

RESULT 11
LOCUS AQ01154/c
DEFINITION HS 3171 A2 H08 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=16 Row=O, DNA sequence.
ACCESSION AQ01154
VERSION AQ01154.1 GI:6357344
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 928)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,D., Zhao,S., Adams,M.D. and Hood,L.
COMMENT Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
CONTACT: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3171 row: O column: 16
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence scop: 928.
Location/Qualifiers
1. 928
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="Plate=3171 Col=16 Row=O"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"
BASE COUNT 240 a 275 c 115 g 298 t
ORIGIN

Query Match 2.6%; Score 126.4; DB 17; Length 928;
Best Local Similarity 72.6%; Pred. No. 2,7e-17;
Matches 193; Conservative 0; Mismatches 66; Indels 7; Gaps 2;

QY 4028 AAGTTTAAATCAGAGTGCATATTTGGCTCCCTGGACACCTGA-----AAG 4081
DB 415 ATACTTAAGACAGGGGCTTCAATCTTTGGCTCCCTGGACACCTGAAGAG 356
QY 4082 AATGTCTTGTACACATATAAATACAGAACATAGCTGATGAGCTAAAAAGTCAT 4141
DB 355 AATGTCTTGTACACATATAAATACAGAACATAGCTGATGAGCTAAAAAAT 296
QY 4142 GCATTAATCTCATCTGTTTAAAGAAAGTTTGAATTTCTGTTAGGCTCATCAAGC 4201
DB 295 ACAAAAAAATAAATTTTAAAGAAAGTTTGAATTTCTGTTAGGCTCAAGGC 237
QY 4202 TGTCCCTGAGGCGATGCGGCTGTGGGCTGCAGGTTGGACAAGCTCTTAAGTAATCT 4261
DB 236 TGTCCCTGAGGCGATGCGGCTGTGGGCTGCAGGTTGTGACAGCTTAAAGAACTG 177
QY 4262 GTCATAGATAGTTTGAAGCTGCAA 4287
DB 176 GAAACATATTAATATCACACAGAAA 151
RESULT 12

AM238510
LOCUS xp27a05.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741552 3'
DEFINITION similar to contains MER30.D2 MER30 repetitive element ;, mRNA
sequence.
ACCESSION AM238510
VERSION AM238510.1 GI:6570899
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 397)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgephs-remail.nih.gov
Tissue Procurement: Edward Shillitoe Ph.D., Silvio Gutkind Ph.D., Chichanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: www-bio.lnl.gov/btrp/image/image.html
Possible reversed clone; polyT not found
Seq primer: -40UP from Gibco
High quality sequence scop: 370.
Location/Qualifiers
1. 397
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:2741552"
/clone_lib="NCI_CGAP_HN10"
/tissue_type="carcinoma in situ from retromolar trigone"
/lab_host="DH10B"
/note="Vector: PAMPI0; cDNA made by oligo-dT priming. Non-directionally cloned into the UDG sites of PAMPI0. Size-selected on agarose gel, average insert size 500 bp. Primary library; non-amplified. CDNA Library Preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
BASE COUNT 128 a 70 c 82 g 117 t
ORIGIN

Query Match 2.6%; Score 124; DB 10; Length 397;
Best Local Similarity 77.4%; Pred. No. 9e-17;
Matches 178; Conservative 0; Mismatches 45; Indels 7; Gaps 2;

QY 4034 TAAATCAGAGTGCATATTTGGCTCCCTGGACACCTGA---AAGATTGCTT 4090
DB 25 TAAATCAGAGTGCATATTTGGCTCCCTGGACACCTGAAGAGATTGCTT 84
QY 4091 GGTACACATATAAATACAGAACATAGCTGATGAGCT---AAAAAGTCATGCAT 4146
DB 85 GGACACATATAAATACAGAACATAGCTGATGAGCTTAACAAAAAATACACAAAAA 144
QY 4147 AATTCATACGTTTAAAGAAAGTTTGAATTTCTGTTAGGCTCATCAAGCTGTC 4206
DB 145 AGTCTCTTAATGTTTAAAGTTTGAATTTCTGTTAGGCTCATCAAGCTGTC 204
QY 4207 TGGGCGATGCGGCTGTGGGCTGCAGGTTGGACAAGCTCTTAAGT 4256
DB 205 TGGGCGATGCGGCTGTGGGCTGCAGGTTGGACAAGCTTGAAGTAAGT 254
RESULT 13
LOCUS AQ108812/c
DEFINITION CIT-HSP-2373M12.TF CIT-HSP Homo sapiens genomic clone 2373M12, DNA

ACCESSION	sequence.
VERSION	AOI08812
KEYWORDS	AOI08812.1 GI:3485502
SOURCE	GS.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 461)
	Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Sub,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready
JOURNAL	Map Building
COMMENT	Unpublished (1998) Other_GSSs: CIT-HSP-2373M12.TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: madams@cigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tcdb/hungen/bac_end_search/bac_end_search.html. Seq primer: M13-21 Class: BAC ends.
FEATURES	Location/Qualifiers
source	1..461 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="2373M12" /clone_id="CIT-HSP" /sex="Male" /cell_type="Sperm" /note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"
BASE COUNT	127 a 97 c 101 g 136 t
ORIGIN	
Query Match	2.6% Score 123.6; DB 17; Length 461;
Best Local Similarity	74.4%; Pred. No. 1.1e-16;
Matches 186; Conservative 0; Mismatches 54; Indels 10; Gaps 2;	
QY	4007 TTCAAAGCATTTAGTAGAGATGTTTAAATCAGAGAGTCCATCATTTGGCTTCCCT
Db	319 TTCAATGGCACTTAAAGGAGTCTTAAAGCAGAAATGTCAGAACTTTAGCTTCCCT
QY	4067 GGACCACTTGAAAGAAATGCTTGGTACACACATTAATACAGACAA-----ATAGC
Db	259 GGGCCACACTGGGAGAAATGCTTGGGGCCACACATTAATACAGTAACAGTAATGATAGA
QY	4121 TGAATGAGTAAAAAAGTCATGC-----ATAATCTCATCTGTTTAAAGAAAGTTTANGA
Db	199 TGAATGAGTAAAAAATTAATCTTAAAAAATATCTCATGATGTTTCAAGAAAGTTTACA
QY	4177 ATTCTGTGTAAGGATTCATCAAGCTGCTCGGGCCATGCGGGCTGTGGGCTGCAGGT
Db	139 ATTGTGTGGGCTGCATTCAAAGCTGTCTTGGGCTTCATGACGCTGTAGAGCTGCGGCT
QY	4237 TGGACAAAGCT 4246
Db	79 TGGACAAAGCT 70
RESULT 14	
LOCUS	BG215075 542 bp mRNA linear EST 21-APR-2001
DEFINITION	R3374733 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION	BG215075
VERSION	BG215075.1 GI:33741096
KEYWORDS	EST.

Source	Organism	Human
REFERENCE	Authors	Human sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 542) Harrington,J.,J., Sheff,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J. ,E., Veloso,N., Kilka,A., Hess,D., Coltrien,K., Lo,K., Offenbacher ,J., Danzig,J. and Ducar,M. Creation of genome-wide protein expression libraries using random activation of gene expression Nat. Biotechnol. 19 (5), 440-445 (2001)
JOURNAL	MEBLINE	21227151
COMMENT	CONTACT	Contact: Scott J. Cain Atherys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@atherys.com
FEATURES	source	High quality sequence stop: 542. Location/Qualifiers 1..542 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="Atherys RAGE Library" /cell_line="HT1080" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology', in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT	ORIGIN	154 a 125 c 101 g 161 t 1 others
Query Match	Best Local Similarity	2.6%; Score 123.4; DB 12; Length 542; Matches 215; Conservative 0; Mismatches 86; Indels 10; Gaps 3;
Qy	3952	TGTTTGCACAAAGAGGTGAATAAGAAAGCCTTAATGATTTGGTGAATACATGATTCAA 4011
Db	540	TTTTTTTTTTTAAAGTGGAACCAAAATTCGATTTGATATCCAGATACAACTTCAA 481
Qy	4012	AGTCATTGAGTAGAGATGTTTAAATCAGAGGTGCCAATCTTTGGCTTCCCTGACC 4071
Db	480	AGTAATAGACT--TGCTGTTCTPAACATAGGGGTGTCGATCTTTGGCTTCCCTGGGCC 423
Qy	4072	ACCTTGA-----AAGATTGCTTGTGTACACACATAAATACAGA--ACATATGCTGA 4122
Db	422	ACATTGGAGAGAGAAATGTCTTTGGGCCACACATAAATATCTTAACACAAATAGCTGA 363
Qy	4124	TGAGCTAAAAAAGCCATGCATTAATCTCATCTGTTTAAAGAAAGTTATGATTTCTG 4183
Db	362	TGACCTTAAAAAAATCCAAAAAATCTCTTAAGTTTAAAGAACTTTAACAAATTTGTG 303
Qy	4184	TTAGGCTGACATTCAAAGCTGCTCGGGCCCATGTGCGGCTGTGGGCTGCAGAGTTGACAA 4243
Db	302	TTGGGCGCCGATTCAAAGCCGCTCTTAGGCCACATGTGGCCCGTGGGCCATGGGTTGACAA 243
Qy	4244	GCTCCTTAATA 4254
Db	242	GTTTGTCTTAA 232
RESULT 15	LOCUS	AO171322 383 bp DNA linear GSS 17-OCT-1998
DEFINITION	LOCUS	HS 3071 B2 D10 MR CIT Approved Human Genomic Sperm Library D Homo
ACCESSION	DEFINITION	sapiens genomic clone Plate=3071 Col=20 Row=H, DNA sequence.
VERSION	ACCESSION	AO171322.1 GI:3568689
KEYWORDS	KEYWORDS	GSS.

PI Dumoutier L, Louahed J, Renaud J;
 XX WPI; 2001-638496/73.
 XX New isolated nucleic acid molecules encoding T cell inducible factors,
 PT useful as markers for expression or effect of interleukin (IL)-9 in a
 PT subject and diagnosing susceptibility to asthma or allergy -
 XX
 PS Claim 1, Page 17-19, 26pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule, which encodes
 CC a T cell derived inducible factor (TIF) which are upregulated by the
 CC cytokine interleukin-9 (IL-9) and induce STAT transcription factor
 CC activation. The TIF proteins (or their mutants) may be used to test IL-9
 CC anti/agonists for their potency against lymphomas, immune system
 CC disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
 CC autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
 CC or inhibit differentiation of tissue types in which they are active and
 CC therefore be used to develop treatments for melanomas and hepatomas.
 CC The present sequence a partial genomic sequence for Human TIF.
 CC
 XX
 XX Sequence 4797 BP; 1339 A; 910 C; 1063 G; 1485 T; 0 other;
 SQ
 Query Match 100.0%; Score 4797; DB 22; Length 4797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 661 AGACCTTAGTCTTTCTTCTCTCCAGGCTAGCTTGCTGATACACACAGACGTTG 720
 Qy 721 TCTCATTTGGGAGAAACCTGTTCCACGAGATCAGTGTAGCTAGTTGACGAGG 780
 Db 721 TCTCATTTGGGAGAAACCTGTTCCACGAGATCAGTGTAGCTAGTTGACGAGG 780
 Qy 781 CCGTGTGCGGTCCATGAGTACTTGGGGTGGTGTATGATGTAGTTAGTTATCCCTTA 840
 Db 781 CCGTGTGCGGTCCATGAGTACTTGGGGTGGTGTATGATGTAGTTAGTTATCCCTTA 840
 Qy 841 TGACCTTTCTGTTTCTTCCACCTGACAGATGAGACCGCTGATCTGAGGAGCAG 900
 Db 841 TGACCTTTCTGTTTCTTCCACCTGACAGATGAGACCGCTGATCTGAGGAGCAG 900
 Qy 901 GGTCTGAATCTACCCCTTGAAGAGGCTTCCCTCAATGTATAGTTTCCAGCTTAT 960
 Db 901 GGTCTGAATCTACCCCTTGAAGAGGCTTCCCTCAATGTATAGTTTCCAGCTTAT 960
 Qy 961 ATGACAGAGGTGGTGGCTTCTGCGCAGGCTCAGCAGAGGCTAAGCATGTGTAGT 1020
 Db 961 ATGACAGAGGTGGTGGCTTCTGCGCAGGCTCAGCAGAGGCTAAGCATGTGTAGT 1020
 Qy 1021 TGAGCTCTAGCTTATGCCACCTTACCCCTCTCTCTCTTCCACAGAGACCCCTTAC 1080
 Db 1021 TGAGCTCTAGCTTATGCCACCTTACCCCTCTCTCTCTTCCACAGAGACCCCTTAC 1080
 Qy 1081 CCCAATCTCTCTCCCTTCCCGCTTACCCCTTACCTAGCTAGCAGAGAGTGTGGCAGCAG 1140
 Db 1081 CCCAATCTCTCTCCCTTCCCGCTTACCCCTTACCTAGCTAGCAGAGAGTGTGGCAGCAG 1140
 Qy 1141 TGTATACAGAGTCAATTTGGGATCATAGATATTTGCTTTCTTGTGACTGATCAGTC 1200
 Db 1141 TGTATACAGAGTCAATTTGGGATCATAGATATTTGCTTTCTTGTGACTGATCAGTC 1200
 Qy 1201 TTGAGTTATAGTGTGAATGGGGTCTGGAACCTTAAGTGTACAGAAACCGCATTTG 1260
 Db 1201 TTGAGTTATAGTGTGAATGGGGTCTGGAACCTTAAGTGTACAGAAACCGCATTTG 1260
 Qy 1261 TCTTGGAAGAAAGGCACTCAGGTTGGCTAAGATGAGAAAGTGTGGAAACATCTTA 1320
 Db 1261 TCTTGGAAGAAAGGCACTCAGGTTGGCTAAGATGAGAAAGTGTGGAAACATCTTA 1320
 Qy 1321 GCTGTGAAATGATCATTTGAGTCTAAGTTGTGAGGGAGGGATGSCATGAGAGAA 1380
 Db 1321 GCTGTGAAATGATCATTTGAGTCTAAGTTGTGAGGGAGGGATGSCATGAGAGAA 1380
 Qy 1381 ATTAGAAGAAAGTGGGAAATGGGAAGGCTTAAAGTGGTGGTGGCAGACTGTT 1440
 Db 1381 ATTAGAAGAAAGTGGGAAATGGGAAGGCTTAAAGTGGTGGTGGCAGACTGTT 1440
 Qy 1441 GCCCTGTGATGTCTATGGGAAGCACAAGATGGAGGGGTGTAAGCTTGTACCGGTGA 1500
 Db 1441 GCCCTGTGATGTCTATGGGAAGCACAAGATGGAGGGGTGTAAGCTTGTACCGGTGA 1500
 Qy 1501 CATTTGAAACTATGAAAAAAGTTTGAAGTGGGAGGAGGAGGAGGAGGAGGAGGAG 1560
 Db 1501 CATTTGAAACTATGAAAAAAGTTTGAAGTGGGAGGAGGAGGAGGAGGAGGAGGAG 1560
 Qy 1561 ACTGAAGAGGCTTAATTTTCACTGAGATGTTTATGTACATTTCTTGTCTTAAGCATG 1620
 Db 1561 ACTGAAGAGGCTTAATTTTCACTGAGATGTTTATGTACATTTCTTGTCTTAAGCATG 1620
 Qy 1621 CAATTTTCTGAGATAGCATTTGAGGTTTATCTTCAAGAAATTTGCAATTAACCTCCG 1680
 Db 1621 CAATTTTCTGAGATAGCATTTGAGGTTTATCTTCAAGAAATTTGCAATTAACCTCCG 1680
 Qy 1681 CTCTTTCAAAATGCAAACTCAGTAGAATTTCCAAAGATGAGAGAGGCTCTCTGTA 1740
 Db 1681 CTCTTTCAAAATGCAAACTCAGTAGAATTTCCAAAGATGAGAGAGGCTCTCTGTA 1740
 Qy 1741 AGGGAAGTACTGATTTCTGGGTCCAGGAAATTCAGAGTCTAGGAAATCTAGTCAAC 1800
 Db 1741 AGGGAAGTACTGATTTCTGGGTCCAGGAAATTCAGAGTCTAGGAAATCTAGTCAAC 1800

QY	1801	1GTTGAATCTAGGCTATTGGGGCAAAATTA	CTTAAGAGCTTTAATTCAGGTGAATTTGT	1860
Db	1801	TGTTGAATCTAGGCTATTGGGGCAAAATTA	CTTAAGAGCTTTAATTCAGGTGAATTTGT	1860
QY	1861	ACTGACCTCATGGGTGGAGGTCA	TAAAGTTTCAGCAACAATTAAATATGTTATG	1920
Db	1861	ACTGACCTCATGGGTGGAGGTCA	TAAAGTTTCAGCAACAATTAAATATGTTATG	1920
QY	1921	CTTGTTATTGTTTTATAGCATATTTGAAGTGAT	ACCTGCATATCCAGAGAAATGTGCA	1980
Db	1921	CTTGTTATTGTTTTATAGCATATTTGAAGTGAT	ACCTGCATATCCAGAGAAATGTGCA	1980
QY	1981	AAGCTGAAGACACAGTGAAAAAGTGAAG	CTGTAACTGTAAAGTCAATG	2040
Db	1981	AAGCTGAAGACACAGTGAAAAAGTGAAG	CTGTAACTGTAAAGTCAATG	2040
QY	2041	AGGAGAGCAAAATGTTTTCTTTCCTTCTT	CTCCATACATTTGGATTTTCA	2100
Db	2041	AGGAGAGCAAAATGTTTTCTTTCCTTCTT	CTCCATACATTTGGATTTTCA	2100
QY	2101	CTTATTTCTCTACACACAGGGCATTA	CTTTGGTGTGTGTATGTATATATCTATA	2160
Db	2101	CTTATTTCTCTACACACAGGGCATTA	CTTTGGTGTGTGTATGTATATATCTATA	2160
QY	2161	TATCTAGATGTCAGTTTCCAAATCTTGCMA	ATTGTAGAAATCTGAATCTGATGCAAT	2220
Db	2161	TATCTAGATGTCAGTTTCCAAATCTTGCMA	ATTGTAGAAATCTGAATCTGATGCAAT	2220
QY	2221	TAGCTTGTCTAGTCACTAACCTCAGAT	CTGGGATGTGTAGTGCGCAGATAGGGCTA	2280
Db	2221	TAGCTTGTCTAGTCACTAACCTCAGAT	CTGGGATGTGTAGTGCGCAGATAGGGCTA	2280
QY	2281	GAATCAGAGTCCGTGAATCCCAAGCCAGCA	CTTTCCGGTGGTGAATACGATTAGTT	2340
Db	2281	GAATCAGAGTCCGTGAATCCCAAGCCAGCA	CTTTCCGGTGGTGAATACGATTAGTT	2340
QY	2341	TGATACCATTAATCTTAGGAAAAATTTCA	GTTCCTATTTGATCATGTAAATCTGAAGAAG	2400
Db	2341	TGATACCATTAATCTTAGGAAAAATTTCA	GTTCCTATTTGATCATGTAAATCTGAAGAAG	2400
QY	2401	TACTTGTTTAAAAACAGAAAAATGCTTAG	GGGCAATTTATTTGAAGTCAATTTTGAAGT	2460
Db	2401	TACTTGTTTAAAAACAGAAAAATGCTTAG	GGGCAATTTATTTGAAGTCAATTTTGAAGT	2460
QY	2461	CATTAATGCAATGCTTTTGAACCTTGAAAG	ATAATCCAGAACATATGAAAAAAGACTGG	2520
Db	2461	CATTAATGCAATGCTTTTGAACCTTGAAAG	ATAATCCAGAACATATGAAAAAAGACTGG	2520
QY	2521	ACTTGCAATATGGGCTAATTTCTGAGAT	TAATAACCTTATTTGAATTAATCATATATC	2580
Db	2521	ACTTGCAATATGGGCTAATTTCTGAGAT	TAATAACCTTATTTGAATTAATCATATATC	2580
QY	2581	TATCAGATATTTAGTTAATAGTTTAAAG	CAGAGACAGAACCCCGATCTCTTTATACAG	2640
Db	2581	TATCAGATATTTAGTTAATAGTTTAAAG	CAGAGACAGAACCCCGATCTCTTTATACAG	2640
QY	2641	GTTCAAAATAGGTAAAAATTAATTAAGAT	TTTATTAAGTAAATGGAAGTCTGAATT	2700
Db	2641	GTTCAAAATAGGTAAAAATTAATTAAGAT	TTTATTAAGTAAATGGAAGTCTGAATT	2700
QY	2701	GGTAGAGCTTTTTTCTTCCCTCTCCCAT	CAAGACCTTCATCTAGTTTCTTCCCTCA	2760
Db	2701	GGTAGAGCTTTTTTCTTCCCTCTCCCAT	CAAGACCTTCATCTAGTTTCTTCCCTCA	2760
QY	2761	CTCCCTCAACAAATCCCTAGGAGCATTTAT	CAATGTGGGCTGTATATTTCTATAG	2820
Db	2761	CTCCCTCAACAAATCCCTAGGAGCATTTAT	CAATGTGGGCTGTATATTTCTATAG	2820
QY	2821	TGAATGATACATCATGTGGCTATTGGTGA	AAAAAACAACAATGGAAGCTTAGACTA	2880
Db	2821	TGAATGATACATCATGTGGCTATTGGTGA	AAAAAACAACAATGGAAGCTTAGACTA	2880

QY	2881	ACAAATAGCATCTCAACCCCAAAACCGGAGGAATGATTTGGAGCACTGAAAGTGAAGCTTCTT	2940
Db	2881	ACAAATAGCATCTCAACCCCAAAACCGGAGGAATGATTTGGAGCACTGAAAGTGAAGCTTCTT	2940
QY	2941	GCAAGCGAGTCAACTAAATCTAGAAACATGAAAGCTCAGTTGATGCAATTTTCAGT	3000
Db	2941	GCAAGCGAGTCAACTAAATCTAGAAACATGAAAGCTCAGTTGATGCAATTTTCAGT	3000
QY	3001	AACAAGCTTAACTTAAATCCCCCTTTTTCCTCTTGACCTTTTAAAAAAGCGTTTCTTC	3066
Db	3001	AACAAGCTTAACTTAAATCCCCCTTTTTCCTCTTGACCTTTTAAAAAAGCGTTTCTTC	3066
QY	3061	CTGAGCATCAATTAAATGATGATGCTGTTTCTTCTCTTGATTAATTGAAGCTTTGACTT	3120
Db	3061	CTGAGCATCAATTAAATGATGATGCTGTTTCTTCTCTTGATTAATTGAAGCTTTGACTT	3120
QY	3121	TTAAATTTGTGAAGCCAGTCTCTGTGTAATGAACTATATCTAGACATGGAAGGCGTAA	3186
Db	3121	TTAAATTTGTGAAGCCAGTCTCTGTGTAATGAACTATATCTAGACATGGAAGGCGTAA	3186
QY	3181	TGTTAGCATGCGACAGACAAAGCATGCTTTACACATCTTGCTTTAAAAATTTACTGATTC	3246
Db	3181	TGTTAGCATGCGACAGACAAAGCATGCTTTACACATCTTGCTTTAAAAATTTACTGATTC	3246
QY	3241	ATCTTGCTTGTTGTTCTTTAGAAAAGTGAAGTGTAGAGAGAGAACTCATGTTGATCTG	3300
Db	3241	ATCTTGCTTGTTGTTCTTTAGAAAAGTGAAGTGTAGAGAGAGAACTCATGTTGATCTG	3300
QY	3301	TGTGATTTTCAAGACCTTTAATCCATTTTGAAGAATCAATTTATATTTTGCAATGGGTT	3366
Db	3301	TGTGATTTTCAAGACCTTTAATCCATTTTGAAGAATCAATTTATATTTTGCAATGGGTT	3366
QY	3361	GCCATGTGGAAGAGATTAATGCTTTTTTGTGTAGTCTCAGAAAGCACAGAGGAGGA	3426
Db	3361	GCCATGTGGAAGAGATTAATGCTTTTTTGTGTAGTCTCAGAAAGCACAGAGGAGGA	3426
QY	3421	GCAATGTTGTTTCAGAGAAAGATCAACAGAGAGAGAAACTGTCAAGGCTGTCTGAATATGG	3486
Db	3421	GCAATGTTGTTTCAGAGAAAGATCAACAGAGAGAGAAACTGTCAAGGCTGTCTGAATATGG	3486
QY	3481	GTTGTTTTGGGAGGCTTTAATCCCTCTCTGTTGGGGGTAAAAAGCAAGACCGAGTTGGTA	3546
Db	3481	GTTGTTTTGGGAGGCTTTAATCCCTCTCTGTTGGGGGTAAAAAGCAAGACCGAGTTGGTA	3546
QY	3541	GTTAAATTCATGACAGACAGTGAAGGAGACGATTAACCTTAAATCTTTATATAGTCTTGAG	3606
Db	3541	GTTAAATTCATGACAGACAGTGAAGGAGACGATTAACCTTAAATCTTTATATAGTCTTGAG	3606
QY	3601	TCTTTGAGATGAAAAGATATCTTTTTTGCCCTATGTCAAAAGAAAGTATGAAAAGGTGA	3666
Db	3601	TCTTTGAGATGAAAAGATATCTTTTTTGCCCTATGTCAAAAGAAAGTATGAAAAGGTGA	3666
QY	3661	AAGGCGGAGAGAAAAGCGAGAAAAGGAAGACATGATTTATATGAGAGCAATGCTGACA	3726
Db	3661	AAGGCGGAGAGAAAAGCGAGAAAAGGAAGACATGATTTATATGAGAGCAATGCTGACA	3726
QY	3721	AGGTTTTCTGGAATATATGCAATPATGATGTAGTAGGAAATTCAGTAGGAGATGCTT	3786
Db	3721	AGGTTTTCTGGAATATATGCAATPATGATGTAGTAGGAAATTCAGTAGGAGATGCTT	3786
QY	3781	TTCACTTGAATTTGGGTTTCTCTTCGATTAATAGTTTGGATCTCATCTGCAATTGACTT	3846
Db	3781	TTCACTTGAATTTGGGTTTCTCTTCGATTAATAGTTTGGATCTCATCTGCAATTGACTT	3846
QY	3841	GGAGAGAGAAAGATGATGTTTAGACCTATATCTGGTTTCTATTTAACTTAAGCAAGTGT	3906
Db	3841	GGAGAGAGAAAGATGATGTTTAGACCTATATCTGGTTTCTATTTAACTTAAGCAAGTGT	3906
QY	3901	GAAAAGACTTATTTGGTATTTTTTCCCAAAAGTGAAGAACTTTCTTTTACTGTTTGTCA	3966
Db	3901	GAAAAGACTTATTTGGTATTTTTTCCCAAAAGTGAAGAACTTTCTTTTACTGTTTGTCA	3966
QY	3961	AAAAAGTGAATAGAAAAAGCCTTAATGTAATGTGTGAATATACATGTTCAAAAGTCATTTG	4026

Db	3361	AAAAGTGGAAATAGAAAACCCTTAATGTATTGGTAATACATGTTCCAAAGTCATTGG	4020
Qy	4021	AGTAGAGATGTTTTAAATCAGAGAGTGCAAATCAATTTGGCTTCCCTGGACCACTTGAA	4080
Db	4021	AGTAGAGATGTTTTAAATCAGAGAGTGCAAATCAATTTGGCTTCCCTGGACCACTTGAA	4080
Qy	4081	GAATTTGCTTGGTACACATTAATAATACAGAACATATGCTGATGAGCTTAAAAAGTCCA	4140
Db	4081	GAATTTGCTTGGTACACATTAATAATACAGAACATATGCTGATGAGCTTAAAAAGTCCA	4140
Qy	4141	TGCATTAATCTCATACGTGTTTTAAAGAAAGTTATGAATTCCTGTTAGGGTGCATTCAAG	4200
Db	4141	TGCATTAATCTCATACGTGTTTTAAAGAAAGTTATGAATTCCTGTTAGGGTGCATTCAAG	4200
Qy	4201	CTGTCTGGGCGCATGTGGCGCTGTGGCTGCAGATTGACAGAGCTCCTTTAATGTAATC	4260
Db	4201	CTGTCTGGGCGCATGTGGCGCTGTGGCTGCAGATTGACAGAGCTCCTTTAATGTAATC	4260
Qy	4261	TGTCATATAGTATGTTTTGGAGCTGCAGAAACAGGCCAAGCATATAGGTGGCACTGGGAT	4320
Db	4261	TGTCATATAGTATGTTTTGGAGCTGCAGAAACAGGCCAAGCATATAGGTGGCACTGGGAT	4320
Qy	4321	CCCCAGATCCAGGCTCATTGAGTCCCTGCTCTGCTGTTAAGAGGGGTGTCAATCC	4380
Db	4321	CCCCAGATCCAGGCTCATTGAGTCCCTGCTCTGCTGTTAAGAGGGGTGTCAATCC	4380
Qy	4381	TCTGCCCCAGCTTTTAAACAGCTTCATTATGATGAGTGACCTGCAGAAATGATAGCTGCTG	4440
Db	4381	TCTGCCCCAGCTTTTAAACAGCTTCATTATGATGAGTGACCTGCAGAAATGATAGCTGCTG	4440
Qy	4441	GTGGCCTCTCAGTCCAGAGAGCCGTCATTTTAAGCTCTTTGGCAATCATCAATACTAA	4500
Db	4441	GTGGCCTCTCAGTCCAGAGAGCCGTCATTTTAAGCTCTTTGGCAATCATCAATACTAA	4500
Qy	4501	AGGATATTTACTATGAATGTTTTACAAATGCTTAAACTCGGTTTTCTGTCTCATCAACC	4560
Db	4501	AGGATATTTACTATGAATGTTTTACAAATGCTTAAACTCGGTTTTCTGTCTCATCAACC	4560
Qy	4561	TAACTTGGCAATTTCTAATTTGTTCACATTGAGAAACATGGCATPAATAGCTCAATPACTT	4620
Db	4561	TAACTTGGCAATTTCTAATTTGTTCACATTGAGAAACATGGCATPAATAGCTCAATPACTT	4620
Qy	4621	TTCGATCTTATTTTTCACAGCTTGGAGAGTGGAGAGATCAAGGCAATTTGAGAACTGG	4680
Db	4621	TTCGATCTTATTTTTCACAGCTTGGAGAGTGGAGAGATCAAGGCAATTTGAGAACTGG	4680
Qy	4681	ATTTCGCTTTATGCTCTGAGAAATGCTTCGATTTGACACAGCAAAAGCTGAAAAATGA	4740
Db	4681	ATTTCGCTTTATGCTCTGAGAAATGCTTCGATTTGACACAGCAAAAGCTGAAAAATGA	4740
Qy	4741	ATAACTAACCCTTTCCCTGCTGTAAGAAATACAAATTTGATGTCGCCCAAGGCAATTTT	4797
Db	4741	ATAACTAACCCTTTCCCTGCTGTAAGAAATACAAATTTGATGATCCCAAGGCAATTTT	4797

Accession	Source	Accession	Source
RESULT 2		AA030646	standard; DNA; 4797 bp.
AA030646			
ID	AA030646		
XX			
AC	AA030646;		
XX			
DT	21-May-2002 (first entry)		
XX			
DE	Human TIF genomic DNA.		
XX			
KW	T cell derived inducible factor; TIF; interleukin-21; IL-21; human;		
KW	STAT transcription factor; acute phase protein; inflammation;		
KW	chromosome 12; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	W0200210393-A2.		

PX	07-FEB-2002.
PD	
PF	27-JUN-2001; 2001WO-US20485.
XX	
PR	27-JUL-2000; 2000US-0626617.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
XX	
PI	Dumontier L, Renaud J;
XX	
DR	WPI; 2002-195964/25.
XX	
CC	Claim 6; Page 56-58; 64pp; English.
XX	
CC	The invention relates to nucleic acid molecules encoding T cell
CC	derived inducible factors (TIFs) also known as interleukin-21 (IL-21).
CC	TIF polynucleotides are upregulated by the cytokine, IL-9, IL-TIF or
CC	IL-21 molecules are implicated in activation of STAT transcription
CC	factors, acute phase proteins and inflammation. The present sequence
CC	is human TIF genomic DNA located on chromosome 12.
SQ	
Seq	Sequence 4797 BP; 1339 A; 910 C; 1063 G; 1485 T; 0 other;
Query Match	100.0%; Score 4797; DB 24; Length 4797;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 4797;	Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 TGCAACAAGCAAAATCTTCAGAACAGATTCTCTCCACGTCACCAGTTGTCTGAGTAGG 60
Db	1 TGCAACAAGCAAAATCTTCAGAACAGATTCTCTCCACGTCACCAGTTGTCTGAGTAGG 60
OY	61 AATTGTCTGCANATGGCGGCCCTGCAGAAAATCTTGAGCTCTTTTCTTAATGGGGACCTGG 120
Db	61 AATTGTCTGCANATGGCGGCCCTGCAGAAAATCTTGAGCTCTTTTCTTAATGGGGACCTGG 120
OY	121 CCACAGACTGCTCTCTCTCTTGCCCTCTTGATGACAGGGAGGAGSACCTGGGCCCATCA 180
Db	121 CCACAGACTGCTCTCTCTCTTGCCCTCTTGATGACAGGGAGGAGSACCTGGGCCCATCA 180
OY	121 GCATCCCACTGCAGGCTTGACAAAGTCCAATCTCCAGAGCCCTATATCACAAACCCACT 240
Db	121 GCATCCCACTGCAGGCTTGACAAAGTCCAATCTCCAGAGCCCTATATCACAAACCCACT 240
OY	241 TCATGCTGGCTTAAGAGGATATACATCTCAATCTGCTCTTTCTGCTGGATCTACTTGA 300
Db	241 TCATGCTGGCTTAAGAGGATATACATCTCAATCTGCTCTTTCTGCTGGATCTACTTGA 300
OY	301 ATCCAAATAGTCTTTAACTTTCTTCAGAGCATCTCTAAGAAGCTTTAGGAACCCACTGT 360
Db	301 ATCCAAATAGTCTTTAACTTTCTTCAGAGCATCTCTAAGAAGCTTTAGGAACCCACTGT 360
OY	361 TTATCCCTGAAGGATATAATTTTCGTTTTTCAGAGACTCTTTGGAAATCTGGCTTT 420
Db	361 TTATCCCTGAAGGATATAATTTTCGTTTTTCAGAGACTCTTTGGAAATCTGGCTTT 420
OY	421 TTTTTCCTTGAACCTCTTCCTTCATTTTGGCCTTATATACATATGATGAATTTT 480
Db	421 TTTTTCCTTGAACCTCTTCCTTCATTTTGGCCTTATATACATATGATGAATTTT 480
OY	481 CCCAAAGAGCGGCATTCAGTATATCATCTGATGATTTTTCCTTTATGCTCTGTG 540
Db	481 CCCAAAGAGCGGCATTCAGTATATCATCTGATGATTTTTCCTTTATGCTCTGTG 540
OY	541 CATGTTCTTAAATCCATGACACATCTGAAATTCGCTTTTATGATGATGATGCTCT 600
Db	541 CATGTTCTTAAATCCATGACACATCTGAAATTCGCTTTTATGATGATGATGCTCT 600
OY	601 GGGGAGACGGGATGGGACATGCTATATGATTAATTTTTTTCTTATTTGCTCAATGTC 660


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Db 601 GGGAGACGGGATGGGACATGTCATATTAATTTTTTTTCTATTGCTCAATGTC 660
Qy 661 AGACCCCTTAGTCTTTTCTTCTCTTCAAGCTAGCTTGATTAACAACAAGAGCTTGG 720
Db 661 AGACCCCTTAGTCTTTTCTTCTCTTCAAGCTAGCTTGATTAACAACAAGAGCTTGG 720
Qy 721 TCTCATTTGGGAGAAACTGTTCCACGAGTCAAGTGAAGTACGACGTTTGACGAAACGAG 780
Db 721 TCTCATTTGGGAGAAACTGTTCCACGAGTCAAGTGAAGTACGACGTTTGACGAAACGAG 780
Qy 781 CCGGTGCCCCGACATGGGTACTTGGGGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 840
Db 781 CCGGTGCCCCGACATGGGTACTTGGGGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 840
Qy 841 TGAACCTTTCTGTTCCCTTCCACCTGACAGATGAGTGAAGCTGATCTGATGAAGCAG 900
Db 841 TGAACCTTTCTGTTCCCTTCCACCTGACAGATGAGTGAAGCTGATCTGATGAAGCAG 900
Qy 901 GTGCTGAACCTTCACTTGAAGAGTGTCTTCCCTCAATCTGATGAGTTCCAGCTTAT 960
Db 901 GTGCTGAACCTTCACTTGAAGAGTGTCTTCCCTCAATCTGATGAGTTCCAGCTTAT 960
Qy 961 ATGAGAGAGTGTGCCCCCTTCTGCGACAGGCTCAGAGCAAGGCTTAAGCAGATGTA 1020
Db 961 ATGAGAGAGTGTGCCCCCTTCTGCGACAGGCTCAGAGCAAGGCTTAAGCAGATGTA 1020
Qy 1021 TCACTCTCAGACCTATGCGCCACCTACCCCTCTTCCCTTCCACAGAGACCCCTTAC 1080
Db 1021 TCACTCTCAGACCTATGCGCCACCTACCCCTCTTCCCTTCCACAGAGACCCCTTAC 1080
Qy 1081 CCCAATCTCTCTCTCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTT 1140
Db 1081 CCCAATCTCTCTCTCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTT 1140
Qy 1141 TGTATATAGAGATCATTTGGGATCATAGATTAATTTGCTTGTGCTTGAATGATCATC 1200
Db 1141 TGTATATAGAGATCATTTGGGATCATAGATTAATTTGCTTGTGCTTGAATGATCATC 1200
Qy 1201 TTGATTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Db 1201 TTGATTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Qy 1261 TCTTTCGAGAAAAAGGCACTCAGGTTGCGTAAGATGAGAAAGTGTGGAAAAATCTTA 1320
Db 1261 TCTTTCGAGAAAAAGGCACTCAGGTTGCGTAAGATGAGAAAGTGTGGAAAAATCTTA 1320
Qy 1321 GCTGTGAGAAATGATCCATTAAGTCTTAAGTGTGAGGGGAGGAGTGGCATGAGAGAA 1380
Db 1321 GCTGTGAGAAATGATCCATTAAGTCTTAAGTGTGAGGGGAGGAGTGGCATGAGAGAA 1380
Qy 1381 ATTGAAGAGAAAGTGGGAAATGGGAAAGCTTAAAGTGGGAGTGGGAGTGGGAGTGG 1440
Db 1381 ATTGAAGAGAAAGTGGGAAATGGGAAAGCTTAAAGTGGGAGTGGGAGTGGGAGTGG 1440
Qy 1441 GCCCTGTTGATGTCATGGGAGCCCAAAATCGAGGCGTGTGAACCTTGATGCCCTGAA 1500
Db 1441 GCCCTGTTGATGTCATGGGAGCCCAAAATCGAGGCGTGTGAACCTTGATGCCCTGAA 1500
Qy 1501 CATTGGAACATATGAAAAAAGTTGATGAGTGGGAGGAGGAGGAGGAGGAGGAGGAG 1560
Db 1501 CATTGGAACATATGAAAAAAGTTGATGAGTGGGAGGAGGAGGAGGAGGAGGAGGAG 1560
Qy 1561 ACTGAAGAGGCTTAATTTTCAATGAGATGTTTATGATACATTTCTTGTCTAAGCAT 1620
Db 1561 ACTGAAGAGGCTTAATTTTCAATGAGATGTTTATGATACATTTCTTGTCTAAGCAT 1620
Qy 1621 CAATTTCTGAGATACATGAGATGAGGATTTATCTTACAGAAATTTGATTAACCTCG 1680
Db 1621 CAATTTCTGAGATACATGAGATGAGGATTTATCTTACAGAAATTTGATTAACCTCG 1680
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Db 1681 CTCCTTCAACAAATGCAATCTCAGATGATTTCCCAAGATGAAGAGGCTCTTGA 1740
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Db 1741 AGGAGATGATGATTTCTGCGCTCCAGAGGAATTCAGAGCTCAGAGAAATCTAGCTAC 1800
Qy 1801 TGTGAAATCTAGGTCATGAGGAGAAATTAATCAAGGCTTAATCCAGGTAATGT 1860
Db 1801 TGTGAAATCTAGGTCATGAGGAGAAATTAATCAAGGCTTAATCCAGGTAATGT 1860
Qy 1861 ACTGTACCTCAATGGGAGTGGAGGATGATTAAGTTCAGAGCAACATTAAGATTA 1920
Db 1861 ACTGTACCTCAATGGGAGTGGAGGATGATTAAGTTCAGAGCAACATTAAGATTA 1920
Qy 1921 CTTGTATTTGTTTATAGCATTTGAAGTGAATCCTGATATCCAGAGAAATGTCAA 1980
Db 1921 CTTGTATTTGTTTATAGCATTTGAAGTGAATCCTGATATCCAGAGAAATGTCAA 1980
Qy 1981 AAGCTGAAGACACAGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2040
Db 1981 AAGCTGAAGACACAGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2040
Qy 2041 AGGAGAGCAAAATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2100
Db 2041 AGGAGAGCAAAATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2100
Qy 2101 CTTGATTTCTCTACACAGAGGCGATTAATTTGAGTGTGATGATGATGATGATGAT 2160
Db 2101 CTTGATTTCTCTACACAGAGGCGATTAATTTGAGTGTGATGATGATGATGATGAT 2160
Qy 2161 TATCTAATGATCAGTTTCCAAATTTGCAAAATTTGCAAAATTTGCAAAATTTGCA 2220
Db 2161 TATCTAATGATCAGTTTCCAAATTTGCAAAATTTGCAAAATTTGCAAAATTTGCA 2220
Qy 2221 TAGCTGTCTAGTACATTAACCTCAGATTCGGGAGTGTGATGAGGAGATAGGCTA 2280
Db 2221 TAGCTGTCTAGTACATTAACCTCAGATTCGGGAGTGTGATGAGGAGATAGGCTA 2280
Qy 2281 GAATGAGGTCCTCTGAAATCCCAAGCCAGACCTTTTCCGGTGTGATGATGATGAT 2340
Db 2281 GAATGAGGTCCTCTGAAATCCCAAGCCAGACCTTTTCCGGTGTGATGATGATGAT 2340
Qy 2341 TGTATCAATTAATCTTAGGAAATTTCAATTCCTATGATGATGATGATGATGATGAT 2400
Db 2341 TGTATCAATTAATCTTAGGAAATTTCAATTCCTATGATGATGATGATGATGATGAT 2400
Qy 2401 TACTGTTTAAAAACAGAAAAATGCTATGAGGCAATTTATTTGAATCTTTTGAAGT 2460
Db 2401 TACTGTTTAAAAACAGAAAAATGCTATGAGGCAATTTATTTGAATCTTTTGAAGT 2460
Qy 2461 CATTATGATGCTTGTGAAACCTTGAAGATTAATCTCAGAACATGAGAAAGAGCTGG 2520
Db 2461 CATTATGATGCTTGTGAAACCTTGAAGATTAATCTCAGAACATGAGAAAGAGCTGG 2520
Qy 2521 ACTTGCAATATGAGGCTAATTTCTGAGTAAATCACTATTTGATTAATCAATATTC 2580
Db 2521 ACTTGCAATATGAGGCTAATTTCTGAGTAAATCACTATTTGATTAATCAATATTC 2580
Qy 2581 ACTTGCAATATGAGGCTAATTTCTGAGTAAATCACTATTTGATTAATCAATATTC 2640
Db 2581 ACTTGCAATATGAGGCTAATTTCTGAGTAAATCACTATTTGATTAATCAATATTC 2640
Qy 2641 GTTCAAAATAGATTAATTAATTAAGATTTATTAATTAATTAATTAATTAATTAAT 2700
Db 2641 GTTCAAAATAGATTAATTAATTAAGATTTATTAATTAATTAATTAATTAATTAAT 2700
Qy 2701 GGTAGAGCTTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2760
Db 2701 GGTAGAGCTTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2760
Qy 2761 CTCCTCAACAAATCCCTAGGAGCATTTATCCATGAGGCTGTGTATCATTTCTATAG 2820
Db 2761 CTCCTCAACAAATCCCTAGGAGCATTTATCCATGAGGCTGTGTATCATTTCTATAG 2820
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2821 TGAATGATACCATCATGTGGCTTATTTGGTGAAGAAACAACATAGGAAGGCTTGACTA 2880
2821 TGAATGATACCATCATGTGGCTTATTTGGTGAAGAAACAACATAGGAAGGCTTGACTA 2880
2881 ACAATATGACTCACCCCAAAACCGAGGAATGATATGAGAGCAAGTGAAGTGCCTCTT 2940
2881 ACAATATGACTCACCCCAAAACCGAGGAATGATATGAGAGCAAGTGAAGTGCCTCTT 2940
2941 GCACAGAGTACAACTTAATCTCAGAAACATGAAAGCTCCAGTTGATGGAATTTTCAGT 3000
2941 GCACAGAGTACAACTTAATCTCAGAAACATGAAAGCTCCAGTTGATGGAATTTTCAGT 3000
3001 AACAGCTTAACCTTAATCTCCCTTTTCCCTCTGACTTTTAAAGAGGCTTCTTC 3060
3001 AACAGCTTAACCTTAATCTCCCTTTTCCCTCTGACTTTTAAAGAGGCTTCTTC 3060
3061 CTGACCATCATTTAATGAGTGTGACTGTTCTTCTTGATTAATGAAAGGCTTGTAGT 3120
3061 CTGACCATCATTTAATGAGTGTGACTGTTCTTCTTGATTAATGAAAGGCTTGTAGT 3120
3121 TTAATTTGTGAAGCCCACTTCTTGTATAGAACTATATCTAGACATGAGGCTGAA 3180
3121 TTAATTTGTGAAGCCCACTTCTTGTATAGAACTATATCTAGACATGAGGCTGAA 3180
3181 TGTAGCATGCGACAGACAGGAGCATGCTTACACATCTTGCTTAAGAAATTAAGTATTC 3240
3181 TGTAGCATGCGACAGACAGGAGCATGCTTACACATCTTGCTTAAGAAATTAAGTATTC 3240
3241 ATCTTCTGTTGTCTTTAGAAAGTGAAGTGAAGTGAAGAGAGAACTCATGATGATCG 3300
3241 ATCTTCTGTTGTCTTTAGAAAGTGAAGTGAAGTGAAGAGAGAACTCATGATGATCG 3300
3301 TGTGATTTTCAAGACCTTTAATCCATTTTGAAGATCAATTTCAATTTGCAATGGGTT 3360
3301 TGTGATTTTCAAGACCTTTAATCCATTTTGAAGATCAATTTCAATTTGCAATGGGTT 3360
3361 GCCATGTGAAGAGTATGCTTTTGTGCTGAGTCTTGAGAAAGACAGAGAGAGAGA 3420
3361 GCCATGTGAAGAGTATGCTTTTGTGCTGAGTCTTGAGAAAGACAGAGAGAGAGA 3420
3421 GCATGTTGTTTCAGAGAAAGATCAACAGAGAGAGAACTGTGAGAGCTGTGAAATAGG 3480
3421 GCATGTTGTTTCAGAGAAAGATCAACAGAGAGAGAACTGTGAGAGCTGTGAAATAGG 3480
3481 GCAATGTTGTTTCAGAGAAAGATCAACAGAGAGAGAACTGTGAGAGCTGTGAAATAGG 3480
3481 GCAATGTTGTTTCAGAGAAAGATCAACAGAGAGAGAACTGTGAGAGCTGTGAAATAGG 3480
3481 GTGGTTTGGAGGCAATTAATTCCTCTGCTGTTGGGGTAAAGACAGAAACGAGGTTGTA 3540
3481 GTGGTTTGGAGGCAATTAATTCCTCTGCTGTTGGGGTAAAGACAGAAACGAGGTTGTA 3540
3541 GTAAATGATGATGACAGACAGTGGGAGAGATTAATTAATTAATTTCTTTATAGTCTTGAG 3600
3541 GTAAATGATGATGACAGACAGTGGGAGAGATTAATTAATTAATTTCTTTATAGTCTTGAG 3600
3601 TCTTTGAGATGAAAGAAATATCTTTTGGCTTATGTCAAAAGAGATGAGAAAGTGA 3660
3601 TCTTTGAGATGAAAGAAATATCTTTTGGCTTATGTCAAAAGAGATGAGAAAGTGA 3660
3661 AAGGCGGAGAAACAGAGAAAGAGAAAGCAATGATATTAATGAGCAATGTGTGACA 3720
3661 AAGGCGGAGAAACAGAGAAAGAGAAAGCAATGATATTAATGAGCAATGTGTGACA 3720
3721 AGGTTTCTTGAATTAATGCAATATGATATGATATGAGAAATTTCAAGAGGATGCTT 3780
3721 AGGTTTCTTGAATTAATGCAATATGATATGATATGAGAAATTTCAAGAGGATGCTT 3780
3781 TTCACTTGAATTTGGGTTCTCTTGATTAAGTTGGAGTCTCATCTGCAATTTGACTT 3840
3781 TTCACTTGAATTTGGGTTCTCTTGATTAAGTTGGAGTCTCATCTGCAATTTGACTT 3840
3841 GGAGAGAGAAAGAAATGATGATGAGACCTATATCTGTTTCTATTAACCTAAAGCAAGT 3900
3841 GGAGAGAGAAAGAAATGATGATGAGACCTATATCTGTTTCTATTAACCTAAAGCAAGT 3900

3901 GAAAGACTTATTTGGTATTTTCCACAAAAGTGAAGAACTTTCTTTACTGTTTCA 3960
3901 GAAAGACTTATTTGGTATTTTCCACAAAAGTGAAGAACTTTCTTTACTGTTTCA 3960
3961 AAAAGTGAATATGAAAGAAAGCCTTAATGATTTGGTGAATATCATGTTCAAAAGTCAATTTG 4020
3961 AAAAGTGAATATGAAAGAAAGCCTTAATGATTTGGTGAATATCATGTTCAAAAGTCAATTTG 4020
4021 AGTAGAGATGTTTAAATCCAGAGTGTCCAAATCAATTTGGGCTCCCTGGACACCTTGAAA 4080
4021 AGTAGAGATGTTTAAATCCAGAGTGTCCAAATCAATTTGGGCTCCCTGGACACCTTGAAA 4080
4081 GAATTTCTTGGTACACATATAATCAAGAAACATAGCTGATGAGCTTAAGAAAGTCA 4140
4081 GAATTTCTTGGTACACATATAATCAAGAAACATAGCTGATGAGCTTAAGAAAGTCA 4140
4141 TGCATTAATCTCATACCTGTTTAAAGAAAGTGAATTTCTGTTAAGGTCATTTCAAG 4200
4141 TGCATTAATCTCATACCTGTTTAAAGAAAGTGAATTTCTGTTAAGGTCATTTCAAG 4200
4201 CTGTCTGGGCGCATGCGGCGCTGGGCTGGAGTGGAGCAAGCTCTTAATGATATC 4260
4201 CTGTCTGGGCGCATGCGGCGCTGGGCTGGAGTGGAGCAAGCTCTTAATGATATC 4260
4261 TGTATATGATATGTTTGGAGCTGCAGAAACAGGCCAATTAATGAGTGCATCGGAT 4320
4261 TGTATATGATATGTTTGGAGCTGCAGAAACAGGCCAATTAATGAGTGCATCGGAT 4320
4321 CCCCAGATCCAGCTCCTACTTCACTTCACTCTCTGCTGTTAAGAGGGTGTCAATC 4380
4321 CCCCAGATCCAGCTCCTACTTCACTTCACTCTCTGCTGTTAAGAGGGTGTCAATC 4380
4381 TCTGCCAGCTTTAAACAGCTTATAGTGAAGTGCACCTGAATTAATGATGCTGCTG 4440
4381 TCTGCCAGCTTTAAACAGCTTATAGTGAAGTGCACCTGAATTAATGATGCTGCTG 4440
4441 GTGGCTCTCAGTCCAGAGAGCCGTCAATTTAACTCTTGGCAATCATCAATACTAA 4500
4441 GTGGCTCTCAGTCCAGAGAGCCGTCAATTTAACTCTTGGCAATCATCAATACTAA 4500
4501 AGGATATTAATGATATGTTTAAACAAATGCTTAAACTCGGTTCTGTCTCATCAAC 4560
4501 AGGATATTAATGATATGTTTAAACAAATGCTTAAACTCGGTTCTGTCTCATCAAC 4560
4561 TTAATCTGCAATTTCTAATTTGTCACCTTAAGAAACATGAGCAATTAATGCTCAATACT 4620
4561 TTAATCTGCAATTTCTAATTTGTCACCTTAAGAAACATGAGCAATTAATGCTCAATACT 4620
4621 TTGCATTTCTAATTTTCAAGCTTGGAGAGAGTGAAGATCAAGCAATTTGAGAACTGG 4680
4621 TTGCATTTCTAATTTTCAAGCTTGGAGAGAGTGAAGATCAAGCAATTTGAGAACTGG 4680
4681 ATTGCTGTTTATGCTCTGAGAAATGCTTGAATTTGACAGCAAAAGCTGAAAGAAATGA 4740
4681 ATTGCTGTTTATGCTCTGAGAAATGCTTGAATTTGACAGCAAAAGCTGAAAGAAATGA 4740
4741 ATAACTAACCCCTTCTCTGCTGTAAGAAATCAATTAATGATGCTCCCAAGGCAATTTT 4797
4741 ATAACTAACCCCTTCTCTGCTGTAAGAAATCAATTAATGATGCTCCCAAGGCAATTTT 4797

RESULT 3
AAB27151
ID AAB27151 standard; DNA; 4797 BP.
XX AAB27151;
AC
XX
XX
DT 09-APR-2002 (first entry)
XX
DE Human T cell derived inducible factor (TIF) beta genomic DNA.
XX T cell derived inducible factor; TIF; cytokine; interleukin-9; IL-9;
KW protein therapy; STAT activation; differentiation; human; ds.

XX Homo sapiens.
OS
XX US6331613-B1.
XX
XX 18-DEC-2001.
XX
XX 18-OCT-1999; 99US-0419568.
XX
XX 26-OCT-1998; 98US-0178973.
XX 16-JUL-1999; 99US-0354243.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Dumoutier L, Loubet J, Renaud J;
XX
XX WPI, 2002-105277/14.
XX
XX Nucleic acids encoding T cell derived inducible factors useful for
XX inducing STAT activation in cells -
XX
XX Claim 1; Column 31-36; 24pp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule, which
XX encodes a T cell derived inducible factor comprising an amino acid
XX sequence encoded by 6 defined nucleotide sequences. The nucleic acid
XX molecules are shown to be up regulated by the cytokine interleukin-9
XX (IL-9) and are described as T Cell Derived Inducible Factors (TIFs). The
XX invention is used in protein therapy. The nucleic acid molecules encode
XX proteins which induce STAT activation in cells. They can be used, for
XX example, in the stimulation of regeneration of targeted tissues.
XX Further, their inhibitors or antagonists can be used to retard, prevent
XX or inhibit differentiation of other tissues. The present sequence is
XX human TIF beta genomic DNA.

Sequence 4797 BP; 1339 A; 910 C; 1063 G; 1485 T; 0 other;

Query Match 100.0%; Score 4797; DB 24; Length 4797;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 4797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACAGCAGATCTTCAGAACAGGTTCTCTCCCAAGTCACAGATGCTCGAGTTG 60
DB 1 TGCACAGCAGATCTTCAGAACAGGTTCTCTCCCAAGTCACAGATGCTCGAGTTG 60
QY 61 AATTGTGCAATGAGCCCGCTGCAAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGG 120
DB 61 AATTGTGCAATGAGCCCGCTGCAAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGG 120
QY 121 CCACAGCTGCTCTCTCTTCTTGGCCCTCTTGTACAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 CCACAGCTGCTCTCTCTTCTTGGCCCTCTTGTACAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 GCTCCACAGCTGAGGCTTGAAGAGTCAAGTTCACAGAGCCCTATATCACCAACCGACCT 240
DB 181 GCTCCACAGCTGAGGCTTGAAGAGTCAAGTTCACAGAGCCCTATATCACCAACCGACCT 240
QY 241 GCTCCACAGCTGAGGCTTGAAGAGTCAAGTTCACAGAGCCCTATATCACCAACCGACCT 240
DB 241 GCTCCACAGCTGAGGCTTGAAGAGTCAAGTTCACAGAGCCCTATATCACCAACCGACCT 240
QY 241 TCAATCTGCTAAGAGAGTATCAATCTCAATCTGCTCTTCTTGTAGATCTACTTGA 300
DB 241 TCAATCTGCTAAGAGAGTATCAATCTCAATCTGCTCTTCTTGTAGATCTACTTGA 300
QY 301 ATCCAAATAGTCTTAAATCTTCTTCAAGAGATCTTAAGAGCTTTAGAAACCCACTGT 360
DB 301 ATCCAAATAGTCTTAAATCTTCTTCAAGAGATCTTAAGAGCTTTAGAAACCCACTGT 360
QY 361 TTAATCTGAGGAGTATCAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 420
DB 361 TTAATCTGAGGAGTATCAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 420
QY 421 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 480
DB 421 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 480

QY 481 CCCAAGAGGGGCGCATTCAGTAATCAATCTGATGATTTTCTTCTTCTTCTTCTTCTTCTG 540
DB 481 CCCAAGAGGGGCGCATTCAGTAATCAATCTGATGATTTTCTTCTTCTTCTTCTTCTG 540
QY 541 CATTGTTTAAATCAGACACACATCTGAATTCGTTTATGCTTTATGATGTTGCTCT 600
DB 541 CATTGTTTAAATCAGACACACATCTGAATTCGTTTATGCTTTATGATGTTGCTCT 600
QY 601 GGGGAGAGCGGATGGGSCATGTCATGATGATTAATTTTCTTCTTCTTCTTCTTCTTCT 660
DB 601 GGGGAGAGCGGATGGGSCATGTCATGATGATTAATTTTCTTCTTCTTCTTCTTCTTCT 660
QY 661 AGACCCCTAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 720
DB 661 AGACCCCTAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 720
QY 721 TCTCATTTGGGAGAAAGTCTTCAAGAGTCAAGTATGATGATGATGATGATGATGATGAT 780
DB 721 TCTCATTTGGGAGAAAGTCTTCAAGAGTCAAGTATGATGATGATGATGATGATGATGAT 780
QY 781 CCGTGTGCGTCCATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 CCGTGTGCGTCCATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 TGACCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
DB 841 TGACCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
QY 901 GTGCTGAATCTCAACCTTGAAGAAAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960
DB 901 GTGCTGAATCTCAACCTTGAAGAAAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960
QY 961 ATGACAGAGTGTGAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020
DB 961 ATGACAGAGTGTGAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020
QY 1021 TCAAGCTTCAAGCTATGAGGCTTCAAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080
DB 1021 TCAAGCTTCAAGCTATGAGGCTTCAAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080
QY 1081 CCCAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140
DB 1081 CCCAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140
QY 1141 TGTATCAGAGTCAATTTGGAGTCAATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1141 TGTATCAGAGTCAATTTGGAGTCAATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 TTGATTTATAGTGTGATGAGGCTTGAAGCTTAAGTGAAGTGAAGGCGCATTTGTTG 1260
DB 1201 TTGATTTATAGTGTGATGAGGCTTGAAGCTTAAGTGAAGTGAAGGCGCATTTGTTG 1260
QY 1261 TCTTGGAAAAAGCACTAGGTTGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1320
DB 1261 TCTTGGAAAAAGCACTAGGTTGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1320
QY 1321 GCTGTGAAAAAGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 GCTGTGAAAAAGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 ATTAAGAGAAAGTGGAGAAATGGAGGCTTAAAGTGTGAGTGTGAGTGTGAGTGTGAG 1440
DB 1381 ATTAAGAGAAAGTGGAGAAATGGAGGCTTAAAGTGTGAGTGTGAGTGTGAGTGTGAG 1440
QY 1441 GCGCTGTGATGATGATGAGGAGGCAAAATGAGAGGCTGTGAAGCTTGAATGCGCTGAA 1500
DB 1441 GCGCTGTGATGATGATGAGGAGGCAAAATGAGAGGCTGTGAAGCTTGAATGCGCTGAA 1500
QY 1501 CATTGAAACTATGAAAAAAGTTGAGTGAAGTGGGCGCAATGAAGGCGCTTGAAGCTT 1560
DB 1501 CATTGAAACTATGAAAAAAGTTGAGTGAAGTGGGCGCAATGAAGGCGCTTGAAGCTT 1560
QY 1561 ACTGAAGAGGCGCTTAATTTTCAATGAGATGTTTATGATCAATTTCTTGTCTAAGATG 1620

Db	1561	ACTGAGAGGGCTTAATTTTTCACATGAGATGTTTATGTACATTTCTTGTTACGATG	1620
Qy	1621	CAATTTTCTGGAGATACGATTGAGGTTTATTTCTTACAGATTTGCATAACTACGCG	1680
Db	1621	CAATTTTCTGGAGATACGATTGAGGTTTATTTCTTACAGATTTGCATAACTACGCG	1680
Qy	1661	CTCTTTCCACAAATGCAAACTCAGTAGGATTTCCCAAAAGTAGAGAGAGTCTCTGTGA	1740
Db	1661	CTCTTTCCACAAATGCAAACTCAGTAGGATTTCCCAAAAGTAGAGAGAGTCTCTGTGA	1740
Qy	1741	AGGGAAGGATCGGATTTCTGGCGTCCAAAGGAAATTCAAGAGCTCAGAAATCTAGTCCAC	1800
Db	1741	AGGGAAGGATCGGATTTCTGGCGTCCAAAGGAAATTCAAGAGCTCAGAAATCTAGTCCAC	1800
Qy	1801	TGTTGAATCTAGGTCATTTGTGGGCAAAATTAAGAGCTTTAATTCACAGTAAATGTG	1860
Db	1801	TGTTGAATCTAGGTCATTTGTGGGCAAAATTAAGAGCTTTAATTCACAGTAAATGTG	1860
Qy	1861	ACTGTAACCTCATGGGTGTGAGGTTCTAAAGTTTCAGCAACAATTAAATAGTATG	1920
Db	1861	ACTGTAACCTCATGGGTGTGAGGTTCTAAAGTTTCAGCAACAATTAAATAGTATG	1920
Qy	1921	CTTGTAATTTGTTTATAGCATATTTGAAGTATACCTCGCATTCACAGGAATGTCCAA	1980
Db	1921	CTTGTAATTTGTTTATAGCATATTTGAAGTATACCTCGCATTCACAGGAATGTCCAA	1980
Qy	1981	AAGCTGAAGACACAGTAAAGGTAGGACTGATACTGCATAGCTAAGTCAATGCAAT	2040
Db	1981	AAGCTGAAGACACAGTAAAGGTAGGACTGATACTGCATAGCTAAGTCAATGCAAT	2040
Qy	2041	AGGAGAGCAAAATGTTTCTTCTCTTCTTCTTCCCATCAGTCTTGATTTTTTCA	2100
Db	2041	AGGAGAGCAAAATGTTTCTTCTCTTCTTCTTCCCATCAGTCTTGATTTTTTCA	2100
Qy	2101	CTTGATTTCTCTACCAACGAGGCGATTACTTTGGTGTGTGTATGATATATCTATA	2160
Db	2101	CTTGATTTCTCTACCAACGAGGCGATTACTTTGGTGTGTGTATGATATATCTATA	2160
Qy	2161	TATCTAGATGTCAAGTTCCAAATCTGCGAAATTTGAGAACTCTAAGCTGGTGGGAATCT	2220
Db	2161	TATCTAGATGTCAAGTTCCAAATCTGCGAAATTTGAGAACTCTAAGCTGGTGGGAATCT	2220
Qy	2221	TAGCTGTCTAGTCACATPAACCTCAGATCTTGGGGATGTGATGCGCAGATAGGCGCTA	2280
Db	2221	TAGCTGTCTAGTCACATPAACCTCAGATCTTGGGGATGTGATGCGCAGATAGGCGCTA	2280
Qy	2281	GAAATGCAGGTTCTCTGAAATCCCAAGCCAGCACTTTCCCGGTGATACAGATTAAGTTT	2340
Db	2281	GAAATGCAGGTTCTCTGAAATCCCAAGCCAGCACTTTCCCGGTGATACAGATTAAGTTT	2340
Qy	2341	TGATACCACTAAATCTTAGGGAAATTTTCAGATTCCTATGTGCTATGATTAATCTAAGAG	2400
Db	2341	TGATACCACTAAATCTTAGGGAAATTTTCAGATTCCTATGTGCTATGATTAATCTAAGAG	2400
Qy	2401	TACTTGTTTAAAAACAGAAATATCCCTATGCGCAAAATTTATTGAAGTCATTTTGAAGT	2460
Db	2401	TACTTGTTTAAAAACAGAAATATCCCTATGCGCAAAATTTATTGAAGTCATTTTGAAGT	2460
Qy	2461	CATTATGCAATGCTTTGAAAACCTTGGAAGATTAACCTAGAACATGAGAAAGAGCTGG	2520
Db	2461	CATTATGCAATGCTTTGAAAACCTTGGAAGATTAACCTAGAACATGAGAAAGAGCTGG	2520
Qy	2521	ACCTGCAATATGAGGCTAATTTCTGAGATTAATAACCTTATTTTGAATATCATTAATATC	2580
Db	2521	ACCTGCAATATGAGGCTAATTTCTGAGATTAATAACCTTATTTTGAATATCATTAATATC	2580
Qy	2581	TATCAGATATTTGATTAATAGTTTAAAGCAGAGCAGCAACCCCGATCTCTTTATACAG	2640
Db	2581	TATCAGATATTTGATTAATAGTTTAAAGCAGAGCAGCAACCCCGATCTCTTTATACAG	2640
Qy	2641	GTTCAATATGAGTAAAAATATTAGTAAAGATTTTATTATAGTTAAATGGAAGTCTGAAT	2700
Db	2641	GTTCAATATGAGTAAAAATATTAGTAAAGATTTTATTATAGTTAAATGGAAGTCTGAAT	2700

Db	2641	GTTCAAATAGAGCTAAAAATATTAGTAAGACATTTATTAATAGTAAATGGAAGCTCGAATT	2700
Qy	2701	GGTAGAGCTTTTCTTCTCTCTCCCATAGACCTTCATCTAGTTCTTCTCTTCA	2760
Db	2701	GGTAAGCTTTTCTTCTCTCTCCCATAGACCTTCATCTAGTTCTTCTCTTCA	2760
Qy	2761	CTCCCTCAACAAATCCCTAGGGAGCATTTATCCATGCTGGCTGTGTACTTTCTATAG	2820
Db	2761	CTCCCTCAACAAATCCCTAGGGAGCATTTATCCATGCTGGCTGTGTACTTTCTATAG	2820
Qy	2821	TGAATGATACATATGTGGCTTATTTGGTAAAGAACAAACATGGAAGGCTTAGACTA	2880
Db	2821	TGAATGATACATATGTGGCTTATTTGGTAAAGAACAAACATGGAAGGCTTAGACTA	2880
Qy	2881	ACAATAGTACCTCACCCCAAAACCGSAGATGATTAGAGCAGTGAAGTACGCTCTT	2940
Db	2881	ACAATAGTACCTCACCCCAAAACCGSAGATGATTAGAGCAGTGAAGTACGCTCTT	2940
Qy	2941	GCAGCAGGTACAACTAAATACTAGAAACATGAAGGCTCCAGTTGATGGAATTTTCACT	3000
Db	2941	GCAGCAGGTACAACTAAATACTAGAAACATGAAGGCTCCAGTTGATGGAATTTTCACT	3000
Qy	3001	AACAAGCTTAACCTTAATTCCTCCCTTTTCCCTCTGACTTTTAAAAAACCGTTCTTC	3060
Db	3001	AACAAGCTTAACCTTAATTCCTCCCTTTTCCCTCTGACTTTTAAAAAACCGTTCTTC	3060
Qy	3061	CTGAGCATCATTTATATGATGTGACTGTTTCTTCTCTTGATTAATGAAGCTTTGATGT	3120
Db	3061	CTGAGCATCATTTATATGATGTGACTGTTTCTTCTCTTGATTAATGAAGCTTTGATGT	3120
Qy	3121	TTAAATGTGGAAGCCAGTTCTCTGTTATAGAACTATATCTAGACATGGAGGCTGAA	3180
Db	3121	TTAAATGTGGAAGCCAGTTCTCTGTTATAGAACTATATCTAGACATGGAGGCTGAA	3180
Qy	3181	TGTTAGCATGCGCACAGACAGGACATGCTTACACATCTGCTTAAAAATTAAGTATTC	3240
Db	3181	TGTTAGCATGCGCACAGACAGGACATGCTTACACATCTGCTTAAAAATTAAGTATTC	3240
Qy	3241	ATCTTGCTGTTGTCTTTAGAAAAGTGAAGGTGAGAGAGAGATCTCATGGTGCATG	3300
Db	3241	ATCTTGCTGTTGTCTTTAGAAAAGTGAAGGTGAGAGAGATCTCATGGTGCATG	3300
Qy	3301	TGTGATTTTCAAGACCTTTAATCCATTTTGAAGAAATCAATTTTGAATGGGTT	3360
Db	3301	TGTGATTTTCAAGACCTTTAATCCATTTTGAAGAAATCAATTTTGAATGGGTT	3360
Qy	3361	GCCATGTGGAAGAGTATATGCTTTTCTGCTAGCTTCAGAAAGCACAGAGGGGAGA	3420
Db	3361	GCCATGTGGAAGAGTATATGCTTTTCTGCTAGCTTCAGAAAGCACAGAGGGGAGA	3420
Qy	3421	GCATGTGTTCAAGAAAGATCAACAGAGAGAAACCTGTCAGAGCTGTCTGAAATGG	3480
Db	3421	GCATGTGTTCAAGAAAGATCAACAGAGAGAAACCTGTCAGAGCTGTCTGAAATGG	3480
Qy	3481	GTGGTTTGGAGGACATTAATTCCTCTCGTGTGGGGTTAAAGACAGAACCGAGGTTGGTA	3540
Db	3481	GTGGTTTGGAGGACATTAATTCCTCTCGTGTGGGGTTAAAGACAGAACCGAGGTTGGTA	3540
Qy	3541	GTAATAATGATAGACAGACAGTAGGGAGACGATTAACCTTTAAATCTTTATATAGTCTTGGAG	3600
Db	3541	GTAATAATGATAGACAGACAGTAGGGAGACGATTAACCTTTAAATCTTTATATAGTCTTGGAG	3600
Qy	3601	TCTTTGAGATAGAAAAGAAATCTTTTGGGCTTATGTCAAAAGAAAGTATGGAAGGTGA	3660
Db	3601	TCTTTGAGATAGAAAAGAAATCTTTTGGGCTTATGTCAAAAGAAAGTATGGAAGGTGA	3660
Qy	3661	AAGGCGGAAAGAAAGCAGAAAGAGAAACATGTATATATAGGAGACAAATGCTGACA	3720
Db	3661	AAGGCGGAAAGAAAGCAGAAAGAGAAACATGTATATATAGGAGCAATGCTGACA	3720
Qy	3721	AGGTTTTTCTTGAATAATATGCAAAATATATATAGATTAGAGAAATTCAGTAGGAATGCTT	3780
Db	3721	AGGTTTTTCTTGAATAATATGCAAAATATATATAGATTAGAGAAATTCAGTAGGAATGCTT	3780


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QY 3781 TTCACTGAAATTTGGGTTTCTTCGATTAAGTTGGAGTCTCATCTGCAATTTGACTT 3840
DB 3781 TTCACTGAAATTTGGGTTTCTTCGATTAAGTTGGAGTCTCATCTGCAATTTGACTT 3840
QY 3841 GGAAGAGAAAGAAATGAAATTTAGGACTATATCTGTTTCTATTAATAAGCAAGTGG 3900
DB 3841 GGAAGAGAAAGAAATGAAATTTAGGACTATATCTGTTTCTATTAATAAGCAAGTGG 3900
QY 3901 GAAAAGACTTATTTGGTATTTTCCACAAAAGTGAAGAACTTTCTTTTACCTGTTTGCA 3960
DB 3901 GAAAAGACTTATTTGGTATTTTCCACAAAAGTGAAGAACTTTCTTTTACCTGTTTGCA 3960
QY 3961 AAAAGGTGAAATAGAAAAAGCCTTAATGTAATGGTGAATACATGTTCAAGTCATTTG 4020
DB 3961 AAAAGGTGAAATAGAAAAAGCCTTAATGTAATGGTGAATACATGTTCAAGTCATTTG 4020
QY 4021 AGTAGAGATGTTTAAATCAGAGAGTCCAAATCATTTGGCTTCCCTGAGCCACTTGAAA 4080
DB 4021 AGTAGAGATGTTTAAATCAGAGAGTCCAAATCATTTGGCTTCCCTGAGCCACTTGAAA 4080
QY 4081 GAATTTGTTGGTACACATTAATAACAGACATAGCTGATGAGCTAAAAAAGTCCA 4140
DB 4081 GAATTTGTTGGTACACATTAATAACAGACATAGCTGATGAGCTAAAAAAGTCCA 4140
QY 4141 TGCAATAAATCTCATCTGTTTAAAGAAATTTATGTAATTTCTGTAGGGTGCATTCAG 4200
DB 4141 TGCAATAAATCTCATCTGTTTAAAGAAATTTATGTAATTTCTGTAGGGTGCATTCAG 4200
QY 4201 CTGTCTGGGCAATGTGCGGCTGTGGCTGCAAGTTGACAGCTCTTATAGTAATC 4260
DB 4201 CTGTCTGGGCAATGTGCGGCTGTGGCTGCAAGTTGACAGCTCTTATAGTAATC 4260
QY 4261 TGTCAATAATGTTTGGAGCTGCAAAACAGGCCAAGCATTAATGGTGGCACTGGGAT 4320
DB 4261 TGTCAATAATGTTTGGAGCTGCAAAACAGGCCAAGCATTAATGGTGGCACTGGGAT 4320
QY 4321 CCCCAGATCCAGGCTCATCTCACTCTCTGCTCTGTTAAAGAGGGGTGTCAACTC 4380
DB 4321 CCCCAGATCCAGGCTCATCTCACTCTCTGCTCTGTTAAAGAGGGGTGTCAACTC 4380
QY 4381 TCTGCCAGCTTTTAAACAGCTTCATTAAGTGTAGGTGACCTGAATTTGATGCTGCTG 4440
DB 4381 TCTGCCAGCTTTTAAACAGCTTCATTAAGTGTAGGTGACCTGAATTTGATGCTGCTG 4440
QY 4441 GTGGCTCTCAGTCCAGAGAGCCGTCATTTAAGCTCTTTGGCAATCATTAATACTTA 4500
DB 4441 GTGGCTCTCAGTCCAGAGAGCCGTCATTTAAGCTCTTTGGCAATCATTAATACTTA 4500
QY 4501 AGGATATTACTATGAATGTTTAAAGCTTAAAGCTCGGTTCTGCTCCATCAACC 4560
DB 4501 AGGATATTACTATGAATGTTTAAAGCTTAAAGCTCGGTTCTGCTCCATCAACC 4560
QY 4561 TAACTTGCATTTTCAATTTGTTGCACTTTAGAAAAACATGGCATTAATGCTCAAACTT 4620
DB 4561 TAACTTGCATTTTCAATTTGTTGCACTTTAGAAAAACATGGCATTAATGCTCAAACTT 4620
QY 4621 TTGCACTTTTATTTTCAAGCTTGGAGAGAGTGAAGATCAAGCAATTTGAGAACTGG 4680
DB 4621 TTGCACTTTTATTTTCAAGCTTGGAGAGAGTGAAGATCAAGCAATTTGAGAACTGG 4680
QY 4681 ATTTCCTGTTATGCTCTGAGAAATGCTGCAATTTGACCAAGCAAGCTGAAAAATGA 4740
DB 4681 ATTTCCTGTTATGCTCTGAGAAATGCTGCAATTTGACCAAGCAAGCTGAAAAATGA 4740
QY 4741 AATACTAACCCCTTTTCCCTGTAGAAATTAACATTAAGTGGCCCAAGCGATTTT 4797
DB 4741 AATACTAACCCCTTTTCCCTGTAGAAATTAACATTAAGTGGCCCAAGCGATTTT 4797

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RESULT 4
AAA28840
ID AAA28840 standard; DNA; 4796 BP.

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XX AC AAA28840;
XX DT 04-SEP-2000 (first entry)
XX DE Human T cell inducible factor genomic DNA.
XX KW TIF; T cell derived inducible factor; interleukin 9; STAT; IL-9;
XX KW Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist;
XX KW probe; chromosome 12q15; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 108..4717
XX FT FT /tag= a
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XX FT intron 258..688
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XX FT exon 689..754
XX FT intron 755..870
XX FT FT /tag= d
XX FT exon 871..1014
XX FT FT /tag= e
XX FT intron 1015..1938
XX FT FT /tag= f
XX FT exon 1939..2004
XX FT FT /tag= g
XX FT intron 2005..3837
XX FT FT /tag= h
XX FT exon 3838..4796
XX FT FT /tag= i
XX FT FT /tag= j
XX PN WO200024758-A1.
XX PD 04-MAY-2000.
XX PF 18-OCT-1999; 99WO-US24424.
XX PR 26-OCT-1998; 98US-0178973.
XX PR 16-JUL-1999; 99US-0354243.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Dumoutier L, Louhed J, Renaud J;
XX DR WPI; 2000-422495/36.
XX DR P-PSDB; AAY92879.
XX PT New nucleic acid molecule encoding a T cell derived inducible factor
XX PS for treating asthma, an allergy or lymphoma
XX PS Claim 1; Page 39-40; 46pp; English.
XX PS
XX CC This DNA encodes a human T cell derived inducible factor (TIF). The gene
XX CC was mapped to chromosome 12q15. The human TIF was identified based on
XX CC homology to a murine TIF, which was identified by subtraction cloning
XX CC from a murine lymphoma cell line BWS147 in the presence or absence of
XX CC interleukin 9 (IL-9). BWS147, can be grown in vitro, without the need to
XX CC add any cytokines to its culture medium. Many IL-9 activities are
XX CC mediated by activation of STAT transcription factors. The novel TIFs were
XX CC expressed in the presence of IL-9, but not in its absence. TIFs induce
XX CC STAT activation in cells. They can be used, e.g. in the stimulation of
XX CC regeneration of targeted tissues. Their inhibitors or antagonists can be
XX CC used to retard, prevent or inhibit differentiation of other tissues. The
XX CC TIFs and their coding sequences are useful in the treatment of asthma,
XX CC allergies and lymphoma (claimed). They are also useful for identifying
XX CC compounds that inhibit or activate T cell induced factor activity in a
XX CC cell (claimed).
XX SQ Sequence 4796 BP; 1339 A; 912 C; 1063 G; 1482 T; 0 other;

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RESULT 6
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 ID AAD30628 standard, DNA; 7445 BP.
 XX AAD30628;
 AC
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Mouse T1F alpha genomic DNA.
 XX
 DE
 XX T cell derived inducible factor; T1F; interleukin-21; IL-21; mouse;
 KW STAT transcription factor; acute phase protein; inflammation; ds.
 XX
 OS Mus musculus.
 XX
 PN W0200210393-A2.

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Db 2561 TACTC-----CTGAGACCCACTGCGGACATACATCTCTAC 2595
QY 629 GATAAATTTTTTTCTATTGCTCAATGTCCAGACCCCTTAGCTTTTTTCTCTCCAG 688
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QY 869 AGATGATGAGCGCTGCTATCTGATGAAGACAGTGTGATTCACCCCTTGAAGAAGTGC 928
Db 2818 AGGCTAAAGATCAGTGTACCTGATGAAGACAGTGTCTCACTTCACTCGAAGACGTTCC 2877
QY 929 TGTTCCTTCATCTGATAGTGTCCAGACCTTATATGACAGAGGTGTGCTTCTGCGCA 988
Db 2878 TGCTCCCCAGTCAACAGGTTCCAGCCCTACATCAGAGAGGTGTATCTTCTTGACCA 2937
QY 989 GGCTGAGAACAGGCTTAAGACATGTTAGTTCAAGTCTCTCAGCTATGCCACTTACC 1048
Db 2938 AACTAGACATAGCTCAGCTCTGTGTATGATCTATCTGTGCTATCTGTCTCTCT 2997
QY 1049 CTCTTCCCTCTCTTCCACAGAGACCCCTTACCCTTCTCTCTCTCTCTCTCTCTCT 1108
Db 2998 CTCTCTCTCTATCTCAGTATGAGAACCCAGGCTCTGCTCTCTCTCTCTCTCTCTCT 3057
QY 1109 TAACTTACAGAGAAAGTGTCTTGGACAGACGTTATTCAGAGTCA-----TTTGGG 1161
Db 3058 GGAGGGGCTCAGACACCAACCATCATAGGCCACTTGAATATGTCACAAAGGCTTTGGC 3117
QY 1162 ATCATAGAGTATTTGCTTTTGTGCTGATGATCACTTGAAGTTATAGTGTGAATG 1221
Db 3118 TTCAATTAGTATATCTTGAAGTTGTATGATGAGCTTTATTTGTTTATCCATGAA 3177
QY 1222 GGGTCTGGAATTAAGTGTACAGAGCCGATTTGTTGTCTTGGAAAAAGGACATCTC 1281
Db 3178 AGAATCAACTCAATTTCTGTAGATGAGAAAGATTTGGGAACAAAAAGGCTTAGAT 3237
QY 1282 A-----GGTTGCTTAAGTATGAAAGGTGTGG 1309
Db 3238 AGAGAAACAGATCTGCTAGTATAGTATCTATATGGGGGAGAGGGGGGATTCACATGA 3297
QY 1310 GAAACATCTAGCTGTGAAATAGATTCATTTGATGATCTTGAAGTTGTGAGGGAGGGGATGG 1369
Db 3298 GTTACAATCTTGTGTGGGAGAGAAATTCATGATGATCAAGTATCTTGTGGCATGAGATC 3357
QY 1370 CATGAGAGAAATTAGAAAGAAAGTGGGAAATGGGAAGGCTTAA----- 1415
Db 3358 CACTAGTAAAGATCTTGTGTGGGGAGGGAATGSCACAGACAAAGTGTGAAGGAAGG 3417
QY 1416 -----GTGGGTGTGGGTGGGACAGCTGTGCTGTGATGTATGGGA 1460

Db 3418 AAGATGAGAGGCTCATAGTGTGGGGGTGAAGGTCACTCTTTTCTATGTATGAG 3477
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Db 3537 ATCCAGAGAGGCGGAGACTGTGGAGACCTGGCATTTAGGGA--AGGCGGCTTTT 3594
QY 1581 CACATGATATGTTTATGATATTTCTTGTCTTGAAGATGACATTTTCTGAGATACAT 1640
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QY 1641 TGAGGTTTATCTCTTACAGAAATTTGCAATTAATCTCGGCTTTCCACAAATGCAAC 1700
Db 3655 TCAAGTTCTGTTCT-----ACGTTCTTGTCTACTGTGTGAAAC 3693
QY 1701 CTCACTAGATTTTCCAAAGATGAAGAGAGTCTTGTGAAGGAAGTGAATCTGTG 1760
Db 3694 TTCACTAGATTTCCCAAGAGAGAGAGAGAGTCTTCTGTAAAGGAGGACCTGATTTCA 3753
QY 1761 GCGTCAAGGGAATTCAGAGCTCAGAAATCTAGTCACTGTGTAATCTAGTCAATG 1820
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QY 1821 TGGGCAAAATTAAGAGCTTATATCCAGTGAATTTGTAAGTCACTGACCTGAGTGTG 1880
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Db 4111 GTCCATTAAGTCTGTTAGCTGACCTGATATCTAGCTGGGTCTATAGATCTTCAATCTGTG 4170
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QY 2237 ATAACTCAGATTTGAGGAGTGTCAAGTGGAGAGATAGGGCTGAATGACGCTCTCTG 2296
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QY 2297 AATCCAGAGCAGACTTCTCCGAGTGTGATACAGATTAATTTTGTGTAACATTAATCT 2356
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QY 2357 TAGGAAATTTCAATTTCTTATGATCATATATCTGAAGAACTGTTTAAACA 2416
Db 4347 TTGGGAAA--GCCAGTTCCACGACCTTACATATCTGAAGAACATGACATTTGAACATA 4404
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Qy 2769 ACAAAATCCCTTAGGAGCATTTATCATGTGGCTGTGTACATTTCTATAGTGAATAT 2828
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Qy 4042 GAGTGCCATCATTTGGCTTCCCTGAGACCACTTGAAGAAATGTCTGTATACACAT 4101
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Qy 4102 AAAATACAAAGACATAGCTGATGAGCTAAATAAGTCCATCATTAATCTATCTGTT 4161
Db 6059 TACCTGTACAGGCCGAGCCCTGTGCTTGTGCTTGTGTTGTTGTTGTTGTTGTTGTTG 6118
Qy 4162 TAAAGAAATTTATGAATTTCTGTTAAGGTGATTCAAAGCTGTCTGGGCCATGTGGCC 4221
Db 6119 TCTGTACTTATGACAGATGAGTGAAGTGAAGCAACCTTTTCTTCC----- 6163
Qy 4222 CTGTGGGCTGAGGTTGGAACAAGCTCCTTAATGAATATCTGTCAADATGATTTTGAGC 4281
Db 6164 -----AACCCCACTAAATTTTATGACAAAGAACTGTATATTG 6205
Qy 4282 TGCAAAACAGGCCAAGCATATAGGTGGCACTCGGGAATCCCGAGATCCAGGCTCACT 4341
Db 6206 TGGGATACAGTGTATATGA----- 6227
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Qy 4402 TTTCAATGTGAGAGTGAAGTCACTGAAATGTAGAGCTGTGTGGGCT--CTCAGTCAAGGA 4460
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 QY 4686 CTGTTATGCTCTGAGAAATGCTGCAATTTGACAGAGCAAAAGCTGAAATGAAATAC 4745
 DB 6584 CTGTTATGCTCTGAGAAATGCTGCAATTTGACAGAGCAAAAGCTGAAATGAAATAC 6643
 QY 4746 TAACCCCTTCCCTCTGAGAAATACATTAATAGATCCCAAGCAATTTT 4797
 DB 6644 TGCTCTCTCTGCTCTGAGAAATACATTAATAGATCCCAAGCAATTTT 6695

RESULT 8
 ID AAA28816 standard; DNA; 7444 BP.
 AC AAA28816;
 XX 04-SEP-2000 (first entry)
 DT Murine T cell inducible factor alpha genomic DNA.
 DE
 XX TIF-alpha; T cell derived inducible factor; interleukin 9; STAT; IL-9;
 KM Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist; ss.
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT exon 1908..1932
 FT /tag= a
 FT /number= 1a
 FT CDS 2080..6615
 FT /tag= b
 FT /product= TIF-alpha
 FT intron 1933..2032
 FT /tag= c
 FT exon 2033..2262
 FT /tag= d
 FT /number= 1b
 FT intron 2263..2654
 FT /tag= e
 FT exon 2655..2720
 FT /tag= f
 FT intron 2721..2819
 FT /tag= g
 FT exon 2820..2963
 FT /tag= h
 FT intron 2964..3930
 FT /number= 3
 FT /tag= i
 FT exon 3931..3996
 FT /tag= j
 FT intron 3997..6538
 FT /tag= k
 FT exon 6539..7137
 FT /tag= l
 FT /number= 5

MO200024758-A1.
 PD 04-MAY-2000.
 PF 18-OCT-1999; 99WO-US24424.
 XX
 PR 26-OCT-1998; 98US-0178973.
 BR 16-JUL-1999; 98US-0354243.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA Dumoutier L, Loubed J, Renaud J;
 PI

XX MPI: 2000-422495/36.
 DR P-PSDB; AAY92877.
 XX
 PT New nucleic acid molecule encoding a T cell derived inducible factor
 PT for treating asthma, an allergy or lymphoma
 XX
 PS Claim 1: Page 34-37; 46pp; English.

CC This DNA encodes T cell derived inducible factor (TIF) alpha identified
 CC by subtraction cloning from a murine lymphoma cell line BW5147 in the
 CC presence or absence of interleukin 9 (IL-9). BW5147, can be grown in
 CC vitro, without the need to add any cytokines to its culture medium. Many
 CC IL-9 activities are mediated by activation of STAT transcription
 CC factors. The novel TIFs were expressed in the presence of IL-9, but not
 CC in its absence. TIFs induce STAT activation in cells. They can be used,
 CC e.g. in the stimulation of regeneration of targeted tissues. Their
 CC inhibitors or antagonists can be used to retard, prevent or inhibit
 CC differentiation of other tissues. The TIFs and their coding sequences are
 CC useful in the treatment of asthma, allergies and lymphoma (claimed). They
 CC are also useful for identifying compounds that inhibit or activate T cell
 CC induced factor activity in a cell (claimed).

XX
 SQ Sequence 7444 BP; 2058 A; 1570 C; 1596 G; 2220 T; 0 other;

Query Match 14.1%; Score 677.4; DB 21; Length 7444;
 Best Local Similarity 53.6%; Pred. No. 1.2e-167;
 Matches 2630; Conservative 0; Mismatches 1891; Indels 388; Gaps 43;

QY 29 CTCCTTCCCGATCACAGCTTGTGAGTATGAAATGCTGCAATGGCCGCTTCAGCA 88
 DB 2034 CTCCTTCCCGATCACAGCTTGTGAGTATGAAATGCTGCAATGGCCGCTTCAGCA 2093
 QY 89 ATCTGTAGAGCTTCTCTTATGAGGAGCCGCGCACAGCTGCTCTCTTGTGAGCCT 148
 DB 2094 ATCTGTAGAGCTTCTCTTATGAGGAGCCGCGCACAGCTGCTCTCTTGTGAGCCT 2153
 QY 149 CTGTGTACAGGAGAGAGAGCTGCGCCATCATGCTCCCATCTGAGAGCTTGTGACATCA 208
 DB 2154 GTGTGTACAGGAGAGAGAGCTGCGCCATCATGCTCCCATCTGAGAGCTTGTGACATCA 2213
 QY 209 CTTCAGAGAGCCCTATATACCAACCGACCTTATGCTGCTAGAGAGTATATATC 268
 DB 2214 CTTCAGAGAGCCCTATATACCAACCGACCTTATGCTGCTAGAGAGTATATATC 2273
 QY 269 AATCTGCTCTTCTCTGAGTATGCTGCAATGCTTAACTTTCTTCA 328
 DB 2274 TCTCTTCTCTGAGTATGCTGCAATGCTTAACTTTCTTCA 2333
 QY 329 GAGCATCTTAAAGAGCTTAAAGACCACTGTTATCCCTGAGAGTAAATTTCTG 388
 DB 2334 CGCTTATCTCGGAGCTCTCACTATATGTTT-----TCGTCTCTTAAAG 2382
 QY 389 TTTTTCAGAGCTTGTGGAATGCTGCTTTTCTTGAAGTCTTCTTCAAT 448
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 QY 449 TTTGAGCTTAAAGATGATGATGATTTTCCCAAGAGGCGCATTCATATCAT 508
 DB 2443 CTGAGCTTAAAGATGATGATGATTTTCCCAAGAGGCGCATTCATATCAT 2500
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 QY 629 GATTAATTTTCTTCTTAAAGCTTCTGCTGCTTCTTAAAGTCAATCTCTTGGC 688
 DB 2596 TTACAGGCTTTCTTCTTAAAGCTTCTGCTGCTTCTTAAAGTCAATCTCTTGGC 2654

QY 689 GCTAGCTGGCTGATTAACAACACAGACCTTGTCTCTATTGGGAGAAACTGTTCCACGGA 748
DB 2655 GCCAGCCTTGGCAGATTAACAACACAGACGCTCCGCTCATCGGGAGAAACTGTTCCGAGGA 2714
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DB 2715 GTCAGTGAAGCTTCCACTGTGATAGCAGGAC-----TACTCGGGAGCT 2761
QY 809 GGTGTGATGATGTTTGAAGCTTATACCTTATGACCCCTTCTGTTTCCCTTCCACTGC 868
DB 2762 GGTGACCCCTCGGGATAG---TGTAGATGATGACCCCTGCTGCTTCTGTCTACTGCTGC 2817
QY 869 AGATGATGAGCGCTGCTATCTGATGAAGCAGCTGTCAACTTCACTTGAAGAACTGC 928
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QY 1282 A-----GGTGGTGAAGTGAAGAAAGTGTGG 1309
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QY 1370 CATGAGAGAAATTAGAAAGAAAGTGGAAATGGGAAAGCTTAA----- 1415
DB 3358 CACTAGTACAAAGTACTTGTGGGGGAGGGGATGGCAAGAGCAAAAGTTGAAGGAAAG 3417
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DB 3418 AAGATGAGAGGCTCATGTGTGGGGGTGTGAAGGTCACTCTTTTCCATGTGATGGAG 3477
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QY 1701 CTCAGTAGGATTTCCAAAGATGAAGAGGTCTTGTGAAGGAAAGTACGTGATTCG 1760

DB 3694 TTCACTAGATTTCCCAAGAGCAGAGACGCTTCTGTAAAGGAGGACCTGGATTTCA 3753
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QY 2540 TTCTGGA-----GTAATTAACAATTTTGAATTAATCAATATCTATCAGATATG 2592
DB 4523 ATTTAGATCACTGTGATTAATAGCTATCATCTTAATTAATTAATAGGCTATATAT 4582
QY 2593 ATTTAGTTTAAAGCAAGACAGACAAAC--CCGATCTCTTTATACAGTTCAAATGA 2651
DB 4583 ATTTAAGATTAACAACAAAGATGATAGCTTCCCAATTTACTGTGCTGGTTTCAAAAG 4642
QY 2652 GTAAATAATTAAGTATGAGATTTATATAGTTAAATGAGAGCTGAATTTGTAAGCTTT 2711
DB 4643 GTAAATAATTAAGTATGATATTAATTAATAGTGTATGAAGTATGAGATGAAACCTTT 4702
QY 2712 TTTTCTCTCTCTCCATCAAGACCTTCAATCTTGAATTTCTTCTTCACTCTCAACA 2771
DB 4703 CTTACTTTTAACTTCA-----TTCTTGAATTTTCTTCTTCAACCCGATCA 4754
QY 2772 AATCCTTAGAGACATTTATCATGTGTGGGTGCTGATCATTTCTATGTATATATACC 2831

4755 AGCCATAGTAGACCACTATCTGCTGAGCTATTATATGACTTTACAGCAACAACACTT 4814
2832 ATCATGTGGCTTATTTGGTGAAGAAACA--ACAATGGAAGCTTAGACTTAACAATAGT 2889
4815 GCTGTGTGGCTCTTTGGGGAAGGAGACAGATAGCAGAGGCTCAGGCTAGCAAGTCTG 4874
2890 ACTCACCCCAAAACCGSAGAAATGATTTAGAGCAGTGAAGAGGCTCTT--GCAGCAG 2948
4875 ACTTCCCTTAAAGCCAGAGGCAATGATGTATAGCAAGAAAGTAGGCTTCTGCAAGTGG 4934
2949 GTACACTAAATACTCAGAAACATAGAGGCTCAGTTGATGGAATTTTCAGTAACAAGCT 3008
4935 GTGTCTTATAGTAATACAGAAACAGAGAGGCTCGTTGATGAAATTAACAGTAATATTC 4994
3009 TAACCTTAATTCCTCCCTTTTCCCTCTGACTTTTAAAAAAGCCTTTCTCTGAGCAT 3068
4995 TACCTTATCTCTCTTATTCGAAAC--TAAATCGTCTCTTTCTTCTGTGT 5044
3069 CATTAAATGAGTGTACTGTTCTCTCTTGTAAATGAAAGCTTTGATTTAAATG 3128
5045 AGCTGATTAACAACACTTGT--TTCTTTGAGTGTCAATGCTTTGATTTTATGTG 5102
3129 TGAAAGCCAGTCTCTGTATATAGAACTATTATCAGACATGAGAGGCTGAATGTAGCA 3188
5103 CTCTGCAAGTCTCTGTAGAG--GGTTGTATACCTTGACACCTGGGCTTGATGTAGCA 5160
3189 TGCCACAGACAAGCATCTTTACATCTTGTCTTAAAAAATTACTGATTTTATCTTCT 3248
5161 TGCCAAAGGACACACTCTGTAATCTGTGTAAGGTATTTATTTCACTTTACT-- 5214
3249 TGTGTCTTTGAAAGTGAAGTGTGAGAGAGAAATCTCATGTGA-- 3296
5215 --TTGTCTTTGAAAGGTGAAGCGTGTGAGAAAGAACTCACAGAGATGTGTCTGTG 5272
3297 -----TCTGTGATTTTCAAGACCTTTATCCATTTTGAAGAAATCAATTCA 3345
5273 TAGAAACTTTTTTTTCCCTTAAATGCCATATATCACTTTAGTCAAC--TTTGA 5329
3346 TATTTGCAATGGTGGCCATGTGAAGATGATTAATGCTTTTGTGCTGATGTAGCA 3405
5330 CTTTATATCAATGCTGTCAATGAAGATGTTTGGCCGCTCATGGCTGTGGAA 5389
3406 AGCA--CAGAGGGAGAGCAATGTTGTTCAGAGAAAGATCAACAGAGAGAAACTGTAG 3464
5390 AGCACAATAGGGAGAGAAATGTATGTGAGAAATCTGACCGGAGGAAACTGTGTAG 5449
3465 AGCTGTCTGAATAGGGTGTGTTTGGAGGCACTTAATCCCTCTGTGGGGGTAAAGC 3524
5450 AGCTCCCCGAAAGCA-----CCACAGTGTTAAGTAGAAC 5487
3525 AGAAGCAGGTTGTGATTAAT--GCATGACAGACAGTAGGAGGAGATTAATTTAAAT 3583
5488 AGTCACAGGTGGGCTCATGTATATGAAATGAAACAAGGAGGAAATAGTACTCAAAAGT 5547
3584 TCTTATATGCTTGGAGCTTTGATGATGAGAAAGAAATCTTTTGGGCTATGTCAAA 3643
5548 TTCAATAGGCTC--CGAGTCTTAAAGATCAAAATATGCTGC--TTGGGCTTCAATACAAAG 5604
3644 GAAATATGAAAG-------TGAAAGGGCGAAGAAAGCAGAGAAAGAGAAAC 3691
5605 GAAGTCTGGAGAGGAGACAGTGAAGAGGAAATGAAAGGAGAAACAGATGTAGAGG 5664
3692 CATGTATATATAGAGCAATAGTGACAGAGTTTCTTGAAATATGCAAAATATGATA 3751
5665 ACTTGAAAGCTACAAATCTCTACAGACATTTTCTTGAAACAATCTAAGAGTAGT 5724
3752 GATTAGAGGAATTTAGTAGGAATGCTTTTCACTGTAATTTGGTTCTCT--TGA 3808
5725 GGAATAGTATGATGAGGGGAGCTGTGTGCAATTTGAATCTGGGTTTTGTCTCTCA 5784
3809 TTAAGTTTGGATCTCATCTGCACTTACT--TGAGAGAGAAAGAAATGATGTAG 3864
5785 TTGAGTTTGAAGGCTACCTTTTACCCTGAAATGAGAGGAAAGAGGGGTAT 5844

3865 GACCTATATCTGTTTCTTATTAACTAAGCAAGTGAAGAAAGCTTATTTGGTATTTTC 3924
5845 GACTCTACCTCGAGGATTTTACTAGTTACGAAATGGAACAGACACTGGGAGCTCTCTT 5904
3925 CCACAAAGTGAAGAACTTTCTTACTGTTGTGCAAAAGGTGGAATATAGAAAGGCT 3984
5905 GACAAAAAATGGAACCTGTTGTGTCTTGTCTTTGTTTGTATTAAGAAAGCAGG 5964
3985 TAATGATTTGGTGAATACATGTTCAAAAGTCATTTGATGAGATGTTTAAATCAGAG 4044
5965 CAAGCCCGACACATAGGTTGATGATGAGGCTTTGATGACAGGCTTTGATGAGCAG 6024
4045 TGTCAATCATTTGGCTTCCCTGACCACTTGAAAGATTTCTTGTATACATATAA 4104
6025 TCATCAATAGTT-----GATCATGTGTCAGGTGAGGAGCTAC 6060
4105 ATACAGAAACAATGATGATGAGCTAAGAAAGTCCATGCAATTAATCTCATCTGTTTAA 4164
6061 CTGTACAGCCGAGCCCTGTGCTGCTCGCACTTAACATCTCCAGGCTTCAGTATCACTTC 6120
4165 GAAAGTTTGAATTTCTGTTAGGGTCAATCAAAAGCTGTCTGGGCATGTGGGCTG 4224
6121 TGCTACTTAGACAGTATAGAGTGTAGCAAACTTTTTC----- 6182
4225 TGGGCTCAGGTTGACAGAGCTCTTATTAAGTAATCTGTCAATAGATAGTTTGAAGCTGC 4284
6163 -----AACCCCACTAAATTTAATTAAGCAAAAGACTGTGTAATTTGGG 6207
4285 AAAACAGCCCAAGCATATAGGTGTGCACTCGGATCCCAAGATCCAGGCTCACTTCA 4344
6208 GATACAGTGTGATTAATGA----- 6226
4345 GTCTCTGTCTCTGTATAGAGGGGTGTCAACTCTGCGCCAGCTTTTAAACAGCTTC 4404
6227 -TCTATGTGTGCAATGTGCAAGGTTCATTAAGATAGATTAAGCCCATCAACAGCTTT 6285
4405 ATTAGTGTAGGTGACCTGCAATGTATGATGCTGTGTGTGCT--CTCAGTCCAGAGAGCC 4463
6286 ATGGGTGTGAATCAATCAATATAGGTAGATGCTGTGTGTGCTTAGGTCAAGAAAGGC 6345
4464 GTCAATTTAAGCTTTTGGCAAAATCAATCAATTAAGGAT--TTAC 4511
6346 ATGATTTAAGGTCTTGGCAAAATCAATTAATTAATCAATTAATTAATTAATTAATTAAT 6405
4512 TATGAATGTTTCAAAATGCTTAAACTCGGTTCTGTCTCCATCAACTATCTTGA 4571
6406 TATTAATCTTTTGAAGAGGCTATTAATCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 6465
4572 TTCT--AATTTGCTACTTTAGAAACAATGCAATTAATGCTCAAAATCTTTTGCATTC 4628
6466 GCTCTTTCAACTGTGTCACCTTTAGAAATGCTAATGCTAATGCTCAAAATGCTTTGTATTC 6525
4629 TTAATTTCAAGCTTGAAGAGAGTGAAGATCAAAATTTGAGAACTTGAATTTGCTG 4688
6526 TTATTTCAATGCTTGAAGAGAGTGAAGATCAAAATGCTAATGCTTGAATTTGCTG 6585
4689 TTTATGCTCTGAAGAAATGCTGATTTGACCAAGAGCAAGCTGAAATTAATTAATTAAT 4748
6586 TTTATGCTCTGAAGAAATGCTGATTTGACCAAGAGCAAGCTTGAATTAATTAATTAAT 4797
4749 CCCCCTTCCCTGTAGAAATTAACATTAATTAATGAGGAGGAGGAGGAGGAGGAGGAGG 4814
6646 TCTTCTGCTGCTTCTAAGAAAGCAATTAATTAATGAGGAGGAGGAGGAGGAGGAGGAGG 6694

RESULT 9
AAA2818
ID AAA2818 standard; DNA; 5935 BP.
AAA2818;
04-SEP-2000 (first entry)

XX DE Murine T cell inducible factor beta genomic DNA.
 XX KW TIF-beta; T cell derived inducible factor; interleukin 9; STAT; IL-9;
 XX KM Anti-asthmatic; anti-allergic; cyostatic; inhibitor; antagonist; ss.
 XX OS Mus sp.
 XX FH Key Location/Qualifiers
 XX FT CDS 399..5302
 XX FT /tag= a
 XX FT /tag= 355..584
 XX FT /tag= b
 XX FT /number= 1
 XX FT intron 585..975
 XX FT /tag= c
 XX FT /tag= 976..1041
 XX FT /tag= d
 XX FT intron 1042..1140
 XX FT /tag= e
 XX FT /tag= 1141..1284
 XX FT /tag= f
 XX FT /number= 3
 XX FT intron 1285..2203
 XX FT /tag= g
 XX FT /tag= 2204..2269
 XX FT /tag= h
 XX FT /number= 4
 XX FT intron 2270..5224
 XX FT /tag= i
 XX FT /tag= 5225..5824
 XX FT /tag= j
 XX FT /number= 5
 XX PN W0200024758-A1.
 XX PD 04-MAY-2000.
 XX PF 18-OCT-1999; 99WO-US24424.
 XX PR 26-OCT-1998; 98US-0178973.
 XX PR 16-JUL-1999; 98US-0354243.
 XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Dumoulier L, Louhed J, Renaud J;
 XX DR WPI: 2000-422495/36.
 XX DR P-PSDB; AA192878.
 XX PT New nucleic acid molecule encoding a T cell derived inducible factor
 XX PT for treating asthma, an allergy or lymphoma
 XX PS Claim 1: Page 41-42; 46pp; English.
 XX CC This DNA encodes T cell derived inducible factor (TIF) beta identified
 CC by subtraction cloning from a murine lymphoma cell line BMS147 in the
 CC presence or absence of interleukin 9 (IL-9). As compared to the coding
 CC region for TIF-alpha (see AA28816), that of TIF-beta has six silent
 CC changes. There are two changes which result in an inconsequential amino
 CC acid change (at both of positions 36 and 103, Val in TIF-alpha becomes
 CC Ile in TIF-beta). There is also a more significant change at position
 CC 112, where Gln becomes Arg. Many IL-9 activities are mediated by
 CC activation of STAT transcription factors. The novel TIFs were expressed
 CC in the presence of IL-9, but not in its absence. TIFs induce STAT
 CC activation in cells. They can be used, e.g. in the stimulation of
 CC regeneration of targeted tissues. Their inhibitors or antagonists can be
 CC used to retard, prevent or inhibit differentiation of other tissues. The
 CC TIFs and their coding sequences are useful in the treatment of asthma,
 CC allergies and lymphoma (claimed). They are also useful for identifying
 CC compounds that inhibit or activate T cell induced factor activity in a
 CC cell (claimed).

SQ Sequence 5935 BF; 1732 A; 1174 C; 1346 G; 1683 T; 0 other;
 Query Match 13.6%; Score 650; DB 21; Length 5935;
 Best Local Similarity 56.5%; Pred. No. 1.8e-160;
 Matches 1863; Conservative 0; Mismatches 1285; Indels 152; Gaps 29;
 29 CTCCTCCCGCAGTCCAGGCTGCTGAGTGAATTTCTGCAATGAGCCCGCTGCAGAA 88
 356 CTCCTCCTCAGATTATTAACCTTTTGACACTTGGCCATCGGTATGCTGCTGCAGAA 415
 89 ATCTGTAGGCTCTTTCCTTAAGGGACCTGGCCACAGCTGCTCTTCTTGGCCCT 148
 416 ATCTATAGTTTTCCTTAAGGGACCTTGGCCGACGCTGCTCTTCTCATTTGCCCT 475
 149 CTGTGTACAGGAGGAGAGAGCTGGCCCATTCAGTCCCATCTGCAGGCTTGAAGTCCA 208
 476 GTGGGCCAGAGAGGCAATGGCGTCCCATCAACACCGGGCAAGCTTGGGTGTCCA 535
 209 CTCACAGAGCCCTATATACCAACCGCACCTTCATGCTGGCTAAGAGGTATACATCTC 268
 536 CTCACAGAGCCCTATATACCAACCGCACCTTCATGCTGGCTAAGAGGTATACATCTC 595
 269 AATCTGCTCTTCTCGTGGATCTAATGCAATTAAGTCTTAACTTTCTTCA 328
 596 TCTCTTCTCTCCATACCGGCTTCCATTTCTGGAAGCACTTCAAACTTTAGGGGC 655
 329 GAGCATCTTAAGGCTTTAGGAACCACTGTTATCCCTGAGGCTAGATAATTTCTG 388
 656 GCTTTATCTCCGAGGCTCAGTCACTATGTTTCTGTCT-----CTTTAGAG 703
 389 TTTTTCAGAGACCTTTGGGAATCTGGCTTTTCTTTTCTTGAACCTTCTCTCAT 448
 704 ACTCTTAAGAGCTGGAATCTTTTCTATTTCTATTTCAAGCTCAGAGCACTTTCTAT 763
 449 TTTGGCCCTTATGATATATATGAAATTTTCCAAAGAGCGCCATTCAGTATCCAT 508
 764 CTGGCCCTTACGACATATATGAAATTTTATCTACAGAGCCCGTT--AGAAAGCA 821
 509 CTGATGATTTTTCCTTTATGCTCTGTCATTTGTTCTTAACTCATGACACATCTG 568
 822 CCGACGACTGCAAACTTCCATCTGTTGCTCTCTTCAACTCATATCTCTTGGC 881
 569 AATCTGCTTTTAACTTATGATGATGCTGGGAGAGACGGATGGGGCACATGCTAT 628
 882 TACTC-----CTGAGCCCACTGGGACATCATCTCTAC 916
 629 GTATTAATTTTTCCTTATTTGCTCAATGTCAGACCCCTTATGCTTTTCTCTTCAG 688
 917 TTACAGGCTTTCTTCCATCTCTTGCACGACCTTAGGGTTTTC-TCTCTTTCAG 975
 689 GCTAGCTTGGCTATTAACACACAGAGCTTGTCTCATTTGGGGAGAACTGTTCCAGGA 748
 976 GCCAGCCTTGCAGATTAACACACAGAGCTCCGGGCTCAACGGGAGAACTGTTCCAGGA 1035
 749 GTCAGTGAACCTACAGTGTGAGGAGAGGCGGTGCGCTCATGGGTACTTGGGGT 808
 1036 GTCAGTGAACCTACAGTGTGAGGAGAGGCGGTGCGCTCATGGGTACTTGGGGT 1082
 809 GATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 868
 1083 GGTGAGCCCTCTGGATATG-----TCTGAGTATGACCCCTGCTGTTCTTGTCTACGTC 1138
 869 AGATGATGAGGCTGCTATCTGATGAGAGAGGCTGATCTTCACTTCAAGAGAGTGC 928
 1139 AGGCTAAGATCAGCTACCTGATGAGAGAGGCTGATCTTCACTTCAAGAGAGTGC 1198
 929 TGTTCCTCATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 988
 1199 TGTTCCTCATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1258
 989 GGCTGAGCAAGAGCTAAGACATGATGATGATGATGATGATGATGATGATGATGATGAT 1048
 1259 AACTGAGCAATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1318

DB 3430 TGGGCTTGATGTTGATGCAATGCCAAGACACACATTCGTAATGCTGTGTAAAGATAT 3489
 QY 3231 TACTGATTTCACTTGTGTTGTTCTTGAAGAAAGTGAAGTGAAGAGAAATCTCA 3290
 DB 3490 TATTCATTACT-----TTGTCTTTGGAAAGGTGAAGTGTGTGTGAAGAAACTCA 3541

RESULT 10
 ID AAS14878 standard; DNA; 5935 BP.
 AC AAS14878;
 XX
 DT 19-DEC-2001 (first entry)
 DE Mouse partial genomic DNA for T cell derived inducible factor, TIFbeta.
 XX
 KW Mouse; T cell derived inducible factor; TIFbeta; ds; anti-allergic;
 KW anti-asthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;
 KW cancer; lymphoma; immune system disorder; allergy; asthma;
 KW acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
 KW thyroiditis; melanoma; hepatoma.
 XX
 OS Mus musculus.
 XX
 PN US2001024652-A1.
 PD 27-SEP-2001.
 XX
 PF 29-DEC-2000; 2000US-0751797.
 XX
 PR 18-OCT-1999; 99US-0419568.
 PR 26-OCT-1998; 98US-0178973.
 PR 16-JUL-1999; 99US-0354243.
 XX
 PA (DUMO/) DUMOUTIER L.
 PA (LOUA/) LOUAHD J.
 PA (RENA/) RENAUD J.
 XX
 PI Dumoutier L, Louahed J, Renaud J;
 DR WPI, 2001-638496/73.
 XX
 PT New isolated nucleic acid molecules encoding T cell inducible factors,
 PT useful as markers for expression or effect of interleukin (IL)-9 in a
 PT subject and diagnosing susceptibility to asthma or allergy
 PS Claim 1; Page 21-23; 26pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule, which encodes
 CC a T cell derived inducible factor (TIF) which are upregulated by the
 CC cytokine interleukin-9 (IL-9) and induce STAT transcription factor
 CC activation. The TIF proteins (or their mutants) may be used to test IL-9
 CC anti-agonists for their potency against lymphomas, immune system
 CC disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
 CC autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
 CC or inhibit differentiation of tissue types in which they are active and
 CC therefore be used to develop treatments for melanomas and hepatomas.
 CC The present sequence a partial genomic sequence for mouse TIFbeta.
 CC
 SQ Sequence 5935 BP; 1732 A; 1174 C; 1346 G; 1683 T; 0 other;

Query Match 13.6%; Score 650; DB 22; Length 5935;
 Best Local Similarity 56.5%; Pred. No. 1.8e-160;
 Matches 1863; Conservative 0; Mismatches 1285; Indels 152; Gaps 29;

QY 29 CTCCTTCCCGAGTACACAGTGTGCTCGAGTTAGATTGTCTGCAATGCGCCCTCGAGAA 88
 DB 356 CTCCTCTCTCAGTATCACTTTTGAACCTTGTCGATGGTGTCTCTCTGAGAA 415
 QY 89 ATGTGAGCTCTTTCTTATAGGGAACCTGGCCACCAAGTCTCTTTCTTGGCCCT 148

DB 416 ATCTATAGATTTTTCCCTTATAGGGAACCTTGGCCGAGCTGCTGCTCTCATTTGCCCT 475
 QY 149 CTGTGATACAGGAGAGAGAGAGAGTGGCCCATAGTCTCCACCTGACGCTTGACAGTCCAA 208
 DB 476 GTGGGCCAGAGAGCAATGTGCTGCCCATGAACCCGGGCAAGCTTGGGTGCA 535
 QY 209 CTCACAGAGCCCTATATACACACCGGACCTTCATGCTGAGCTAAGAGATATCATCTC 268
 DB 536 CTCACAGAGCCCTGACATGCTGACACCGGACCTTTATGCTGACAGAGAGTACAGCTCA 595
 QY 269 AATCCGCTCTTTCCTGTTGATCTACTGTGAATCCAAATGTTCTTAATCTTTCTTCA 328
 DB 596 TCTCTTTCTCCATACCGCCCTTGCCATTTCTGAAACACTGTGAACCTTTTAGGGCC 655
 QY 329 GAGCATCTTAAGACCTTTAGAACCCACTGTTATCCCTGAGGTAATATTTCTG 388
 DB 656 GCTTATCTCCGACAGTCTCACTACTATGTTTCTGTCT-----CTTTAGANG 703
 QY 389 TTTTTCAGAGACTTTTGGGAATCTGCTTTTTTTTTTTCTGTAACCTTCTCTCCAT 448
 DB 704 ACTCTTTAAGACTGGATCTTTTCTATTTCTAATTTCAAGTCTGAGACATTTCTAT 763
 QY 449 TTTGGCCTTTATGATACATATGATGATTTTTCCTCAAGAGCGGCATTCATATCAT 508
 DB 764 CTGGCCTTCAGAGACATATCTGATTTTATCTACAGAGCGGCTTT--AGAAAGCA 821
 QY 509 CTGATGATTTTTTTTCCCTTATGCTCTGTCATTTGTTCTAACTGACACATCTG 568
 DB 822 CCACAGACTGCAATCTTTCCATCTGTTGCTCTCTGAACTCACTCTCTGGC 881
 QY 569 AATCTGCTTTAGTCTTTATGATGTTGCTCTGAGGAACCGGATGGGACATGCTAT 628
 DB 882 TACTC-----CTGAACCCACTGCGACATATATCTTAC 916
 QY 629 GATTAATTTTTTTCTATTTGCTCATGTCAGACCTTATGTTTCTCTCTTCCAG 688
 DB 917 TTACAGGCTTTCTTCATCTCTCTGTGTACCCAGGACCTTAGGGTTTC-TCTCTTACG 975
 QY 689 GCTAGCTTGGCTGATACAGACAGAGCTGCTCATTTGGGGAGAACTGTTCCAGCA 748
 DB 976 GCCAGCCTTGAGATACAGACAGACAGCGCCGCTCATCGGGAGAACTGTTCCAGGA 1035
 QY 749 GTCAGTGAAGCTACAGTTGTGACGAAGAGCGCGTGTCCATGGGTCTTGGGT 808
 DB 1036 CTCAGTGAAGCTCTCAGCTGTGATGAGAGGCG-----TAGCTGCGGAGGT 1082
 QY 809 GGTGTGATGATGTTTATGCTTATCCCTTATGACCTTTGTTCCCTTCCACTGC 868
 DB 1083 GGTGACCCCTCTGGATAG--TCTGACGTATGACCCCTGCTCTTGTGTACTTGC 1138
 QY 869 AGATAGTAGAGGCTGCTATCTGATGAGACAGGCTGTAACCTTGAAGAAGTGC 928
 DB 1139 AGGCTAAGATAGAGTCTACGTAGAGAGAGGTCTCACTCACTCCGGAAGCATTC 1198
 QY 929 TGTTCCTCATCTGATAGAGTTCACGCTTATATGAGAGAGTGTGCTTCTGAGCA 988
 DB 1199 TCTCTCCCGACAGCAAGGTTCCGCTTATATCAGAGGTGTGCTTCTTCCAGCA 1258
 QY 989 GGCTCAGCAACAGGCTAGACATGTTAAGTTAGCTCTCAGCTATGCCACCTACCC 1048
 DB 1259 AACTGACATAGCTAGCTGCTGTGTAAGTGTGCTGTGCTACTATGCTCTCT 1318
 QY 1049 CTCCTTCCCTCTCCACAGAGACCCCTTACCCCACTCTCTCTCCCTCCCAACCC 1108
 DB 1319 CTCCTCTCTTATCTCAATGAAGACCGAGGCTGCTCTCTCTCTTCAAGAGTGA 1378
 QY 1109 TAAGTACGAGAGAGAGTGTCTTGGACAGCACTGTTATAGAGATCA-----TTGGG 1161
 DB 1379 GGAAGGCTCAGACACACCATCATATGGCCACTGTAATAGTTCACAAAGCTTTGGC 1438
 QY 1162 ATCATAGAGATTTGTTGTTTGTGAGTGAAGTCACTTATAGTTATATGATGATG 1221
 DB 1439 TTCAATGATATACCTTTGAGTTGTATTAAGCTTTATTTGTTTATCATGGA 1498

QY 1222 GGGCTCGAAGCTTAAGTGTACAGAGCCCGCATGGTTGTCTTGGAAAAAGGCAATC 1281
DB 1499 AGAAATCAACTCAAAATTCGTAGGATGAGAAAGATGTGGAAACGAAAAAGGCTTAGAT 1558
QY 1282 AGGTTGGCGTAA---GATGAGAAAGGTGTGGGAAAAATCTAGCTGTGGAAATGATCCA 1338
DB 1559 AGGAAACAGATCTGCTGAGTACAGTACTTATGGGGGGGGGGGCGAGCATATCCA 1618
QY 1339 TTGAGTCTAAGTTGTTGAGGGGAGGGGATGCGATGAGAGAAATTTAGAGAGAAAGTGGG 1398
DB 1619 CTGAGTCCAGTACTGTTGGGAGAGAAATCCACTAGTACAAAGTCTTGTGGGGGAAAG 1678
QY 1399 AAATGGGAAGGCTTAAAGTCGTGTGGGTGGGCGAGACTGTGCCC-----TGTTGA 1450
DB 1679 AATGGCACAGAGCAAAAGTTGAAGGAAAGAGAGATGAGAGGCGCTCAATGTTGGGG 1738
QY 1451 TGTCAATGGGAGCGCAAAATGGGAGCGGTGTGAATGTATGCGCGCTGAACATTTGAAC 1510
DB 1739 TGTGAAGGTCACTCTTTTCCATGTATGAGAGATTAAGAAAAATCAGTGTGAGTT 1798
QY 1511 TATGAAAAAAGTTGAGTGAAGTGGGCCAGTAAAGGCCCTAGGACTTACTGAAGAG 1570
DB 1799 TGAATGCTTACAGACACCCCACTATGCGAGACTGTGGGAGACTGGCAATTTAGGA-AGG 1857
QY 1571 GCTTAATTTTCACTAGAGATGTTTATATGATCAATTTCTTGTCTTACGATGCAATTTCTG 1630
DB 1858 CCGCGCTTTTACACAGAAACTTATATGCTCACTCTTGCTACACTCCACCTTTGAT 1917
QY 1631 GAGATACGATGAGGTTTATTCCTTACAGAAATTTGCAATACTCCGCTTTTCCAC 1690
DB 1918 GAGGTTAAGCTCAGGTTGCTTCT-----ACCGTCTTGTCTAC 1956
QY 1691 AAATGCAAACTCAGTAGATTTCCCAAGATGAGAGAGTCTCTTTGAAGGAAGTGA 1750
DB 1957 TGGTGAATCTTCAAGTGAATTCCTCCAAAGACGAGACGCTCTTGTGAAGGAGGAC 2016
QY 1751 CTGATTTGCGGCTCCAGGGAATTCAGAGCTCAGAAATCTAGTCACTGTTGAATC 1810
DB 2017 CTGGAATTCAGTCTCTAGAGAAACGAAATAGCTCAGAGATCTAGGTCACGTAATCT 2076
QY 1811 TTAGTATTTGCGGCAAAATTTACTAAGACTTTAATTCAGGTGAATTTACTGTACTC 1870
DB 2077 AGGTCAAGCGGCAAAATGACTGAACGCTCTAATTCAGGTGAACGCTCACTGCTCC 2136
QY 1871 CATGGGTGAGAGTTCATAAAGTTTCAAGACAACTTAAGATGATGCTGTATG 1930
DB 2137 AATATACTAGAGTATGGGCTCCACCGGATTAAGTCTGTATGA-GTCTGCTTTTA 2195
QY 1931 TTTTATAGCATATTGAAGTGAATGACTTCATATCCAGAGAAATGTGCAAAAGCTGAG 1990
DB 2196 TTTTGCAGACATCAGTGTGAGACCAAGACATCCAGAAAGATGCAAGAGCTGAG 2255
QY 1991 AACAGTGAAGAAAGTGAAGTGAATGATCTCAATGCTAAGTCAATAGAGAGACA 2050
DB 2256 AACAGTGAAGAAAGTGAATGATGAGCAACAAATCTAAGCCATTCAGTGAAGAGCTG 2315
QY 2051 AATGTTGTTTCTTCTCTTCTTCTCCATCACTGTTGTGATTTTCACTGATCTC 2110
DB 2316 GGGATTTCTTCTCTGCTTCCAGTCT--CTTCTACTTTGTAACATTTTCTTGAATCT 2373
QY 2111 CTACCAACAGGCGGAT---ACTTGAGTGTGTGTATGATATATCTATATCTTA 2166
DB 2374 CTACGTCGTGTGCAATTACTCACTTGTGACACCTGCACTAGCTGGGTCTATAGATCT 2433
QY 2167 GATGTCAAGTTCCAAATCTTGCAAATTTGAGAAATTTAGAACTGGTGGGATCTTACCT 2226
DB 2434 TCAATCTGTCTTAAATTT---GTAGTCAAAATCTGAGGCTAGAGAAAGCTTAGCTC 2490
QY 2227 GTCTAGTCAATTAAGTCAATCTGAGATTTGGGAGTGTGAGTGAAGTGAAGTGAAGTGC 2286
DB 2491 AGCGAGTCTCATGAGCACTTGTCTGGAGGATGCTTTGTACAGAGTCAATGCTAGAGAC 2550

QY 2287 AGGTCTCTGAATCCCAAGCCAGCACTTTTCCCGTGTGATACAGATTTAGTTGTGATC 2346
DB 2551 AGCATCCCTGATTTCCCACTCTGCAC--TTGCTAGTGGCCAGGTGTAATTACTTAGCCT 2609
QY 2347 CATTAATTTCTAGGAATTTTCAATTTCTATATGATCTATGATCTGAGAGTACTTG 2406
DB 2610 GATTAAGTATTTGGGAAA--GCCAATTTCCACCGCTTACATTAATCCGAAGACATGCA 2667
QY 2407 TTTAAAAACAGAAAAATGCTTATGGGCAAAATTTATTTGAAGTCAATTTGAAGTCA 2466
DB 2668 TTGAAAACTAGAAA---GCTGGGCAAAACTTACTAGAGATGATTTTGAAGTCAATTA 2723
QY 2467 TGCATTTCTTGAACCTTGAAGAAATTAATCTCAGAACTGAGAAAGAGCTGAGCTTC 2526
DB 2724 ACTGATGCTGTAATGATGATCAATTCACAGATTAACAAAGAGCTGAGATTTGC 2783
QY 2527 AATAGGCTAATTTCTGAGATTAATAACACTTA-----TTGAATTTCTATTA 2578
DB 2784 AATATGACAGATTTTGAATCACTGATTAACAGCTGTATCATCTTAATTAATATAG 2843
QY 2579 TCT---ATCAGATATTGATTTATAGTTTAAAGCAAGAGAGCAAC--CCGATCTCTTT 2634
DB 2844 TGTCTATTTAGCTGCTATTTAAGATTTAAACCAAGAGTGAATTACTTCCATTTACTG 2903
QY 2635 ATACAGTTCAAAATAGTAAATAATTAATGAGATTTATTAATGTTAAATGAAGTCT 2694
DB 2904 GGCCTGTTTCAATAGATTAATAATATCAGTATGATTAATTAATAGTGTATGAAGTA 2963
QY 2695 TGAATTTGTAAGCTTTTCTTCTCTCTCCATCAAGACCTTCCATTTCAATTTCTT 2754
DB 2964 TGAAGTGAAGACC---CTTCTCTTACTTTTAACTTCACTTCTTATTAATTAATTTT 3020
QY 2755 CTTTCACTCCCTCAACAAATCCCTAGGAGCACTTATTCATGATGGGTGCTGATTA 2814
DB 3021 TCTTACACCTGATCAAGCCACTGTAAGCACTTATGCTGCGAGCTATTAATGAT 3080
QY 2815 CTATAGTGAATGATACATCATGTGGCTTATTTGTTGAAGAAACA--ACAATGAAGC 2872
DB 3081 TTACAGCAAAACAATCTGCTGTGGCTCTTTGGGAAAGGAAAGATACAGAGAGC 3140
QY 2873 TTAGCTAACA--TAGTACATCAACCCCAAAACCGAGAAATTAAGAGCACTGAAT 2931
DB 3141 TCAGGCTGCAAGTGTGACTTCACTTAAGCAAGAGCAAGTGTGATGACAGAAAGT 3200
QY 2932 GACGCTCTT--GCAAGCAGTACCACTAATACTCAGAAATGAGAGCTCCAGTTGATG 2990
DB 3201 GAGGCTCTTCAAGTGGGTGTGCTTAAGTATCGAAACAGAAAGCTCTGTGTGATG 3260
QY 2991 AATTTTCAATCAAGCTTAACCTTAATTTCCCTTTTCCCTCTGACTTTTAAAAA 3050
DB 3261 AATATCAATGAATATATCACTTATCTCC-----TTCTTATTAAGAACTTAACG 3313
QY 3051 GCGTTTCTTCTGAGCATATTAATGATGTGACTGTTTCTCTTTGATTAATGAAG 3110
DB 3314 TCTCTCTCTTGTGTGTAGGCTGATTAACAGCTGTGT--TTCTTTGAGTGTTCATG 3371
QY 3111 CTGTGATTTTAAATTTGGAAGCCAGTCTCTGTTATTAAGAACTTATTAAGACATG 3170
DB 3372 CTTTCAAGATTTTCACTGTCTCTGCGAGTCTTGT--TAGAGGTTTGTAACTTACAC 3429
QY 3171 GAGGCTGAATTTAGATGCCACAGACAGAGCATGCTTTACATCTTGTCTTAAAAAT 3230
DB 3430 TGGGCTGAGATTTAGATGCAAGGACACACACTTGAATGCTGTGTAAGAGTAT 3489
QY 3231 TACTGATTTCACTTCTGTTGTTGTTTGAAGAAAGTGAAGTGAAGAGCAATCTCA 3290
DB 3490 TATTCATTTACT-----TTGTCTTTGAAGAGTGAAGTGTGTGTAAGAAAGCACTCA 3541

RESULT 11
AAB30660
ID AAB30660 standard; DNA; 5935 BP.
XX

AC AAD30660;
 XX 21-MAY-2002 (first entry)
 DT Mouse TIF beta genomic DNA.
 XX
 DE
 XX T cell derived inducible factor; TIF; Interleukin-21; IL-21; mouse;
 KM STAT transcription factor; acute phase protein; inflammation; ds.
 XX
 OS Mus musculus.
 XX
 PN W0200210393-A2.
 XX
 PD 07-FEB-2002.
 XX
 XX 27-JUN-2001; 2001WO-US20485.
 PF
 XX 27-JUL-2000; 2000US-0626617.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Dumoutier L, Renaud J;
 PI
 XX WPI; 2002-195964/25.
 DR
 XX Stimulating expression of STAT transcription factor and inducing
 PT production of acute phase protein in a cell, involves contacting a cell
 PT capable of expressing STAT with T cell derived inducible factors -
 XX
 XX Example 9; Page 61-64; 64pp; English.
 XX
 CC The invention relates to nucleic acid molecules encoding T cell
 CC derived inducible factors (TIFs) also known as interleukin-21 (IL-21).
 CC TIF polynucleotides are upregulated by the cytokine, IL-9. IL-TIF or
 CC IL-21 molecules are implicated in activation of STAT transcription
 CC factors, acute phase proteins and inflammation. The present sequence
 CC is mouse TIF beta genomic DNA.
 CC
 SQ Sequence 5935 BP; 1732 A; 1174 C; 1346 G; 1683 T; 0 other;

Query Match 13.6%; Score 650; DB 24; Length 5935;
 Best Local Similarity 56.5%; Pred. No. 1,8e-160;
 Matches 1863; Conservative 0; Mismatches 1285; Indels 152; Gaps 29;

29 CTCCTCCCACTGTCACCAAGTCTGAGTGAATTTGCTGCAATGCGCGCCCTGACAGA 88
 356 CTCCTCTCTCAAGTTTCACTTTTGAACCTTGTGCGATGCGATGCGTCTCTGACAGA 415
 89 ATCTGTAGCTCTTCTCTTATGGGAGCCCTGGCCACAGCTGCTCTTCTTGAGCCCT 148
 416 ATCTATAGTGTCTTCTCTTATGGGAGCCCTGGCCACAGCTGCTCTTCTTGAGCCCT 475
 149 CTGTGTACAGAGAGAGAGAGCTGCGCCCATCAGCTCTGCTGCTGAGAGTTCACAA 208
 476 GTGGGCGCCAGAGAGAGAGAGTGGCTGCGCCCATCAGCTGCTGCTGAGAGTTCACAA 535
 209 CTTCAGAGAGCCCTTATACCAACGACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 268
 536 CTTCAGAGAGCCCTTATACCAACGACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 595
 269 AATCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 328
 586 TCTCTTCT 655
 329 GAGCATCTCTTAAGAGCTTGAAGACCCACTGTTATCTCTGAGAGGTAGATAAATTTCTG 388
 656 GCTTATCT 703
 389 TTTTTCAGAGAGCTCTTGGAGATGCGCTTTTCTTTTCTTGAATCTTCTCTCTCAT 448
 704 ACTCTTAAAGAGAGCTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 763
 449 TTTGAGCTTATGAT 508

DB 764 CTTGCGCTTCAGAGACATATCTGATTTTATCTACAGAGCGCGCTT--AGAAAGCA 821
 509 CTGATGATTTTCTTCTTATAGCTCTGTGCAATGTTTAACTCATGACACATCTG 568
 822 CCGACGACTGCAATATCTTCTGATCTGTGTGCTCTCTTCTGAACTCATCTCTTGGC 881
 569 AATCTGCTTTAGTCTTTATGATGTGCTCTGTGGAGACGGGATGGGGGCACTGTCTAT 628
 882 TATCT-----CTGAGACCACTGGCGACATATCTCTAC 916
 629 GTATATAATTTTCTTATTTGCTCAATGTCCACACCTTATGCTTTTCTCTCTCTCCAG 688
 917 TTACAGGCTTTCTTCTCATCTCTCTGTTCACCCAGCACTTAGGTTTCT--TCTCTTAC 975
 689 GCTAGCTTGGCTGATTAACAACAGAGCTTGTCTCATTTGGGAGAACTGTTCCACGA 748
 976 GCCAGCTTGGAGATTAACAACAGAGCTTGTCTCATTTGGGAGAACTGTTCCAGGA 1035
 749 GTCACTGATGACTACAGTTGTGAGAACAGGCGCGTGTCCGCTCATGGGTACTTGGGGT 808
 1036 GTCACTGATGACTACAGTTGTGAGAACAGGCGCGTGTCCGCTCATGGGTACTTGGGGT 1082
 809 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 868
 1083 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1138
 869 AGATGAG 928
 1139 AGGTAG 1198
 929 TGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 988
 1199 TGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1258
 989 GGTTCAG 1048
 1259 AACTGAG 1318
 1049 CTCCTTCCCTCTTCCACAG 1108
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 1379 GAG 1438
 1162 ATCATAG 1221
 1439 TTCAATGAG 1498
 1222 GGGTCTGAG 1281
 1499 AGAATCACTCAAAATTTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1558
 1282 AGTTGCTGAA--GATGAG 1338
 1559 AGAAG 1618
 1339 TTGACTTAAGTTTGTAG 1398
 1619 CTGAGTCCAGATCTTGTGGAG 1678
 1399 AAATGAG 1450
 1679 AATGAG 1738
 1451 TGTCTAG 1510
 1739 TGTGAAAGTCACTCTTTTCTCATGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1798
 1511 TATGAG 1570

Db 1799 TGATGCTTCAGACACCCCACTATGAGAGAGTGTGGAGACCTGGCAATTAGGA-AGG 1857
 Qy 1571 GCTTAATTTTCACATAGATGTTTATGTAACATTCTTGTCTTAACATGCAATTTTCG 1630
 Db 1858 CCGGGCTTTTCACACAGAAACCTTATGCTCATCTCTTGCTACACTCCCACTTTGAT 1917
 Qy 1631 GAGATACGATGAGTTTATTCCTTACAGAAATTTGCATTAATACTACCGCTTTCCAC 1690
 Db 1918 GAGGTAAAGCTCAGGTTTCTTCT-----ACCGTCTTGTCTAC 1956
 Qy 1691 AATATGAAACCTCAGTAGAATTTCCCAAGATGAGAGAGTCTCTTGTAGAGGAAGTA 1750
 Db 1957 TGGTGAACCTTCAGTAGATTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2016
 Qy 1751 CTGAGATTCGGGCTCCAGAGGAATTAAGAGCTCAGAGAAATCTAGTCACTGTTGAATC 1810
 Db 2017 CTGAGATTCAGTCTCTAGAGAACGAAATAGCTCAGAGAAATCTAGTCAAGCTGAATCT 2076
 Qy 1811 TAGGTCAATGTGGGCAAAATTAATAAGACTTTAATTCAGAGTAATTTGACTGTAACCTC 1870
 Db 2077 AGGTACAGAGGGGCAAAATTAAGCTGTAAGCGCTCTTATTCAGAGTAAGAGAGAGAG 2136
 Qy 1871 CATGGGTGAGAGTTCATTAAGTTTACAGACAACTTAAGATAGTATGTTGTTATG 1930
 Db 2137 AGATATCTGAGGTATTTGGGCTCCACCGGATTAAGTTCTGTTAGTA-GTCTGCTTTTA 2195
 Qy 1931 TTTTATAGCATTTGAAGTGATGACCTGCAATATCCAGAGAAATGCAAAAGCTGAAG 1990
 Db 2196 TTTTCAGACATCACTAGTGTGACGACAGAAATCATCAGAAAGATGCAAGAGCTGAAG 2255
 Qy 1991 ACAGAGTGAAGAGTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATG 2050
 Db 2256 AGACATGGAAGAGTACTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2315
 Qy 2051 AATGTTGTTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2110
 Db 2316 GGGATTTCTTCTCTGCTTCCAGTCT--CTTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 2373
 Qy 2111 CTACACAGAGGCGAT-----ACTTTGTGCTGTGATGATGATGATGATGATGATGATG 2166
 Db 2374 CTACTGCTGCTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 2433
 Qy 2167 GATGCACTTCCAAATCTTGAATTTGAATTTCTGAATTTCTGAATTTCTGAATTTCTGA 2226
 Db 2434 TCAATCTGTCTTAAATTT--GTAGTCACAATTTCTGAGCTTACCAAAAGCTTACCTC 2490
 Qy 2227 GTCTAGTCAATTAACCTCAGATTTCTGGGATGATGATGATGATGATGATGATGATGATG 2286
 Db 2491 AGCCAGTCTCATGAGCACTTGTGAGAGATGCTTGTGAGAGATGATGATGATGATGATG 2550
 Qy 2287 AGGTCTCTGATTCAG 2346
 Db 2551 AGCATCCCTGATTCAGAGCTGTGAC--TTGCTAGTGTGAGAGAGAGAGAGAGAGAGAG 2609
 Qy 2347 CATTAATCTTGAAGAAATTTCAATTTCTTATGATGATGATGATGATGATGATGATGATG 2406
 Db 2610 GATTAAGTATTTGGAAA--GCCAATTCACCGAGCTTCAATTAATTCAGAGAGAGAGAG 2467
 Qy 2407 TTTAAAAACAGAAATGCTATGAGGCAATTTAATTTGAATGATGATGATGATGATGATG 2466
 Db 2668 TTGAAACTGAAA-----GCTGGGCAAACTTACTAGAGATGATTTTGTAGCTCATTTAA 2723
 Qy 2467 TGCATTTGCTTGAACCTTGAAGATTAATCAGAAATGAGAGAGAGAGAGAGAGAGAGAG 2526
 Db 2724 ACTGATGCTGAAATGATGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2783
 Qy 2527 ATATAGGCTAATTTCTGAGATTAATTAACACTTAT-----TTGATATTAATTAATA 2578
 Db 2784 AATATGAGCAAGTATTTAGATCACTGTATTAACAGTGTCACTTAAATTAATTAATTAAT 2843
 Qy 2579 TCT--ATCAGATATTTAGTATTTAGTATTTAAAGCAAGAGAGAGAGAGAGAGAGAGAG 2654
 Db 2844 TGTCTATTTAGCTGCTATTTAAGATTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2903

Qy 2635 ATACAGTTCAATAGATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2694
 Db 2904 GGCTGTTTCAATAGATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2963
 Qy 2695 TGAATTTGATGCTTTTCTTCT 2754
 Db 2964 TGAGTTGAAACCC--CTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3020
 Qy 2755 CCTTCT 2814
 Db 3021 TCTTACACCT 3080
 Qy 2815 CTATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2872
 Db 3081 TTACAGCAACAACTTCTGT 3140
 Qy 2873 TTAGCTAACAA-TAGTACTTCACTCCCAAAACCGAGAGATGATTAAGAGAGAGAGAG 2931
 Db 3141 TCAGGCTAGCAAGTCTGACTTCACTTAAAGCCAGAGAGAGATGATTAAGAGAGAGAGAG 3200
 Qy 2932 GAGGCTCTT-GAAGAGAGTACAACTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 2990
 Db 3201 GAGGCTCTTCAAAAGT 3260
 Qy 2991 AATTTTCAATCAAGCTTAACCTTAATTTCCCTTTTCCCTCTTGAATTTTAAAAA 3050
 Db 3261 AATTTTCAATCAAGCTTAATTTCCCTTTTCCCTCTTGAATTTTAAAAA 3110
 Qy 3051 GCGTTTCTTCTGAGATCAATTAATGAGTGTGATGATGATGATGATGATGATGATGATG 3110
 Db 3314 TCTCTCTCTCTGTTGT 3371
 Qy 3111 CTGT 3170
 Db 3372 CTGT 3429
 Qy 3171 GAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3230
 Db 3430 TGGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3489
 Qy 3331 TACTGATTTCACTTGT 3290
 Db 3490 TATTCATTTACT-----TTGTCTTGAAGAGTGAAGTGTGTGTGTGTGTGTGTGTGT 3541

RESULT 12
 AAD27153
 ID AAD27153 standard, DNA, 5935 BP.
 XX AAD27153;
 AC
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Mouse T cell derived inducible factor (TIF) beta genomic DNA.
 XX
 KW T cell derived inducible factor; TIF; cytokine; interleukin-9; IL-9;
 XX protein therapy; STAT activation; differentiation; mouse; ds.
 OS Mus musculus.
 XX
 PN US6331613-B1.
 XX
 PD 18-DEC-2001.
 XX
 XX 18-OCT-1999; 99US-0419568.
 XX
 PF 26-OCT-1998; 98US-0178973.
 PR 16-JUL-1999; 99US-0354243.
 XX
 PA (LUDWIG-) LUDWIG INST CANCER RES.
 XX
 PI Dumoutier L, Louheid J, Renaud J;

CC interleukin 9 (IL-9). BM5147, can be grown in vitro, without the need to
CC add any cytokines to its culture medium. Many IL-9 activities are
CC mediated by activation of STAT transcription factors. The novel TIFs were
CC expressed in the presence of STAT, but not in its absence. TIFs induce
CC STAT activation in cells. They can be used, e.g., in the stimulation of
CC regeneration of targeted tissues. Their inhibitors or antagonists can be
CC used to retard, prevent or inhibit differentiation of other tissues. The
CC TIFs and their coding sequences are useful in the treatment of asthma,
CC allergies and lymphoma (claimed). They are also useful for identifying
CC compounds that inhibit or activate T cell induced factor activity in a
CC cell (claimed).

XX Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;

SO Query Match 5.4%; Score 258; DB 21; Length 690;

Best Local Similarity 100.0%; Pred. No. 1.7e-57;

Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACAGCAGAAATCTTCAGACAGGTTCTCTCCAGTCCAGGTTCTCGAGTTAG 60

DB 1 TGCACAGCAGAAATCTTCAGACAGGTTCTCTCCAGTCCAGGTTCTCGAGTTAG 60

QY 61 AATTGCTGCAATGGCCGCGCTCAGAAATCTGTGAGCTTCTTATGAGGACCTGG 120

DB 61 AATTGCTGCAATGGCCGCGCTCAGAAATCTGTGAGCTTCTTATGAGGACCTGG 120

QY 121 CCACAGCTGCT 180

DB 121 CCACAGCTGCT 180

QY 181 GCTCCAGCTGCTGAGGCTTTCAGCAAGTCCCACTTCAGCAGCCCTATATCAACCAACCGACCT 240

DB 181 GCTCCAGCTGCTGAGGCTTTCAGCAAGTCCCACTTCAGCAGCCCTATATCAACCAACCGACCT 240

QY 241 TCATGCTGGCTAAGAGG 258

DB 241 TCATGCTGGCTAAGAGG 258

RESULT 14

AA514875 standard; cDNA; 690 BP.

XX AA514875;

DT 19-DEC-2001 (first entry)

XX Human cDNA encoding T cell derived inducible factor, TIF.

XX Human; T cell derived inducible factor; TIF; ss; anti-allergic;

XX antileukemic; cytokine; interleukin-9; IL-9; STAT transcription factor;

XX cancer; lymphoma; immune system disorder; allergy; asthma;

XX acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;

XX thyroiditis; melanoma; hepatoma.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 72..611

XX /tag= a

XX /product= "TIF"

XX /transl_except= (pos:159..161,aa:Glu)

XX /transl_except= (pos:378..380,aa:11e)

XX /transl_except= (pos:405..407,aa:Arg)

XX /transl_except= (pos:519..521,aa:Cys)

XX US2001024652-A1.

XX 27-SEP-2001.

XX 29-DEC-2000; 2000US-0751797.

XX 18-OCT-1999; 99US-0419568.

PR 26-OCT-1998; 98US-0178973.

PR 16-JUL-1999; 98US-0354243.

XX (DUMO/) DUMOUTIER L.

XX (LOUA/) LOUAHED J.

XX (RENA/) RENAUUD J.

XX Dumoutier L, Louahed J, Renaud J,

XX WPI; 2001-638496/73.

XX P-PSDB; AAU09091.

XX New isolated nucleic acid molecules encoding T cell inducible factors,

XX useful as markers for expression or effect of interleukin (IL)-9 in a

XX subject and diagnosing susceptibility to asthma or allergy

XX Claim 1; Page 17; 26pp; English.

XX The invention relates to an isolated nucleic acid molecule, which encodes

XX a T cell derived inducible factor (TIF) which are upregulated by the

XX cytokine interleukin-9 (IL-9) and induce STAT transcription factor

XX activation. The TIF proteins (or their mutants) may be used to test IL-9

XX ant/agonists for their potency against lymphomas, immune system

XX disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),

XX autoimmune diabetes and thyroiditis. TIF molecules promote regeneration

XX or inhibit differentiation of tissue types in which they are active and

XX therefore be used to develop treatments for melanomas and hepatomas.

XX The present sequence encodes human TIF.

XX Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;

SO Query Match 5.4%; Score 258; DB 22; Length 690;

Best Local Similarity 100.0%; Pred. No. 1.7e-57;

Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACAGCAGAAATCTTCAGACAGGTTCTCTCCAGTCCAGGTTCTCGAGTTAG 60

DB 1 TGCACAGCAGAAATCTTCAGACAGGTTCTCTCCAGTCCAGGTTCTCGAGTTAG 60

QY 61 AATTGCTGCAATGGCCGCGCTCAGAAATCTGTGAGCTTCTTATGAGGACCTGG 120

DB 61 AATTGCTGCAATGGCCGCGCTCAGAAATCTGTGAGCTTCTTATGAGGACCTGG 120

QY 121 CCACAGCTGCT 180

DB 121 CCACAGCTGCT 180

QY 181 GCTCCAGCTGCTGAGGCTTTCAGCAAGTCCCACTTCAGCAGCCCTATATCAACCAACCGACCT 240

DB 181 GCTCCAGCTGCTGAGGCTTTCAGCAAGTCCCACTTCAGCAGCCCTATATCAACCAACCGACCT 240

QY 241 TCATGCTGGCTAAGAGG 258

DB 241 TCATGCTGGCTAAGAGG 258

XX Homo sapiens.

XX Key Location/Qualifiers

XX AAD30645 standard; cDNA; 690 BP.

XX AAD30645;

XX 21-MAY-2002 (first entry)

XX Human TIF cDNA.

XX T cell derived inducible factor; TIF; interleukin-21; IL-21; human;

XX STAT transcription factor; acute phase protein; inflammation;

XX chromosome 12; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT	72.611
FT	/tag= a
FT	/product= "Human TIF protein"
XX	

WO200210393-A2.

07-FEB-2002.

27-JUN-2001; 2001WO-US20485.

27-JUL-2000; 2000US-0626617.

(LUDW-) LUDWIG INST CANCER RES.

Dumoulier L, Renauld J;

WFL: 2002-195964/25.
P-PSDB: AAE19237.

P-PSDB; AAE19237.

Stimulating expression of STAT transcription factor and inducing production of acute phase protein in a cell, involves contacting a cell capable of expressing STAT with T cell derived inducible factors -

Card No: Page 55-56; 64pp; English.

The invention relates to nucleic acid molecules encoding T cell derived inducible factors (TIFs) also known as interleukin-21 (IL-21). TIF polynucleotides are upregulated by the cytokine, IL-9, IL-TIF or IL-21 molecules are implicated in activation of STAT transcription factors, acute phase proteins and inflammation. The present sequence is human TIF cDNA. The TIF gene is located on chromosome 12.

sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;

Query Match	5.4%	Score 258; DB 24;	Length 690;
Best Local Similarity	100.0%	Pred. No. 1.7e-57;	
Matches . 258; Conservative	0;	Mismatches	0; Indels . 0; Gaps 0

QY	1	TGACACAGCGAATCTTCAAGAACAGGTTCTCCTTCCCAAGTCACCAAGTTGCTCGAGTTAG	60
Db	1	TGCACACAGCAAGATCTTCAAGAACAGGTTCTCCTTCCCAAGTCACCAAGTTGCTCGAGTTAG	60
QY	61	AATGTTCTGCATATGAGCGCGCTTCGCAAAATCTGTAGCTCTTCTTATGGGAACTCGG	120
Db	61	AATGTTCTGCATATGAGCGCGCTTCGCAAAATCTGTAGCTCTTCTTATGGGAACTCGG	120
QY	121	CCACACAGCTGCCCTCTCTCTTGTGGCCTTTTGGTACAGGAGAGACAGCTGCGCCATCA	180
Db	121	CCACACAGCTGCCCTCTCTCTTGTGGCCTTTTGGTACAGGAGAGACAGCTGCGCCATCA	180
QY	181	GCTCCCACTGCAGGCTTGAACAAGTCCAATTGCACAGCCCTTATATCAACAACCGGCACT	240
Db	181	GCTCCCACTGCAGGCTTGAACAAGTCCAATTGCACAGCCCTTATATCAACAACCGGCACT	240
QY	241	TGATGTGTGCTAAGAGG	258
Db	241	TGATGTGTGCTAAGAGG	258

Search completed: July 19, 2003, 09:44:01
Job time : 709.876 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 16:17:16 ; Search time 678.702 Seconds
(without alignments)
14581.096 Million cell updates/sec

Title: US-09-751-797-25

Perfect score: 4797
Sequence: 1 tgcacagcagcagatcttcag.....gagccccaagcagcttctt 4797

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4797	100.0	4797	10	US-09-751-797-25
2	1073.6	22.4	1074	15	US-10-027-632-118181
3	686	14.3	7445	10	US-09-751-797-8
4	650	13.6	5935	10	US-09-751-797-29
5	611.8	12.8	637	15	US-10-027-632-208140
6	611.8	12.8	637	15	US-10-027-632-208141
7	611.8	12.8	637	15	US-10-027-632-208142
8	258	5.4	690	10	US-09-751-797-24
9	244	5.1	1152	11	US-09-870-574-1
10	244	5.1	1152	14	US-10-063-588-153
11	244	5.1	1152	15	US-10-006-867-153
12	244	5.1	1152	15	US-10-066-500-125
13	244	5.1	1152	15	US-10-063-547-153
14	244	5.1	1152	15	US-10-063-616-153
15	244	5.1	1152	15	US-10-063-502-153
16	244	5.1	1152	15	US-10-227-884-243

17	244	5.1	1152	15	US-10-002-796-125	Sequence 125, App
18	244	5.1	1152	15	US-10-066-273-125	Sequence 125, App
19	244	5.1	1152	15	US-10-066-494-125	Sequence 125, App
20	244	5.1	1152	15	US-10-230-163-243	Sequence 243, App
21	244	5.1	1152	15	US-10-066-269-125	Sequence 125, App
22	244	5.1	1152	15	US-10-066-211-125	Sequence 125, App
23	244	5.1	1152	15	US-10-066-193-125	Sequence 125, App
24	244	5.1	1152	15	US-10-230-338-243	Sequence 243, App
25	244	5.1	1152	15	US-10-218-631-243	Sequence 243, App
26	244	5.1	1152	15	US-10-063-518-153	Sequence 153, App
27	244	5.1	1152	15	US-10-230-414-243	Sequence 243, App
28	244	5.1	1152	15	US-10-063-598-153	Sequence 153, App
29	244	5.1	1152	15	US-10-227-693-153	Sequence 153, App
30	244	5.1	1152	15	US-10-063-567-153	Sequence 153, App
31	244	5.1	1152	15	US-10-216-159A-243	Sequence 243, App
32	244	5.1	1152	15	US-10-218-849-243	Sequence 243, App
33	244	5.1	1152	15	US-10-227-873-243	Sequence 243, App
34	244	5.1	1152	15	US-10-227-883-243	Sequence 243, App
35	244	5.1	1152	15	US-10-219-076-243	Sequence 243, App
36	244	5.1	1152	15	US-10-230-434-243	Sequence 243, App
37	244	5.1	1152	15	US-10-063-599-153	Sequence 153, App
38	244	5.1	1152	15	US-10-063-595-153	Sequence 153, App
39	244	5.1	1152	15	US-10-219-003-243	Sequence 243, App
40	244	5.1	1152	15	US-10-219-075-243	Sequence 243, App
41	244	5.1	1152	15	US-10-219-464-243	Sequence 243, App
42	244	5.1	1152	15	US-10-219-466-243	Sequence 243, App
43	244	5.1	1152	15	US-10-219-479-243	Sequence 243, App
44	244	5.1	1152	15	US-10-219-481-243	Sequence 243, App
45	244	5.1	1152	15	US-10-230-260-243	Sequence 243, App

ALIGNMENTS

RESULT 1
US-09-751-797-25
Sequence 25, Application US/09/751797
Patent No. US20010024652A1
GENERAL INFORMATION:
APPLICANT: Dumontier, Laure
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/751,797
CURRENT FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 09/419,568
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 25
LENGTH: 4797
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-751-797-25
Query Match 100.0%; Score 4797; DB 10; Length 4797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGACAGCAGATCTTCAGAACAGGTCCTCCCGATCAGCAGTGTGCTGAGTTAG 60
DB 1 TGACAGCAGATCTTCAGAACAGGTCCTCCCGATCAGCAGTGTGCTGAGTTAG 60
QY AATTGCTGCAATGAGCCGCGCTTCAGAAATCTGTGAGCTTTCTTATGAGGACCTGG 120
DB AATTGCTGCAATGAGCCGCGCTTCAGAAATCTGTGAGCTTTCTTATGAGGACCTGG 120
QY 121 CCACGAGCTCCCTCTTCTTCTTGTATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180

Db 121 CCAACGAGCTGCTCTTCTTCTGCGCTCTTGCTACAGGAGAGACGCTGGCCCATCA 180
Qy 181 GCTCCCACTGACAGCTTGACACAGTCCAACTTCCAGAGCCCTATATCAACCAACCGACCT 240
Db 181 GCTCCCACTGACAGCTTGACACAGTCCAACTTCCAGAGCCCTATATCAACCAACCGACCT 240
Qy 241 TCAATGCTGCTGAAGAGGATATATCATCTCATCTCTCTTCTCTTGATCTACTTGA 300
Db 241 TCAATGCTGCTGAAGAGGATATATCATCTCATCTCTCTTCTCTTGATCTACTTGA 300
Qy 301 ATCCAAATAGTTTAACTTCTTCAAGAGCATCTCTAAGAGCTTAAAGCCACTGT 360
Db 301 ATCCAAATAGTTTAACTTCTTCAAGAGCATCTCTAAGAGCTTAAAGCCACTGT 360
Qy 361 TATCCCTGAGGAGTAAATTTTCTGTTTTTCAAGACATCTTTGGAACTGCTCTT 420
Db 361 TATCCCTGAGGAGTAAATTTTCTGTTTTTCAAGACATCTTTGGAACTGCTCTT 420
Qy 421 TTTTTTTTCTGAACCTTCTCTCTTCCATTTTGCCCTTATGATACATATGATATTTT 480
Db 421 TTTTTTTTCTGAACCTTCTCTCTTCCATTTTGCCCTTATGATACATATGATATTTT 480
Qy 481 CCAAAAGAGGAGCATTCAGTATCCATGATGATTTTTTTTCCCTTATGCTCTGTG 540
Db 481 CCAAAAGAGGAGCATTCAGTATCCATGATGATTTTTTTTCCCTTATGCTCTGTG 540
Qy 541 CATTTGTTCTAACTGACACATGCTGAATCTGCTTTTATGCTTATGATGTTGCTCT 600
Db 541 CATTTGTTCTAACTGACACATGCTGAATCTGCTTTTATGCTTATGATGTTGCTCT 600
Qy 601 GGGGAGACGGGATGAGGACATGCTATGATATAATTTTTTTTCTATTTGCTCAATGCTC 660
Db 601 GGGGAGACGGGATGAGGACATGCTATGATATAATTTTTTTTCTATTTGCTCAATGCTC 660
Qy 661 AGACCCCTGAGTCTTCTCTCTCTTCCAGGCTAGCTTGGCTGATAAACAACAGAGCTGTG 720
Db 661 AGACCCCTGAGTCTTCTCTCTCTTCCAGGCTAGCTTGGCTGATAAACAACAGAGCTGTG 720
Qy 721 TCTCATTTGGGAGAACTGTTCCACGAGAGTCACTGATAGCTACAGTTGTGACGAAACAGG 780
Db 721 TCTCATTTGGGAGAACTGTTCCACGAGAGTCACTGATAGCTACAGTTGTGACGAAACAGG 780
Qy 781 CCGTGTGCCCTCCATGGGTACTTGGGGTGTGTGATGATGTTTATGCTTATCCCTTA 840
Db 781 CCGTGTGCCCTCCATGGGTACTTGGGGTGTGTGATGATGTTTATGCTTATCCCTTA 840
Qy 841 TGAACCTTTCTGTTTTCCCTTCCACCTGACAGATGATGAGCGCTGCTATCTGATGAAACAG 900
Db 841 TGAACCTTTCTGTTTTCCCTTCCACCTGACAGATGATGAGCGCTGCTATCTGATGAAACAG 900
Qy 901 GTGCTGAACCTTCAACCTTGAAGAAGTGTCTTCCCTCAATCTGATAGTTTCAAGCTTAT 960
Db 901 GTGCTGAACCTTCAACCTTGAAGAAGTGTCTTCCCTCAATCTGATAGTTTCAAGCTTAT 960
Qy 961 ATGACAGAGAGTGTGCTCTTCCCTGAGAGCTCAGCAACAGGCTAAGCAATGTGTAAAGT 1020
Db 961 ATGACAGAGAGTGTGCTCTTCCCTGAGAGCTCAGCAACAGGCTAAGCAATGTGTAAAGT 1020
Qy 1021 TCAAGCTCTAGAGCTATGACCAACCTTCCCTCTCTCTCTTCCACAGAGACCCCTTAC 1080
Db 1021 TCAAGCTCTAGAGCTATGACCAACCTTCCCTCTCTCTCTTCCACAGAGACCCCTTAC 1080
Qy 1081 CCAAACTCTCTCTCTTCCCTTCAACCTTAAAGCTAGAGAGAGAAAGTGTGTGGCAGAG 1140
Db 1081 CCAAACTCTCTCTCTTCCCTTCAACCTTAAAGCTAGAGAGAGAAAGTGTGTGGCAGAG 1140
Qy 1141 TGTATATAGAGATATTTGGGATCATAGATATTTGCTTTTGTGCTTATGATGAGCATATC 1200
Db 1141 TGTATATAGAGATATTTGGGATCATAGATATTTGCTTTTGTGCTTATGATGAGCATATC 1200
Qy 1201 TTGAGTTATATGAGTGAATGGGCTGGAACCTTAAGTATACAGAACCGGATGAGTTTG 1260
Db 1201 TTGAGTTATATGAGTGAATGGGCTGGAACCTTAAGTATATGATGACAGAACCGGATGAGTTTG 1260

Qy 1261 TCTTGGAAAAAGGCAACTCAGGTGCTGAAGATGAGAAAGGTGTGGAAAAATCATCTA 1320
Db 1261 TCTTGGAAAAAGGCAACTCAGGTGCTGAAGATGAGAAAGGTGTGGAAAAATCATCTA 1320
Qy 1321 GCTGTGAAAAATGATCCATTTGATGCTTGAAGTGTGAGGAGGAGGATGAGATGAGAGNA 1380
Db 1321 GCTGTGAAAAATGATCCATTTGATGCTTGAAGTGTGAGGAGGAGGATGAGATGAGAGNA 1380
Qy 1381 ATTAGAAGAAAGTGGGAAATGGGAAGCTTTAAAGTGTGTGTGGGTGGGACATGTT 1440
Db 1381 ATTAGAAGAAAGTGGGAAATGGGAAGCTTTAAAGTGTGTGTGGGTGGGACATGTT 1440
Qy 1441 GGCCTGTTGATGCTCATGGGAAGCCCAAAATGAGAGGGGTGTGAACCTTGAATCCCTGTA 1500
Db 1441 GGCCTGTTGATGCTCATGGGAAGCCCAAAATGAGAGGGGTGTGAACCTTGAATCCCTGTA 1500
Qy 1501 CATTTGAAACTATGAAAAAAGTTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
Db 1501 CATTTGAAACTATGAAAAAAGTTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
Qy 1561 ACTGAAGAGGAGGCTTAATTTTCAATGAGATGTTTTATGATATTTCTGTTCTAAAGCATG 1620
Db 1561 ACTGAAGAGGAGGCTTAATTTTCAATGAGATGTTTTATGATATTTCTGTTCTAAAGCATG 1620
Qy 1621 CAATTTTCTGAGATACGATGAGGTTTTATTTCTTACAGAAATTTGCAATACTCTCG 1680
Db 1621 CAATTTTCTGAGATACGATGAGGTTTTATTTCTTACAGAAATTTGCAATACTCTCG 1680
Qy 1681 CTTCTTCCAAATCCAAATCCCTCAGTAGGATTTCCCAAGAGAGAGAGAGGCTCTGTGA 1740
Db 1681 CTTCTTCCAAATCCAAATCCCTCAGTAGGATTTCCCAAGAGAGAGAGAGGCTCTGTGA 1740
Qy 1681 CTTCTTCCAAATCCAAATCCCTCAGTAGGATTTCCCAAGAGAGAGAGGCTCTGTGA 1740
Db 1681 CTTCTTCCAAATCCAAATCCCTCAGTAGGATTTCCCAAGAGAGAGAGGCTCTGTGA 1740
Qy 1741 AGGGAAGTGAAGTGAATTTGAGGAGTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800
Db 1741 AGGGAAGTGAAGTGAATTTGAGGAGTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800
Qy 1801 TGTGAAATCTAGATATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860
Db 1801 TGTGAAATCTAGATATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860
Qy 1861 ACTGATACCTCAATGGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
Db 1861 ACTGATACCTCAATGGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
Qy 1921 CTTGTTATTTGTTTATGACATATGAAAGTGAATCTTCCATATCCAGAGAAATGTCAA 1980
Db 1921 CTTGTTATTTGTTTATGACATATGAAAGTGAATCTTCCATATCCAGAGAAATGTCAA 1980
Qy 1981 AAGCTGAAGACACAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2040
Db 1981 AAGCTGAAGACACAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2040
Qy 2041 AGGAGAGCAAAATGTTGTTTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2100
Db 2041 AGGAGAGCAAAATGTTGTTTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2100
Qy 2101 CTTGATTTCTTCAACCAAGGAGGAGTACTTTGTTGTTCTGTGATGATATATCTATA 2160
Db 2101 CTTGATTTCTTCAACCAAGGAGGAGTACTTTGTTGTTCTGTGATGATATATCTATA 2160
Qy 2161 TATCTGATGATGATTTTCCAAATCTTGAAGATTTGATGAATCTGAGATGAGGATCT 2220
Db 2161 TATCTGATGATGATTTTCCAAATCTTGAAGATTTGATGAATCTGAGATGAGGATCT 2220
Qy 2221 TAGCTGTCTAGACATATTAACCTCAGATTTGAGGAGTGTCAAGTGCAGAGATAGGCTTA 2280
Db 2221 TAGCTGTCTAGACATATTAACCTCAGATTTGAGGAGTGTCAAGTGCAGAGATAGGCTTA 2280
Qy 2281 GAATGAGGATCTCTGAAATCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340
Db 2281 GAATGAGGATCTCTGAAATCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340

QY 2341 TGGTACATTAATTTCTAGGGAATTTGAGATTCCATTTGACTCATGTAAATCTGAAG 2400
DB 2341 TGGTACATTAATTTCTAGGGAATTTGAGATTCCATTTGACTCATGTAAATCTGAAG 2400
QY 2401 TACTGTTTAAAAAAGAGAAAAATGCTATGGCAATTTAAATTTGAAGTCAATTTTGAAGT 2460
DB 2401 TACTGTTTAAAAAAGAGAAAAATGCTATGGCAATTTAAATTTGAAGTCAATTTTGAAGT 2460
QY 2461 CATTAATGCAATTTGCTTTGAAAATGAGAAATTAATCTAGAAATTAAGAAAAAGCTGG 2520
DB 2461 CATTAATGCAATTTGCTTTGAAAATGAGAAATTAATCTAGAAATTAAGAAAAAGCTGG 2520
QY 2521 ACTTGCAATATGAGGCTAATTTTGTGAGTAAATTAACATTTATTTTGAATTAATATATC 2580
DB 2521 ACTTGCAATATGAGGCTAATTTTGTGAGTAAATTAACATTTATTTGATATATATATC 2580
QY 2581 TATCAGATATGATATATGATTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2640
DB 2581 TATCAGATATGATATATGATTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2640
QY 2641 GTTCAATATGAGTAAATATATGATATGAGATTTATATGATTAATGAGAGCTGAAAT 2700
DB 2641 GTTCAATATGAGTAAATATATGATATGAGATTTATATGATTAATGAGAGCTGAAAT 2700
QY 2701 GGTAAAGCTTTTCTTCT 2760
DB 2701 GGTAAAGCTTTTCTTCT 2760
QY 2761 CTCCCTCAACAAATTCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
DB 2761 CTCCCTCAACAAATTCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
QY 2821 TGAATGATATGATATGATATGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
DB 2821 TGAATGATATGATATGATATGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
QY 2881 ACAATATGATATGATATGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940
DB 2881 ACAATATGATATGATATGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940
QY 2941 GCAAGAGAGTATGATATGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3000
DB 2941 GCAAGAGAGTATGATATGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3000
QY 3001 AACAGAGTATGATATGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3060
DB 3001 AACAGAGTATGATATGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3060
QY 3061 CTGAGAGATATGATATGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120
DB 3061 CTGAGAGATATGATATGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120
QY 3121 TTAATATGAG 3180
DB 3121 TTAATATGAG 3180
QY 3181 TGTGAG 3240
DB 3181 TGTGAG 3240
QY 3241 ATCTGAGTATGATATGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3300
DB 3241 ATCTGAGTATGATATGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3300
QY 3301 TGTGATTTTCAAG 3360
DB 3301 TGTGATTTTCAAG 3360
QY 3361 GGCATGAG 3420
DB 3361 GGCATGAG 3420
QY 3421 GCAATGTTGTTGAG 3480

DB 3421 GCAATGTTGTTGAG 3480
QY 3481 GTGTTTTTGGAG 3540
DB 3481 GTGTTTTTGGAG 3540
QY 3541 GTAAATGATATGAG 3600
DB 3541 GTAAATGATATGAG 3600
QY 3601 TCTTTGATATGAG 3660
DB 3601 TCTTTGATATGAG 3660
QY 3661 AAGGCGAG 3720
DB 3661 AAGGCGAG 3720
QY 3721 AGGTTTTTCTGAAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3780
DB 3721 AGGTTTTTCTGAAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3780
QY 3781 TTCACTTGAATTTGGGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3840
DB 3781 TTCACTTGAATTTGGGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3840
QY 3841 GAG 3900
DB 3841 GAG 3900
QY 3901 GAAAAG 3960
DB 3901 GAAAAG 3960
QY 3961 AAAAG 4020
DB 3961 AAAAG 4020
QY 4021 AGTGAAG 4080
DB 4021 AGTGAAG 4080
QY 4081 GAATGTTGTTGATATGAG 4140
DB 4081 GAATGTTGTTGATATGAG 4140
QY 4141 TGCATTAATGATATGAG 4200
DB 4141 TGCATTAATGATATGAG 4200
QY 4201 CTGTCCTGGGAG 4260
DB 4201 CTGTCCTGGGAG 4260
QY 4261 TGTGATATGATATGAG 4320
DB 4261 TGTGATATGATATGAG 4320
QY 4321 CCCCAG 4380
DB 4321 CCCCAG 4380
QY 4381 TGTGCGAG 4440
DB 4381 TGTGCGAG 4440
QY 4441 GTGAGCTCTGAG 4500
DB 4441 GTGAGCTCTGAG 4500
QY 4501 AGGATATTAATGATATGAG 4560

Db 4501 AGGATATATCTATGATGATGTTTACAAATGCTTAAACCTGGTTTCTGCTCCATCAACC 4560
Qy 4561 TAATCTGCAATTTCTAATTTGTTCACTTTAGAAAACATGSCATTAATGCTCAATACTT 4620
Db 4561 TAACTTGCATTTCTAATTTGTTCACTTTAGAAAACATGSCATTAATGCTCAATACTT 4620
Qy 4621 TTGCAATTTTATTTTACAGCTTGAGAGAGATGAGATCAAAAGCAATGGAGAACTGG 4680
Db 4621 TTGCAATTTTATTTTACAGCTTGAGAGAGATGAGATCAAAAGCAATGGAGAACTGG 4680
Qy 4681 ATTGCTGTTTATGTTCTGAGAAATGCTGCAATTTGACAGCAAAAGCTGAAAATGA 4740
Db 4681 ATTGCTGTTTATGTTCTGAGAAATGCTGCAATTTGACAGCAAAAGCTGAAAATGA 4740
Qy 4741 ATAATAACCCCTTTCCCTCTGAGAAATTAACAATAGATGCCCCAAAGCATTTT 4797
Db 4741 ATAATAACCCCTTTCCCTCTGAGAAATTAACAATAGATGCCCCAAAGCATTTT 4797

RESULT 2

US-10-027-632-118181/c

Sequence 118181, Application US/10027632

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

POLYMERISMS IN THE HUMAN GENOME

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 118181

LENGTH: 1074

TYPE: DNA

ORGANISM: Human

US-10-027-632-118181

Query Match 22.4%; Score 1073.6; DB 15; Length 1074;

Best Local Similarity 99.9%; Pred. No. 1.6e-254;

Matches 1073; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2472 TGCCTTGAACCTTGAGATTAATCACTGAGAAATGAGAAAGAGCTGAGCTGAGATTA 2531
Db 1074 TGCCTTGAACCTTGAGATTAATCACTGAGAAATGAGAAAGAGCTGAGCTGAGATTA 1015
Qy 2532 GGGCTAATTTCTGAGATTAATCACTTATTTGATTAATCATATATCTATCAGATAT 2591
Db 1014 GGGCTAATTTCTGAGATTAATCACTTATTTGATTAATCATATATCTATCAGATAT 955
Qy 2592 GATTAATTTTAAAGCAAGCAAGCAACCCCGATCTCTTTATACAGTTCAATATGA 2651
Db 954 GATTAATTTTAAAGCAAGCAAGCAACCCCGATCTCTTTATACAGTTCAATATGA 895
Qy 2652 GTAAAAATATAGTAAAGATTTATATAGTTAAATGAGAGCTGAAATGGTAACTTTT 2711
Db 894 GTAAAAATATAGTAAAGATTTATATAGTTAAATGAGAGCTGAAATGGTAACTTTT 835
Qy 2712 TTTCTTCTCTCTCCATCAAGACCTTCAATTCATGTTTCTTCTTCACTCCCTCAACA 2771

Db 834 TTTCTTCTCTCTCCATCAAGACCTTCAATTCATGTTTCTTCTTCACTCCCTCAACA 775
Qy 2772 ATCCCTAGGAGATTTATTCATTTGAGGCTGGTGTACATTTCTATAGTAAATGATACC 2831
Db 774 ATCCCTAGGAGATTTATTCATTTGAGGCTGGTGTACATTTCTATAGTAAATGATACC 715
Qy 2832 ATCATGTCCTTATTTGTTGAAAAAACAATATGAGGCTTATGATTAACATATGAC 2891
Db 714 ATCATGTCCTTATTTGTTGAAAAAACAATATGAGGCTTATGATTAACATATGAC 655
Qy 2892 TCACCCCAAAACCGAGAGATTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGTA 2951
Db 654 TCACCCCAAAACCGAGAGATTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGTA 595
Qy 2952 CAATTAATATCTGAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTA 3011
Db 594 CAATTAATATCTGAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTA 535
Qy 3012 CTTTATTTCCCTTTTCCCTCTTGAATTTTAAAGAGGTTCTTCTGAGAGATCAT 3071
Db 534 CTTTATTTCCCTTTTCCCTCTTGAATTTTAAAGAGGTTCTTCTGAGAGATCAT 475
Qy 3072 TTAATGAGTGTACTGTTTCTTCTTGTATTAATGAGGCTTGTATTAATGAGTA 3131
Db 474 TTAATGAGTGTACTGTTTCTTCTTGTATTAATGAGGCTTGTATTAATGAGTA 415
Qy 3132 AGCCAGTCTCTGTTATATGAACTATATATATATATATATATATATATATATATAT 3191
Db 414 AGCCAGTCTCTGTTATATGAACTATATATATATATATATATATATATATATATAT 355
Qy 3192 CACAGCAAGTA 3251
Db 354 CACAGCAAGTA 295
Qy 3252 TGTCTTGAAGTA 3311
Db 294 TGTCTTGAAGTA 235
Qy 3312 AGACCTTAT 3371
Db 234 AGACCTTAT 175
Qy 3372 GAGTAT 3431
Db 174 GAGTAT 115
Qy 3432 CAGAGAAAGATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTA 3491
Db 114 CAGAGAAAGATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTA 55
Qy 3492 AGGATTAATTTCCCTCTGTTGGGGGTAAGAGAGAGAGAGAGAGAGAGAGTA 3545
Db 54 AGGATTAATTTCCCTCTGTTGGGGGTAAGAGAGAGAGAGAGAGAGAGAGTA 1

RESULT 3

US-09-751-797-8

Sequence 8, Application US/09751797

Patent No. US20010024652A1

GENERAL INFORMATION:

APPLICANT: Dumoulier, Laure

APPLICANT: Louhe, Jamila

APPLICANT: Renaud, Jean-Christophe

TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible 1

FILE REFERENCE: LUD 5543.2

CURRENT APPLICATION NUMBER: US/09/751,797

PRIOR APPLICATION NUMBER: 09/419,568

PRIOR FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: US09/178,973

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 8
 LENGTH: 7445
 TYPE: DNA
 ORGANISM: Mus musculus
 FEATURE:
 US-09-751-797-8

Query Match 14.3%; Score 686; DB 10; Length 7445;
 Best Local Similarity 53.8%; Pred. No. 3e-158;
 Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;

29 CTCCTTCCCGACGACAGTGTGCTGAGTAAATGTGCGAAATGCGCGCCCTGAGAA 88
 2034 CTCTCTCTCACTTATCAACTGTGACACTGTGCGACATCTTGATGAGCTGTCTGAGAA 2093
 89 ATCTGTAGACTCTTCTCTTATGAGGACCCGTGCGACAGCTGCTCTCTTCTGAGCCCT 148
 2094 ATCTATGAGTCTTCTCTTATGAGGACCTTGGCCGCGACAGCTGCTCTCTCTCATGGCCT 2153
 149 CTTGGTACAGGAGAGACAGCTGCGCCCATCAGCTCCCACTGCAAGCTTGACAAATCCAA 208
 2154 GTGGGCGCCAGAGAGCAATGCGCTGCGCCGTCACACCCGAGTCAAGCTTGAGGTGCCAA 2213
 209 CTTGACGACGCCCTATATACCAACCGGACCTTCAGCTGGCGTAAAGAGTATACATCTC 268
 2214 CTTCCAGACGCCGATACATGTCACACCGACCTTATGCTGGCCCAAGAGGTACAGCTGCA 2273
 269 AATCTGCTCTTCTCTGCTGAGATCTTCTGGAATCCAAATAGTCTTAACTTTCTTCA 328
 2274 TCTCTTCTCTCATACCGCCCTTGCATTTCTCTGAGACACTTGCAAACTCTTTAGGGG 2333
 339 GAGCATCTCTAAAGCTTTAGGAACCCACTGTTATCCCTGAGGGTAAATTAATTTCTG 388
 2334 CCGTTATCTCGCAGGTCTCACTACCTATGTTT-----TCTGCTCTTTAGAG 2382
 389 TTTTTCAGAGACTCTTGGGAATCTGGCTTTTCTTTTCTTGAACCTTCTCTCCAT 448
 2383 ACTCTTAAAGACTGGGCTTTTCTTATTTTCAATTTCAAGTCTCGAGCACTTCTCTAT 2442
 449 TTGGCCCTTATGATATGATGATGATTTTCCCAAGAGCGGCCATTCAATATCCAT 508
 2443 CTTGGCTTCAAGACATATGATGATTTTATCTACAGAGGCGCATTT--AGAAAGCCA 2500
 509 CTGATGATTTTCTTCTTATGCTCTGCTGCTGCTTCTTAACTCATGACACATCTG 568
 2501 CCCAGCATGCAATACCTTCTGCTGCTCTCTTCTGAACTCATACCTCTTGGC 2560
 569 AATTCTGCTTTAGTCTTATGATGATGCTCTGAGGAGACGGGATGGGCACTGTCTAT 628
 2561 TACTC-----CTGAGACCACTGCGACATACATCTCTAC 2595
 629 GATATAATTTTCTTATTTGCTCAATGCTCAAGCCCTTACCTTCTCTCCAG 688
 2596 TTACAGGCTTTCTTCTCTCTCTCTCTCTCAAGGACCTTAAAGGTTTCT--TCTCTTCA 2654
 689 GCTAGCTGCTGATTAACAACAAGAGCTGCTCTCTTATTTGGGAGAACTGTTCCAGGA 748
 2655 GCCAGCTTGCAGATTAACAACAAGAGCTGCTCTCTCTATGCGGAGAACTGTTCCAGGA 2714
 749 GTGATGTAGCTACAGTTGTGACGAACAGGCGGTGCTGCTCAATGAGTACTTGGGCT 808
 2715 GTGAGTGAAGTCTCTCACTGTGATGAGCAGGCG-----TAGCTGCGGAGGCT 2761
 809 GGTGAGTGAAGTGTAGGCTTATCCCTTATGACCCCTTCTGTTTCTCTTCCACTG 868
 2762 GGTGAGCCTCTGGGATAG---CTGAGATGACCCCTGCTCTTCTTGTCTTACTG 2817
 869 AGATGATGAGGCTCTCTCTGATGAGAGGCTGCTGAATTCACCTTGAAGAAGTGC 928
 2818 AGGCTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2877
 929 TGTTCCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 988

2878 TGCTCCCCAGTCAAGAGTTCAGCCCTACATGAGAGGTGATCTTCTCTGACA 2937
 989 GGCTCAGCAACAGGCTAAGACATGTGTAAGTTCACTCTCAGCCTATGCCACTACCC 1048
 2938 AACTCAGCAATCAGCTCAGCTCTGTGTAAGTCTGCTGCTACCTATGCTCTCTCT 2997
 1049 CTCCTTCCCTCTCTCAGAGAACCCCTTACCCCACTCTCTCTCTCTCTCTCTCTCT 1108
 2998 CT 3057
 1109 TAAGTACAGAGAAAGTGTCTTGGCAGCAGTGTATCAGAGTCA-----TTTGGG 1161
 3058 GAGAGGCTCAGACCAACCATCATATGAGCCACTGAAATAGTATCAAAAGCTTTGGC 3117
 1162 ATCATAGAGTATTTGCTTTGCTTGTAGTCACTGATCATCTTGAATATAGTGTGAATG 1221
 3118 TTCAATGTAGTATATCTTGTAGTGTATGAGTGAAGCTTTATTTGTTATTCATAGAA 3177
 1222 GGTCTGGAATTTAAGTATACGAAGCCCATTTGTTGTCTTGGAAAAAGCAATC 1281
 3178 AGAATCAACTCAAAATCTGTAGATGAGAAAGATGTTGGAACGAAAAAGGCTTAGAT 3237
 1282 A-----GGTTGGTAAATGAGAAAGTGTGG 1309
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 1310 GAAACATCTAGCTGTGAAATGATATCATGATGATGATGATGATGATGATGATGATG 1369
 3298 GTACAGTACTTGTGGGAGAGAAATCCACTGATGATGATGATGATGATGATGATGATG 1415
 1370 CATGAGAGAAATTTAGAGAGAAAGTGGAAATGGAAGCTTAA-----1415
 3358 CACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3417
 1416 -----GTGGTGTGGGTGGGAGACTGTGCGCTGTGATGATGATGATGATGATGATG 1460
 3418 AAGATGAGAGGCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3477
 1461 AGCCCAAAATCGAGGCTGTGAACTTGATGCTGCTGCAATTTGAAATGATGAAATA 1520
 3478 AGTTAAGAAACAGT--GTGAGATGATGATGATGATGATGATGATGATGATGATGATG 3536
 1521 AGTTAGTGAAGTGGGCCCAAGTAAAGCCCTAGACATTTAGTGAAGAGGCTTAAATTT 1580
 3537 ATCCAGAGAGAGGCGGCACTGTGAGAACCTGAGTATTAAGGA--AGGCGGCTTTT 3594
 1581 CACATGAGATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1640
 3595 CACAGAGAACTTATGCTCATCTTGTGCTACCTCCACCTTGTGATGAGGTTCAAG 3654
 1641 TGAGTTTATCTCTTACAGATTTGATTAACCTCTGCTCTTCCAAATGCAAC 1700
 3655 TCAAGTTGTTCT-----ACGTTCTTCTCTCTCTGATGAAAC 3693
 1701 CTCAGTGAATTTCCCAAGATGAAAGAGTCTCTTGAAGGAAATGATGATGATGATGAT 1760
 3694 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3753
 1761 GGTCTCAAGGAAATTCAGAGTCAAGAAATCTAGTCACTGTTGAATCTTAGTATG 1820
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 3814 GGGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3873
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 3874 AGGTATGAGGCTCCCAAGGATTAAGTCTGTTAGGA--GTCTGCTTTATTTTTCAGCA 3932
 1941 TATGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2000
 3933 CATCAAGGCTGACGACCAAGATCATCAAGAAATGATGATGATGATGATGATGATGATGAT 3992

QY 2001 AAAGTAGACTGATTAAGTCAATGCTAGTCAATGAGAGCAAAATGTTT 2060
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D 4111 GTCCATTAATCTGCTAGCTGACCTGTATCTAGCTGGGCTATAGATCTTCAATCTGTG 4170
QY 2177 TCCAAATCTGCAATTTGTATTAATTTCTAGAACTGTGGGATCTTGAAGTCTGTAC 2236
D 4171 TCTAAATTT---GTAGTCAAAATTTCTGAGCTAGCAAAAGCTTAGCTCAGCCAGTCTC 4227
QY 2237 ATAACTCAGATTTCTGGGATGTCTAGTGCAGAGATAGGCTAGAAATGAGTCTCTCTG 2296
D 4228 ATGAGCACTGTCTGGAGATGTGCTTGTACAGAGTCAATCTGAAAGACAGCATCCCTG 4287
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QY 2477 TGAATCTGGAATTAATCACTCAGAACATGAGAAAAGAGCTGATCTGATAGAGCT 2536
D 4461 TGAATGTGGCAAAATCAACCCAGATTAACAAAGAGAGCTGATTTGCAATAGAGCA 4520
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D 4753 TCAAGCACTATGATAGCACTATCTGTGATGATTAATTAATTAATTAATTAATTAAT 4812
QY 2829 ACCATCATGTGCTTATTTGTGTAAGAGACA--ACAATGAGAGCTTATGATTAACATA 2886
D 4813 ATGCTGTGTGCTCTTGTGGGAGAGGAGACAGATTAAGAGAGGCTCAGCTGCAAGT 4872
QY 2887 GTGACTCAAGCCCAAAAGGAGATGATTAAGAGAGTGAAGTGAAGCTCTT--GCAAG 2945
D 4873 CTGACTTGTGCTTAAAGCAGAGGATGTGTATGATGAGAGAGTGAAGGCTCTTCTGCAAG 4932
QY 2946 CAGGATCAATTAATTAATCAAGAAATGAGAGCTTCAAGTATGATGAATTTCAATCAAA 3005
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QY 3006 GCTTAACTTAATTTCCCTTTTCTCTCTGATCTTTTAAAGAGGCTTTCTCTCTGAG 3065
D 4993 ATCTACCTTATCTCTTCTATGAGAC-----TAAATGTCTCTTTCTCTGTG 5042

QY 3066 CATCATTAATGAGTGTGACTGTTTCTCTTGTATTAATGAAAGCTTTGATTTAAA 3125
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D 5216 ----TTGTCTTGTGAAGATGAGAGCTGTGTGAAGAAATCAACAGAGATGTCTTCT 5270
QY 3297 -----TCTGTGATTTTCAAGACCTTTAATCAATTTTGAAGAAATCAAT 3342
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D 5448 CAGAGCTTCCCGAGACCA-----CCAGGTGTTTAAGTAAAG 5485
QY 3522 AGCAGAGCAGAGTGTGATTAAT--GCATGACAGACAGTAGGAGAGATTAATCTTAA 3580
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QY 3641 AAAGAGTATGAAAGS-----TGAAGAGGCGGAGAGAGAGAGAGAGAGAG 3668
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QY 3669 AACCATGATTAATATAGAGCAATAGTGAAGAGTTTCTTGAATTAATGCAATATAG 3748
D 5663 AGAGCTTGAACAGTAAATCTCTTACAGAGATTTTCTTGAACATCTAGAGAGT 5722
QY 3749 ATGATTAAGAGATTTCAATGAGAGATGCTTTTCACTTGAATTTGGGTTCTCT--T 3805
D 5723 AGTGAATTAAGTATGACAGAGGAGACTTGTGCTTGAATCTGGGTTTGTCTCT 5782
QY 3806 CGATTAAGTTGGAGTCTCATGCTGATTTGACT---TGAAGAGAGAGAGAGAGAGT 3861
D 5783 CATTTAGTTGAAGCTGACCTCTTTTACCTTCAATGAGAGAGAGAGAGAGAGAGT 5842
QY 3862 TAGAGCTATATCTGTTTCTTATTAATTAAGCAATGAGAGAGAGAGAGAGAGT 3921
D 5843 TAGAGCTTCACTGAGATTTTCTAGTTTACCAATGAAGAGAGAGAGAGAGAGT 5902
QY 3922 TTCCACAAAGTGAAGAACTTTCTTCTTCTGTTTGTCAAAAGAGTGAAGATGAAGAAAG 3961
D 5903 CTTGACAAAGAAATGAGAACTGTTGTGTTGTCTTGTGTTTGTGTTGTTGTTGTTGTTGTT 5962
QY 3982 CTTAATGATTTGTGATATCATGTTCAAGATCATTTGAGTGAAGATTTTAAATCAG 4041
D 5963 AGGCAAGCCGAGACACATGAGTGAATGTGAGTCTTTGAGTCAAGGCTTTGAGTTGAG 6002
QY 4042 GAGTGTCCATTAATTTGGCTTCCCTGAGCAGCTTGAAGAAATGTCTTGTGATACACAT 4101
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QY 4102 AAATATCAAGAAATAGCTGATGAGCTAAAGAGTCAATGATCAATTAATCTCATGCTTT 4161

Db 6059 TACCTGACAGCCGACGCTGCTGCTCCGACTTAACATCTCCAGGCTTCAGATCACT 6118
 Qy 4162 TAAGAAAGTTAATGAAATTTCTGTAGGTCATTCAAAGCTGTCCTGCGCATGTGCGC 4221
 Db 6119 TCTGCTACTTACAGACGTTAGAGGTTAGCAAAACCTTTTTC----- 6163
 Qy 4222 CTGTGGGCTGCAAGTTGACAAAGCTCTTAAAGTAATCTGTCAATAGTAGTTTGGAGC 4281
 Db 6164 -----AACCCCACTAAATTTAATGACAAAMAACTGTGTAAATTG 6205
 Qy 4282 TGCAAAACAGCCCAAGCAATATAGGTGACCTGGATCCCCAGATCCAGAGCTCACT 4341
 Db 6206 TGGGATACAGTGTGATTAATGA----- 6227
 Qy 4342 TCAGTCTCTGCTGCTGTGAAGAGGGTGTGTCACCTCTGCGCAGCTTTTAAAGC 4401
 Db 6228 -----TCTATGTGTGACATGTGCAAGTTCAATAGATAGATTAATAGCCCATCAAGC 6283
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 Qy 4461 GCGGTCAATTTAAGCTTTGGCAAAATCAATCAATACTTAAAGGATA-----T 4508
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 Qy 4509 TACTATGATGTTTAAAGTCTTAAACCTGGTCTCTGCTCATCAACCTTATCTTG 4568
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 Qy 4569 CAATTTCT---AATTGTCACTTTAGAAAACATGGCATTAATGCTCAATCTTTTGA 4625
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 Db 6524 TTCTTATTTTCAAGCTTGAAGAGAGTGAAGATCAAGCAATTTGAGAACTGATTTG 6583
 Qy 4686 CTGTATATGCTCTGAGAAATGCTGATTTGACCAAGCAAGCTGAAATTAATTAAC 4745
 Db 6584 CTGTTTATGCTCTGAGAAATGCTGCTGTGACGAGAAAGACTGAAATACAGAGAC 6643
 Qy 4746 TAAACCCCTTCTCCTGTAGAAATTAACATTAATGAGCCCAAGCAATTTT 4797
 Db 6644 TGTCTCTCTGCTCTTAATAAGAACATTAAGATCCGTGATGAGCTTTT 6695

 RESULT 4
 US-09-751-797-29
 ; Sequence 29, Application US/09751797
 ; Patent No. US20010024652A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumoulier, Laure
 ; APPLICANT: Leoued, Jamila
 ; APPLICANT: Renaud, Jean-Christophe
 ; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
 ; FILE REFERENCE: LIND 5543.2
 ; CURRENT APPLICATION NUMBER: US/09/751,797
 ; CURRENT FILING DATE: 2000-12-29
 ; PRIOR APPLICATION NUMBER: 09/419,568
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: US09/178,973
 ; PRIOR FILING DATE: 1998-10-26
 ; NUMBER OF SEQ ID NOS: 29
 ; SEQ ID NO 29
 ; LENGTH: 5935
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 US-09-751-797-29

Query Match 13.6%; Score 650; DB 10; Length 5935;
 Best Local Similarity 56.5%; Pred. No. 2e-149; Indels 152; Gaps 29;
 Matches 1863; Conservative 0; Mismatches 1285;
 Qy 29 CTCCTTCCAGTACAGGTTGCTCGAGTATGATGTCGAATGAGCCGCTGAGAA 88
 Db 356 CTCCTCTCAGATTATCACTTTTGAACCTGTGGCATGGTATAGGCTGCTGAGAA 415
 Qy 89 ATCTGTAGCTCTTCTTATGAGGAACTGTGCAACAGCTGCTCTTCTTTGGCCCT 148
 Db 416 ATCTATAGATTTTCTTATGAGGAACTTTGGCGCAGCTGCTCTTCTTATGCTCT 475
 Qy 149 CTGTGTAAGAGGAGAGAGCTGCGCCATCACTGCCACTGAGAGCTTACAGTCAA 208
 Db 476 GTGGGCCAGAGAGCAAAATGCTGCCATCAACACCCGATGAGCTTATAGGTTCAA 535
 Qy 209 CTTCAGACAGCCCTATATCAACAAGCAGCACTTATGCTGAGTAAAGAGTATATCTC 268
 Db 536 CTTCAGACAGCCCTATATCAACGACCTTATGCTGAGTAAAGAGTATATCTC 595
 Qy 269 AATCTGCTCTTCTGCTGATCTATCTGAAATCAATATGTTCTTAACTTTTCTCA 328
 Db 596 TCTCTTCTCTCATACCGCTTGCATTTCTGAAAGCACTTGAACCTTTAGGGGC 655
 Qy 329 GAGCATCTTAAGAGCTTGAAGAACCACTTTATCCCTGAGAGTATATTTCTG 388
 Db 656 GCTTTATCTCCGAGAGCTACATATGTTTCTGCT-----CTTTAGAG 703
 Qy 389 TTTTTCAGAGCTCTTGGAAATGAGCTTTTCTTTTCTTGAATCTTCTCTTCAT 448
 Db 704 ACTCTTATAGAGCTGATCTTTTCTTATTTCTTATCAAGTCTCAGACATTTCTAT 763
 Qy 449 TTTGGCTTATGATATATATATGAAATTTTCCAAAGAGCGGCAATGATATCAT 508
 Db 764 CTGGCTTACAGACATATATGATTTTATCTACAGAGGCGGCTT--AGAAAGCA 821
 Qy 509 CTGATGATTTTCTTATGCTCTGATGATTTTAACTATACACATCTG 568
 Db 822 CCCAGACTGCAATATCTTCACTGCTGTGTCTCTTCTGAAATCATATCTCTTGGC 881
 Qy 569 AATTGCTTTTATGCTTATATGTTGCTGTGGGAGAGGGATGGGACATGTTAT 628
 Db 882 TACTC-----CTAGAACCACTGCGGACATATCTTAC 916
 Qy 629 GATTAATTTTCTTATGCTCAATGTCAGACCTTATGTTCTTCTTCTCAG 688
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 Qy 689 GCTAGCTGCTATTAACAACAGAGCTTCTCATTTGGGAGAACTGTTCCAGGA 748
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 Qy 869 AGATGAGTACGCTGTATCTATATGAGAGAGTGTGAACTTACCTTGAAGAGTGC 928
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 Qy 929 TGTTCCTCATCTGATAGTGTTCAGGCTTATATGAGAGAGTGTGCTTCTTCTGAGCA 988
 Db 1199 TGTCTCCCACTAGACAGAGTTCCGCTTATCATGAGAGAGTGTGCTTCTTCTGAGCA 1258
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 Qy 1049 CTCCTTCTCTTCCACAGAGACCCCTTAACCCCAACTCTCTCTCTTCTTCTTCTTCTT 1108

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Qy 1691 AAATGCAAACTCAGTAGATTTTCCAAAGATGAAGAGGCTCTTTGAAAGGAGTGA 1750
Db 1957 TGTGAGAACTTCAAGTAGATTTCCCAAGAGAGAGCAGCTCTTCTGTAAGGAGGAGC 2016
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Qy 1811 TAGGCTATGTGGGCAAAATTAAGAGCTTAAATTCAGGTAATTTGACTGACTC 1870
Db 2077 AGGTACAGCGGGCAAAATGACTGAAAGCTCTTATTCAGGTGAAGGTCACTGCTTC 2136
Qy 1871 CATGGGTGAGGTTCAATAAGTTTCAACAACATTTAGATTTATGCTTGTATATG 1930
Db 2137 AGATTAATCTGAGATTTGGGCTCCACCGGATTAAGATTTCTGTATGA-GTCTGCTTTTA 2195
Qy 1931 TTTTATAGCATTTTAAAGTATGATGACTGATATTCAGAGAAATGCAAAAGCTGAAG 1990
Db 2196 TTTTGCACACATCAGTGTGTGCGACAGAACATCAGAAAGATTCAGAAAGGCTGAAG 2255
Qy 1991 ACACAGTAAAAAGTAGACTGATTAATCTGATGCTAAGTCAATGAGAGAGACA 2050
Db 2256 AGACAGTAAAAAGTAACTATTGGAGAGCACAATCTAAGGCAATTCAGTAGAGAGCTG 2315
Qy 2051 AATGTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2110
Db 2316 GGGATTTCTTCTCTGCTTCCAGTCT--CTTCTACTTTGTAACATTTTCTTGTGACTGT 2373
Qy 2111 CTACACACAGGCGATT-----ACTTGGTGTGTGTATGATATATCTATATATCTA 2166

Db 2374 CTACTGTGTGTCATTAATCTCACTTACTGACACCTGATCTAGCTGGGTCTATGATCTT 2433
Qy 2167 GATGTCAAGTTTCCAAATCTTGCAAAATTGTGAATTTAGAACTGTGGATCTTACTT 2226
Db 2434 TCATCTGTGTCTAAATTT---GTAACTCAAAATTTGGAGCTGACGAAAGCTTAGCTC 2490
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Qy 2287 AGGTCTGCTGAATCCAGACAGACTTTTCCGGGTGTATACAGATTAGTTTGTGTAC 2346
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Qy 2347 CATTAATTTCTAGGAAATTTCAAGATTCCTATAGTACTATGTAATCTGAAAGTACTTG 2406
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Qy 2407 TTTAAAAACGAAAAATGCTATGCGCAATTTATTTGAAGTCAATTTTGAAGTCTTAA 2466
Db 2668 TTGAAAACTAGAAA---GCTGGGCACAAACTTACTAGAGATGATTTTGTGCTCATTA 2723
Qy 2467 TGCAATGCTTTGAACTTGAAGAATAAATCAAGATGAGAGAAAGAGCTGACTGC 2526
Db 2724 ACTGATCTCTGAAATGTGATCAATCAACCCAGAAATTAACAAGAGCTGGAATTTGC 2783
Qy 2527 ATATAGGCTTAATTTCTGAGATAATAAACAATTAT-----TTGATATATCATATA 2578
Db 2784 AAATAGCAAGATTTTGAATCTCTGTATTTAAGCTGTCACTTAAATTAATTAATAG 2843
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Qy 2755 CTTCACCTCTCAACAAATCCTAGGAGATTTATTCATGTGGGCTGTGTACATTT 2814
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Qy 2815 CTATAGGATGATACATCATCATGAGCTATTTGGTGAAGAACAA-ACAATGAGAGC 2872
Db 3081 TTACAGCAAAACAACTTGTGTGTGGCTCTTTGGGAGGGAACAGATGCAAGAGGC 3140
Qy 2873 TTAGACTAACAA-TAGTACTCACCCCAAAACCGAGAGATGATTAAGAGCAGTGAAGT 2931
Db 3141 TCAGGCTAGCAAGTGTGACTCAACCTAAGCCAGAGGCAATGATTAAGCAGAGAAAGT 3200
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Qy 2991 AATTTTCAATCAAGCTTAACCTTAATTTCCCTTTTCCCTGTGACTTTTAAAAAA 3050
Db 3261 AATTAATCAATGATTAATCTACCTTAATCTC-----TTCTTATTAAGAGCTTAACCG 3313
Qy 3051 GCGTTTCTCTCTGAGATCATTTATGATGATGATGATGATGATGATGATGATGATGATG 3110
Db 3314 TCTCTCTCTCTGT 3371
Qy 3111 CTGT 3170
Db 3372 CTGT 3429
Qy 3171 GAGGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3230
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QY 3231 TACTGATTCATCTGCTTCTTCTTTAGAAAAAGTGAAGTGTGAGAGAGCAATCTCA 3290
DB 3490 TATCATCTTACT-----TTGTCTTGGAAAGGTGAAGTGTGTGTGAGAAAGAACTCA 3541

RESULT 5
US-10-027-632-208140

/ Sequence 208140, Application US/10027632
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 208140
/ LENGTH: 637
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-208140

Query Match 12.8%; Score 611.8; DB 15; Length 637;
Best Local Similarity 99.2%; Pred. No. 1.4e-140;
Matches 632; Conservative 3; Mismatches 0; Indels 2; Gaps 2;

QY 3289 CATGTGATCTGTGATTTTCAAGACCTTTAATCCA-TTTTGAAGAAATCAATTTTCATA 3347
DB 1 CATGTGATCTGTGATTTTCAAGACCTTTAATCCAATTTTGAAGAAATCAATTTTCATA 60
QY 3348 TTTGCAATGGGTTGCCATGTGAAGAGTATATGTTTTGCTGTGGCTTCAGAAAG 3407
DB 61 TTTGCAATGGGTTGCCATGTGAAGAGTATATGTTTTGCTGTGGCTTCAGAAAG 120
QY 3408 CACAGAGGAGAGAGCAATGTGTCA-GAGAAAGATCAACAGAGAGAAACTGTCAAG 3466
DB 121 CACAGAGGAGAGAGCAATGTGTCAAGAGAAATCAACAGAGAGAAACTGTCAAG 180
QY 3467 CTGTCTGAATAAGGGTGTGTTGGAGGCAATTAATTCCTCTCGTTGGGGGTAAAGCAG 3526
DB 181 CTGTCTGAATAAGGGTGTGTTGGAGGCAATTAATTCCTCTCGTTGGGGGTAAAGCAG 240
QY 3527 AACGCAAGTTGTGTAAGTAAATGATACACAGACAGTGGGAGCATTAATCTTTAAATTTCT 3586
DB 241 AACGCAAGTTGTGTAAGTAAATGATACACAGACAGTGGGAGCATTAATCTTTAAATTTCT 300
QY 3587 TTATAGTCTTGAGTCTTTGAGATAGAAAAGATATCTTTTGGCCTTAATGTCAAAAGAA 3646
DB 301 TTATAGTCTTGAGTCTTTGAGATAGAAAAGATATCTTTTGGCCTTAATGTCAAAAGAA 360
QY 3647 GTATGAAAAGTGAAGGCGGAGAAAGACAGAGAAAGAAACCATGTATTATATAGA 3706
DB 361 GTATGAAAAGTGAAGGCGGAGAAAGACAGAGAAAGAAACCATGTATTATATAGA 420
QY 3707 GGCATATGTGACAAAGTTTCTTTGAAAATATGCAATATGATAGATTAGAGAAATTC 3766
DB 421 GGCATATGTGACAAAGTTTCTTTGAAAATATGCAATATGATAGATTAGAGAAATTC 480

QY 3767 AGTAGGGAATGCTTTTCACTTGAATTTGGGTTTCTCTTGCATTAAGTTGGGATCTCA 3826
DB 481 AGTAGGGAATGCTTTTCACTTGAATTTGGGTTTCTCTTGCATTAAGTTGGGATCTCA 540
QY 3827 TCTGCATTTGACTTGAGAGAGAAAGATGATGTAGACCTTAATCTGTTTCTATT 3886
DB 541 TCTGCATTTGACTTGAGAGAGAAAGATGATGTAGACCTTAATCTGTTTCTATT 600
QY 3887 AACTAAGCAAGTGAAGAAAGCTTATTGTAATTTT 3923
DB 601 AACTAAGCAAGTGAAGAAAGCTTATTGTAATTTT 637

RESULT 6
US-10-027-632-208141

/ Sequence 208141, Application US/10027632
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 208141
/ LENGTH: 637
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-208141

Query Match 12.8%; Score 611.8; DB 15; Length 637;
Best Local Similarity 99.2%; Pred. No. 1.4e-140;
Matches 632; Conservative 3; Mismatches 0; Indels 2; Gaps 2;

QY 3289 CATGTGATCTGTGATTTTCAAGACCTTTAATCCA-TTTTGAAGAAATCAATTTTCATA 3347
DB 1 CATGTGATCTGTGATTTTCAAGACCTTTAATCCAATTTTGAAGAAATCAATTTTCATA 60
QY 3348 TTTGCAATGGGTTGCCATGTGAAGAGTATATGTTTTGCTGTGGCTTCAGAAAG 3407
DB 61 TTTGCAATGGGTTGCCATGTGAAGAGTATATGTTTTGCTGTGGCTTCAGAAAG 120
QY 3408 CACAGAGGAGAGAGCAATGTGTCA-GAGAAAGATCAACAGAGAGAAACTGTCAAG 3466
DB 121 CACAGAGGAGAGAGCAATGTGTCAAGAGAAATCAACAGAGAGAAACTGTCAAG 180
QY 3467 CTGTCTGAATAAGGGTGTGTTGGAGGCAATTAATTCCTCTCGTTGGGGGTAAAGCAG 3526
DB 181 CTGTCTGAATAAGGGTGTGTTGGAGGCAATTAATTCCTCTCGTTGGGGGTAAAGCAG 240
QY 3527 AACGCAAGTTGTGTAAGTAAATGATACACAGACAGTGGGAGCATTAATCTTTAAATTTCT 3586
DB 241 AACGCAAGTTGTGTAAGTAAATGATACACAGACAGTGGGAGCATTAATCTTTAAATTTCT 300
QY 3587 TTATAGTCTTGAGTCTTTGAGATAGAAAAGATATCTTTTGGCCTTAATGTCAAAAGAA 3646
DB 301 TTATAGTCTTGAGTCTTTGAGATAGAAAAGATATCTTTTGGCCTTAATGTCAAAAGAA 360

QY 3647 GTATGAAAGGTGAAGGCGGAGAAAGCAAGAAAGAAACCATGATTTATATAGA 3706
DB 361 GTATGAAAGGTGAAGGCGGAGAAAGCAAGAAAGAAACCATGATTTATATAGA 420
QY 3707 GCACATATGTACAGAGGTTTCTTGAATATATGAAATATGATATAGATTAAGGAATTC 3766
DB 421 GCACATATGTACAGAGGTTTCTTGAATATATGAAATATGATATAGATTAAGGAATTC 480
QY 3767 AGTAGGAATGCTTTTCACTTGAATTTGGGTTTCTCTTCGATTAAAGTTGGATCTCA 3826
DB 481 AGTAGGAATGCTTTTCACTTGAATTTGGGTTTCTCTTCGATTAAAGTTGGATCTCA 540
QY 3827 TCTGATTTGACTTGGAGAGAGAAAGAAATGATATGATAGACCTATATCTGTTTCTATT 3886
DB 541 TCTGATTTGACTTGGAGAGAGAAAGAAATGATATGATAGACCTATATCTGTTTCTATT 600
QY 3887 AACTAAAGCAAGTGAGAAAGCACTATTGTTATTTT 3923
DB 601 AACTAAAGCAAGTGAGAAAGCACTATTGTTATTTT 637

RESULT 7
US-10-027-632-208142
Sequence 208142, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMERASE: Polymorphisms in the Human Genome
FILE REFERENCE: 108827, 129
CURRENT APPLICATION NUMBER: US/10/027, 632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218, 006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198, 676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193, 483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185, 218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167, 363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156, 358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146, 002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 208142
LENGTH: 637
TYPE: DNA
ORGANISM: Human
US-10-027-632-208142

Query Match 12.8%; Score 611.8; DB 15; Length 637;
Best Local Similarity 99.2%; Pred. No. 1,4e-140;
Matches 632; Conservative 3; Mismatches 0; Indels 2; Gaps 2;

QY 3289 CATGATCTGTGTGATTTTCAAGACCTTAATCCA-TTTTGAAGAAATCAATTCATA 3347
DB 1 CATGATCTGTGTGATTTTCAAGACCTTAATCCA-TTTTGAAGAAATCAATTCATA 60
QY 3348 TTTCGATGCTGTGATTTTCAAGACCTTAATCCA-TTTTGAAGAAATCAATTCATA 3407
DB 61 TTTCGATGCTGTGATTTTCAAGACCTTAATCCA-TTTTGAAGAAATCAATTCATA 120
QY 3408 CACAGAGGAGAGGAGCAATGTTTCA-GAGAAAGATTAACAGAGGAGAACTGTCTAG 3466
DB 121 CACAGAGGAGAGGAGCAATGTTTCA-GAGAAAGATTAACAGAGGAGAACTGTCTAG 180
QY 3467 CTGTCTGAATATAGGAGGTTTGGAGGAGCAATTAATTCCTGCTGGGGGTAAAGCAG 3526
DB 181 CTGTCTGAATATAGGAGGTTTGGAGGAGCAATTAATTCCTGCTGGGGGTAAAGCAG 240

QY 3527 AACGCAAGTGTAGTAAATATGATGACAGACAGTAGGAGGACATTAATCTTAAATCT 3586
DB 241 AACGCAAGTGTAGTAAATATGATGACAGACAGTAGGAGGACATTAATCTTAAATCT 300
QY 3587 TTATAGCTTGGAGCTCTTTGATAGTAAAGAAATATCTTTTGGCTTATGCTAAAGAA 3646
DB 301 TTATAGCTTGGAGCTCTTTGATAGTAAAGAAATATCTTTTGGCTTATGCTAAAGAA 360
QY 3647 GTATGAAAGGTGAAGGCGGAGAAAGCAAGAAAGAAACCATGATTTATATAGA 3706
DB 361 GTATGAAAGGTGAAGGCGGAGAAAGCAAGAAAGAAACCATGATTTATATAGA 420
QY 3707 GCACATATGTACAGAGGTTTCTTGAATATATGAAATATGATATAGATTAAGGAATTC 3766
DB 421 GCACATATGTACAGAGGTTTCTTGAATATATGAAATATGATATAGATTAAGGAATTC 480
QY 3767 AGTAGGAATGCTTTTCACTTGAATTTGGGTTTCTCTTCGATTAAAGTTGGATCTCA 3826
DB 481 AGTAGGAATGCTTTTCACTTGAATTTGGGTTTCTCTTCGATTAAAGTTGGATCTCA 540
QY 3827 TCTGATTTGACTTGGAGAGAGAAAGAAATGATATGATAGACCTATATCTGTTTCTATT 3886
DB 541 TCTGATTTGACTTGGAGAGAGAAAGAAATGATATGATAGACCTATATCTGTTTCTATT 600
QY 3887 AACTAAAGCAAGTGAGAAAGCACTATTGTTATTTT 3923
DB 601 AACTAAAGCAAGTGAGAAAGCACTATTGTTATTTT 637

RESULT 8
US-09-751-797-24
Sequence 24, Application US/09751797
Patent No. US20010024652A1
GENERAL INFORMATION:
APPLICANT: Dumoulier, Laure
APPLICANT: Renauld, Yamila
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/751, 797
CURRENT FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 09/419, 568
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/178, 973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 24
LENGTH: 690
TYPE: DNA
ORGANISM: Homo sapiens
US-09-751-797-24

Query Match 5.4%; Score 258; DB 10; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.5e-53;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACAGAGAAATCTTCAAGACAGGTTCTCTCCAGTCAACAGTTGCTGAGTTAG 60
DB 1 TGCACAGAGAAATCTTCAAGACAGGTTCTCTCCAGTCAACAGTTGCTGAGTTAG 60
QY 61 AATTGCTGCAATGCGCGCGCTGCAAGAAATCTGTAGCTCTTCTTATGAGGACCTGG 120
DB 61 AATTGCTGCAATGCGCGCGCTGCAAGAAATCTGTAGCTCTTCTTATGAGGACCTGG 120
QY 121 CCACAGCTGCTCTCTTCTTGGCCCTTGTGACAGGAGAGAGAGAGCTGCGCCATCA 180
DB 121 CCACAGCTGCTCTCTTCTTGGCCCTTGTGACAGGAGAGAGAGAGCTGCGCCATCA 180
QY 181 GCTCCAGCTGAGGCTTGAAGAGTCAATCTTCAGAGAGCCCTATATCAACAGCACT 240

Db 181 GCTCCACTGACGCTTGACAACTCCACTTCACAGAGCCCTATATACCAACCGACCT 240
Qy 241 TCATGCTGGCTAAGAGG 258
Db 241 TCATGCTGGCTAAGAGG 258

RESULT 9

US-09-870-574-1

Sequence 1, Application US/09870574

Patent No. US20020102723A1

GENERAL INFORMATION:

APPLICANT: Gurney, Austin L.

APPLICANT: Aggarwal, Sudeepa

APPLICANT: Xie, Ming-Hong

APPLICANT: Maruoka, Ellen M.

APPLICANT: Foster, Jessica S.

APPLICANT: Goddard, Audrey

APPLICANT: Wood, William I.

TITLE OF INVENTION: INTERLEUKIN-22 POLYPEPTIDES, NUCLEIC ACIDS ENCODING

FILE REFERENCE: P2806-1(US)

CURRENT APPLICATION NUMBER: US/09/870,574

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: US 60/169,495

PRIOR FILING DATE: 1999-12-07

PRIOR APPLICATION NUMBER: PCT/US00/14042

PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: PCT/US00/23328

PRIOR FILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 1

LENGTH: 1152

TYPE: DNA

ORGANISM: Homo Sapien

US-09-870-574-1

Query Match 5.1%; Score 244; DB 11; Length 1152;

Best Local Similarity 100.0%; Pred. No. 1.4e-49;

Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTTGACAGAGGTTCTCTTCCCTCCAGTCACAGTTGCTGCAATTGCTGCAATG 74
Db 1 CTTGACAGAGGTTCTCTTCCCTCCAGTCACAGTTGCTGCAATTGCTGCAATG 60
Qy 75 GCGGCCCTGACAAATCTGTAGCTCTTCTTATGGGACCCCTGGCCACCAAGCTGCTC 134
Db 61 GCGGCCCTGACAAATCTGTAGCTCTTCTTATGGGACCCCTGGCCACCAAGCTGCTC 120
Qy 135 CTTCTCTTGGCCCTCTTGTACAGAGGAGAGAGCTGCGCCATCAGCTCCACTGAGG 194
Db 121 CTTCTCTTGGCCCTCTTGTACAGAGGAGAGAGCTGCGCCATCAGCTCCACTGAGG 180
Qy 195 CTTGACAGGTCACCTTCCAGAGAGCCCTATATACCAACCGACCTTCAATGCTGCTAAG 254
Db 181 CTTGACAGGTCACCTTCCAGAGAGCCCTATATACCAACCGACCTTCAATGCTGCTAAG 240
Qy 255 GAGG 258
Db 241 GAGG 244

RESULT 10

US-10-063-588-153

Sequence 153, Application US/10063588

Publication No. US20030130483A1

GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.

APPLICANT: Filvaroff, Ellen

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,588
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 153
LENGTH: 1152
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-588-153

Query Match 5.1%; Score 244; DB 14; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTTGACAGAGGTTCTCTTCCCTCCAGTCACAGTTGCTGCAATTGCTGCAATG 74
Db 1 CTTGACAGAGGTTCTCTTCCCTCCAGTCACAGTTGCTGCAATTGCTGCAATG 60
Qy 75 GCGGCCCTGACAAATCTGTAGCTCTTCTTATGGGACCCCTGGCCACCAAGCTGCTC 134
Db 61 GCGGCCCTGACAAATCTGTAGCTCTTCTTATGGGACCCCTGGCCACCAAGCTGCTC 120
Qy 135 CTTCTCTTGGCCCTCTTGTACAGAGGAGAGAGCTGCGCCATCAGCTCCACTGAGG 194
Db 121 CTTCTCTTGGCCCTCTTGTACAGAGGAGAGAGCTGCGCCATCAGCTCCACTGAGG 180
Qy 195 CTTGACAGGTCACCTTCCAGAGAGCCCTATATACCAACCGACCTTCAATGCTGCTAAG 254
Db 181 CTTGACAGGTCACCTTCCAGAGAGCCCTATATACCAACCGACCTTCAATGCTGCTAAG 240
Qy 255 GAGG 258
Db 241 GAGG 244

RESULT 11

US-10-006-867-153

Sequence 153, Application US/10006867

Publication No. US20020119130A1

GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.

APPLICANT: Filvaroff, Ellen

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3230R1C1

CURRENT APPLICATION NUMBER: US/10/006,867

CURRENT FILING DATE: 2001-12-06

PRIOR APPLICATION NUMBER: 60/063435

PRIOR FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: 60/064215

PRIOR FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: 60/082797

PRIOR FILING DATE: 1998-04-22

PRIOR APPLICATION NUMBER: 60/083495

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/085579

PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/087759

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/088021

;; PRIOR FILING DATE: 1999-04-16
;; PRIOR APPLICATION NUMBER: 60/131291
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/138387
;; PRIOR FILING DATE: 1999-06-09
;; PRIOR APPLICATION NUMBER: 60/144791
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/169495
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/175481
;; PRIOR FILING DATE: 2000-01-11
;; PRIOR APPLICATION NUMBER: 60/191007
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/199397
;; PRIOR FILING DATE: 2000-04-25
;; PRIOR APPLICATION NUMBER: 09/380139
;; PRIOR FILING DATE: 1998-08-25
;; PRIOR APPLICATION NUMBER: 09/311832
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 09/380137
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380138
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380142

Query Match 5.1%; Score 244; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAACAGGTTCTCTTCCGACGACAGTGTCTGCAAGTATGATGCTGCAATG 74
DB 1 CTTGAGAACAGGTTCTCTTCCGACGACAGTGTCTGCAAGTATGATGCTGCAATG 60
QY 75 GCGGCCCTGAGAAATGTGAGCTCTTCTTATGGGACCTGGCCACAGCTGCTC 134
DB 61 GCGGCCCTGAGAAATGTGAGCTCTTCTTATGGGACCTGGCCACAGCTGCTC 120
QY 135 CTTCTCTGGCCCTCTTGTATGAGGAGGAGAGCAGCTGCGCCATCAGCTCCAGTGCAGG 194
DB 121 CTTCTCTGGCCCTCTTGTATGAGGAGGAGAGCAGCTGCGCCATCAGCTCCAGTGCAGG 180
QY 195 CTTGACAGTCCAACTTCCAGCAGCCTTATATCAACACCGCAGCTTCACTGCTGCTAAG 254
DB 181 CTTGACAGTCCAACTTCCAGCAGCCTTATATCAACACCGCAGCTTCACTGCTGCTAAG 240
QY 255 GAGG 258
DB 241 GAGG 244

RESULT 12
US-10-066-500-125
; Sequence 125, Application US/10066500
; Publication No. US2002017165A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerltzen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Matheer
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni

;; APPLICANT: Margaret Ann Roy
;; APPLICANT: Timothy A. Stewart
;; APPLICANT: Daniel Tumas
;; APPLICANT: Colin K. Watanabe
;; APPLICANT: P. Mickey Williams
;; APPLICANT: William I. Wood
;; APPLICANT: Zemin Zang
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; TITLE OF INVENTION: ACIDS ENCODING THE SAME
;; FILE REFERENCE: P3130R1C7
;; CURRENT APPLICATION NUMBER: US/10/066,500
;; PRIOR FILING DATE: 2002-02-01
;; PRIOR APPLICATION NUMBER: 10/002,796
;; PRIOR FILING DATE: 2001-11-15
;; PRIOR APPLICATION NUMBER: 60/056974
;; PRIOR FILING DATE: 1997-08-26
;; PRIOR APPLICATION NUMBER: 60/059115
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059568
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/062285
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/062816
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063082
;; PRIOR FILING DATE: 1997-10-31
;; PRIOR APPLICATION NUMBER: 60/063329
;; PRIOR FILING DATE: 1997-10-27
;; PRIOR APPLICATION NUMBER: 60/063733
;; PRIOR FILING DATE: 1997-10-29
;; PRIOR APPLICATION NUMBER: 60/066364
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: 60/066840
;; PRIOR FILING DATE: 1997-11-25
;; PRIOR APPLICATION NUMBER: 60/069694
;; PRIOR FILING DATE: 1997-12-16
;; PRIOR APPLICATION NUMBER: 60/074086
;; PRIOR FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: 60/074092
;; PRIOR FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/081049
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/085998
;; PRIOR FILING DATE: 1998-08-10
;; PRIOR APPLICATION NUMBER: 60/097000
;; PRIOR FILING DATE: 1998-08-18
;; PRIOR APPLICATION NUMBER: 60/099601
;; PRIOR FILING DATE: 1998-09-09
;; PRIOR APPLICATION NUMBER: 60/099803
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099811
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099812
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/100858
;; PRIOR FILING DATE: 1998-09-17
;; PRIOR APPLICATION NUMBER: 60/101922
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/106032
;; PRIOR FILING DATE: 1998-10-28
;; PRIOR APPLICATION NUMBER: 60/109304
;; PRIOR FILING DATE: 1998-11-20
;; PRIOR APPLICATION NUMBER: 60/125778
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/139695
;; PRIOR FILING DATE: 1999-06-15
;; PRIOR APPLICATION NUMBER: 60/145070
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145698


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1 PRIOR APPLICATION NUMBER: 09/870574
2 PRIOR FILING DATE: 2001-05-30
3 PRIOR APPLICATION NUMBER: 09/872035
4 PRIOR FILING DATE: 2001-06-01
5 PRIOR APPLICATION NUMBER: 09/886342
6 PRIOR FILING DATE: 2001-06-19
7 PRIOR APPLICATION NUMBER: PCT/US98/14552
8 PRIOR FILING DATE: 1998-07-14
9 PRIOR APPLICATION NUMBER: PCT/US98/18824
10 PRIOR FILING DATE: 1998-03-10
11 PRIOR APPLICATION NUMBER: PCT/US98/19093
12 PRIOR FILING DATE: 1998-09-14
13 PRIOR APPLICATION NUMBER: PCT/US98/19330
14 PRIOR FILING DATE: 1998-09-16
15 PRIOR APPLICATION NUMBER: PCT/US98/19437
16 PRIOR FILING DATE: 1998-09-17
17 PRIOR APPLICATION NUMBER: PCT/US98/24855
18 PRIOR FILING DATE: 1998-11-20
19 PRIOR APPLICATION NUMBER: PCT/US98/25108
20 PRIOR FILING DATE: 1998-12-01
21 PRIOR APPLICATION NUMBER: PCT/US98/25190
22 PRIOR FILING DATE: 1998-11-25
23 PRIOR APPLICATION NUMBER: PCT/US99/05028
24 PRIOR FILING DATE: 1999-03-08
25 PRIOR APPLICATION NUMBER: PCT/US99/12252
26 PRIOR FILING DATE: 1999-06-02
27 PRIOR APPLICATION NUMBER: PCT/US99/20111
28 PRIOR FILING DATE: 1999-09-01
29 PRIOR APPLICATION NUMBER: PCT/US99/20594
30 PRIOR FILING DATE: 1999-09-08
31 PRIOR APPLICATION NUMBER: PCT/US99/21090
32 PRIOR FILING DATE: 1999-09-15
33 PRIOR APPLICATION NUMBER: PCT/US99/21547

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Query Match	5.1%	Score 244;	DB 15;	Length 1152;
Best Local Similarity	100.0%;	Pred. No. 1.4e-49;		
Matches 244; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	15	CTTCAGAAACAGGTTCTCTTCCCAAGTACACAGATTGCTCGATTAGAAATGTCTGCATG	74
Db	1	CTTCAGAAACAGGTTCTCTTCCCAAGTACACAGATTGCTCGATTAGAAATGTCTGCATG	60
QY	75	GCCGCCTCTCAGAAATCTGTGAGCTCTTTCCTATAGGGACCCCTGCGCCACAGCTGCCTC	134
Db	61	GCCGCCTCTCAGAAATCTGTGAGCTCTTTCCTATAGGGACCCCTGCGCCACAGCTGCCTC	122
QY	135	CTTCTCTTGGCCCTCTTGTGTACAGGAGAGACAGCTGGGCCATCAGTCCCACTGCAGG	199
Db	121	CTTCTCTTGGCCCTCTTGTGTACAGGAGAGACAGCTGGGCCATCAGTCCCACTGCAGG	180
QY	195	CTTGCACAGTCCCACTTCAGAGAGCCATATACCAACGCACCTTCATGCTGGCTAG	254
Db	181	CTTGCACAGTCCCACTTCAGAGAGCCATATACCAACGCACCTTCATGCTGGCTAG	240
QY	255	GAGG 258	
Db	241	GAGG 244	

RESULT 13
US-10-063-547-153

; Sequence 153, Application US/10063547
; Publication No. US20020182638A1
CENTRAL INTELLIGENCE

GENERAL INFORMATION:

APPLICANT: Filvaco

APPLICANT: Gerrit

APPLICANT: Goddard

APPLICANT: Godowsk

APPLICANT: Gilmartin

APPLICANT: Watanabe

APPLICANT: Wood, wi

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 153
LENGTH: 1152
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-547-153

Query Match 5.1%; Score 244; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAACAGGTTCTCTCCAGTGCAGGAGTGTGAGTGAATTGTCTGCATG 74
DB 1 CTTGAGAACAGGTTCTCTCCAGTGCAGGAGTGTGAGTGAATTGTCTGCATG 60
QY 75 GCCGCCCTGCAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGGCCACAGCTGCCTC 134
DB 61 GCCGCCCTGCAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGGCCACAGCTGCCTC 120
QY 135 CTTCTCTTGGCCCTCTTGTGTAACAGGAGAGAGAGCTGGCCCATCATGCTCCACTGCAGG 194
DB 121 CTTCTCTTGGCCCTCTTGTGTAACAGGAGAGAGAGCTGGCCCATCATGCTCCACTGCAGG 180
QY 195 CTTGACAGTCCAACTTCCAGAGCCCTATATACCAACCGACCTTATGCTGCTAG 254
DB 181 CTTGACAGTCCAACTTCCAGAGCCCTATATACCAACCGACCTTATGCTGCTAG 240
QY 255 GAGG 258
DB 241 GAGG 244

RESULT 14

US-10-063-616-153
Sequence 153, Application US/10063616
Publication No. US20030013855A1
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,616
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 153
LENGTH: 1152
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-616-153

Query Match 5.1%; Score 244; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAACAGGTTCTCTCCAGTGCAGGAGTGTGAGTGAATTGTCTGCATG 74
DB 1 CTTGAGAACAGGTTCTCTCCAGTGCAGGAGTGTGAGTGAATTGTCTGCATG 60

QY 75 GCCGCCCTGCAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGGCCACAGCTGCCTC 134
DB 61 GCCGCCCTGCAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGGCCACAGCTGCCTC 120
QY 135 CTTCTCTTGGCCCTCTTGTGTAACAGGAGAGAGAGCTGGCCCATCATGCTCCACTGCAGG 194
DB 121 CTTCTCTTGGCCCTCTTGTGTAACAGGAGAGAGAGCTGGCCCATCATGCTCCACTGCAGG 180
QY 195 CTTGACAGTCCAACTTCCAGAGCCCTATATACCAACCGACCTTATGCTGCTAG 254
DB 181 CTTGACAGTCCAACTTCCAGAGCCCTATATACCAACCGACCTTATGCTGCTAG 240
QY 255 GAGG 258
DB 241 GAGG 244

RESULT 15

US-10-063-502-153
Sequence 153, Application US/10063502
Publication No. US20030023042A1
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,502
CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 153
LENGTH: 1152
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-502-153

Query Match 5.1%; Score 244; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAACAGGTTCTCTCCAGTGCAGGAGTGTGAGTGAATTGTCTGCATG 74
DB 1 CTTGAGAACAGGTTCTCTCCAGTGCAGGAGTGTGAGTGAATTGTCTGCATG 60
QY 75 GCCGCCCTGCAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGGCCACAGCTGCCTC 134
DB 61 GCCGCCCTGCAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGGCCACAGCTGCCTC 120
QY 135 CTTCTCTTGGCCCTCTTGTGTAACAGGAGAGAGAGCTGGCCCATCATGCTCCACTGCAGG 194
DB 121 CTTCTCTTGGCCCTCTTGTGTAACAGGAGAGAGAGCTGGCCCATCATGCTCCACTGCAGG 180
QY 195 CTTGACAGTCCAACTTCCAGAGCCCTATATACCAACCGACCTTATGCTGCTAG 254
DB 181 CTTGACAGTCCAACTTCCAGAGCCCTATATACCAACCGACCTTATGCTGCTAG 240
QY 255 GAGG 258
DB 241 GAGG 244

Search completed: July 20, 2003, 03:46:16
Job time : 692.702 secs

Db 301 ATCCAAATAGTCTTAACTTTCTTCAGAGCATCTCTAAGACCTTTAGAAACCCACTGT 360
Qy 361 TTAATCCCTGAGGATAGATAAATTTCTGTCTTTTCAGAGACCTCTTGGGAATCGCTT 420
Db 361 TTAATCCCTGAGGATAGATAAATTTCTGTCTTTTCAGAGACCTCTTGGGAATCGCTT 420
Qy 421 TTTTCTTTCTGAACTTCT 480
Db 421 TTTTCTTTCTGAACTTCT 480
Qy 481 CCCAAGAGCGGCGCATTCAGTAATCCATCTGATGATTTTCTCTCTCTCTCTCTCTCT 540
Db 481 CCCAAGAGCGGCGCATTCAGTAATCCATCTGATGATTTTCTCTCTCTCTCTCTCTCT 540
Qy 541 CATGTTCTTAACTACATGACACATGATGATCTGATTTAGCTTTATGATGATGCTCT 600
Db 541 CATGTTCTTAACTACATGACACATGATGATCTGATTTAGCTTTATGATGATGCTCT 600
Qy 601 GGGGAGACGGGATGGGGACATGTCATGTAATTAATTTTCTATTTTCTCAATGCTC 660
Db 601 GGGGAGACGGGATGGGGACATGTCATGTAATTAATTTTCTATTTTCTCAATGCTC 660
Qy 661 AGACCTTATGCTTTTCT 720
Db 661 AGACCTTATGCTTTTCT 720
Qy 721 TCTCATTTGGGGAGAACTGTCTCCAGGAGCTGATGATGATGATGATGATGATGATG 780
Db 721 TCTCATTTGGGGAGAACTGTCTCCAGGAGCTGATGATGATGATGATGATGATGATG 780
Qy 781 CCGTGTGCCGTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Db 781 CCGTGTGCCGTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Qy 841 TGAACCTTTCTGTTTCCCTTCCACCTGACATGATGATGATGATGATGATGATGATG 900
Db 841 TGAACCTTTCTGTTTCCCTTCCACCTGACATGATGATGATGATGATGATGATGATG 900
Qy 901 GTGCTGAATCTTCACTTGAAGAGTGTGCTGCTCAATCTGATGATGATGATGATGATG 960
Db 901 GTGCTGAATCTTCACTTGAAGAGTGTGCTGCTCAATCTGATGATGATGATGATGATG 960
Qy 961 ATGACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 961 ATGACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Qy 1021 TGAAGCTCTAGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 1080
Db 1021 TGAAGCTCTAGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 1080
Qy 1081 CCCAATCT 1140
Db 1081 CCCAATCT 1140
Qy 1141 TGTATCAGAGTCAATTTGGGATCATGAGATATTTGCTTTGCTTTGCTTTGCTTTGCT 1200
Db 1141 TGTATCAGAGTCAATTTGGGATCATGAGATATTTGCTTTGCTTTGCTTTGCTTTGCT 1200
Qy 1201 TTGAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
Db 1201 TTGAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
Qy 1261 TCTTTCGAAAAAGGCACTCAGGTGCTGATGATGATGATGATGATGATGATGATGATG 1320
Db 1261 TCTTTCGAAAAAGGCACTCAGGTGCTGATGATGATGATGATGATGATGATGATGATG 1320
Qy 1321 GCTGTGAAATGATCATTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Db 1321 GCTGTGAAATGATCATTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Qy 1381 ATTAGAAGAAAGTGGGAAATGGGAAAGCTTAAATCGGTGCTGCTGCTGCTGCTGCT 1440

Db 1381 ATTAGAAGAAAGTGGGAAATGGGAAAGCTTAAATCGGTGCTGCTGCTGCTGCTGCT 1440
Qy 1441 GCCCTGTGATGTCATGGAAGCCCAAAATCGAGGGCTGTAATCTGATCCGCTGAA 1500
Db 1441 GCCCTGTGATGTCATGGAAGCCCAAAATCGAGGGCTGTAATCTGATCCGCTGAA 1500
Qy 1501 CATTTGAAACTATGAAAAAAGTTTGAATGATGATGATGATGATGATGATGATGATGAT 1560
Db 1501 CATTTGAAACTATGAAAAAAGTTTGAATGATGATGATGATGATGATGATGATGATGAT 1560
Qy 1561 ACTGAAGAGGCTTAAATTTTCAATGATGATGATGATGATGATGATGATGATGATGATG 1620
Db 1561 ACTGAAGAGGCTTAAATTTTCAATGATGATGATGATGATGATGATGATGATGATGATG 1620
Qy 1621 CAATTTCTGAGATACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
Db 1621 CAATTTCTGAGATACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
Qy 1681 CTCTTTCCAAATGCAAACTCAGTATGATGATGATGATGATGATGATGATGATGATGAT 1740
Db 1681 CTCTTTCCAAATGCAAACTCAGTATGATGATGATGATGATGATGATGATGATGATGAT 1740
Qy 1741 AGGGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
Db 1741 AGGGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
Qy 1801 TGTGAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
Db 1801 TGTGAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
Qy 1861 ACTGATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
Db 1861 ACTGATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
Qy 1921 CTTGTTATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Db 1921 CTTGTTATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Qy 1981 AAGCTGAAGACACAGTGAAGAAAGTGAAGATGATGATGATGATGATGATGATGATGAT 2040
Db 1981 AAGCTGAAGACACAGTGAAGAAAGTGAAGATGATGATGATGATGATGATGATGATGAT 2040
Qy 2041 AGGAGAGCAAAATGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2100
Db 2041 AGGAGAGCAAAATGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2100
Qy 2101 CTTGATTTCTCTACCAAGGAGGCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2160
Db 2101 CTTGATTTCTCTACCAAGGAGGCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2160
Qy 2161 TATCTAGATGCTAGTTTCCAAATCTTGAATTTGAAATTTGAAATCTGATGATGATGAT 2220
Db 2161 TATCTAGATGCTAGTTTCCAAATCTTGAATTTGAAATTTGAAATCTGATGATGATGAT 2220
Qy 2221 TAGCTTGTCTAGTCAATTAATCTGATGATGATGATGATGATGATGATGATGATGATG 2280
Db 2221 TAGCTTGTCTAGTCAATTAATCTGATGATGATGATGATGATGATGATGATGATGATG 2280
Qy 2281 GAATGAGGCTCTCTGAAATCCCAAGCAGACTTTTCCCGGTGATGATGATGATGATGAT 2340
Db 2281 GAATGAGGCTCTCTGAAATCCCAAGCAGACTTTTCCCGGTGATGATGATGATGATGAT 2340
Qy 2341 TGTGACATTAATTTCTTGAAGAAATTTGATGATGATGATGATGATGATGATGATGATG 2400
Db 2341 TGTGACATTAATTTCTTGAAGAAATTTGATGATGATGATGATGATGATGATGATGATG 2400
Qy 2401 TACTTGTTTAAAAACAGAAAAATGCTTATGCTTATGATGATGATGATGATGATGATGAT 2460
Db 2401 TACTTGTTTAAAAACAGAAAAATGCTTATGCTTATGATGATGATGATGATGATGATGAT 2460
Qy 2461 CATTAATCATGCTTTGAAATTTGAAAGAAATTAATCTGAAATGATGATGATGATGATGAT 2520
Db 2461 CATTAATCATGCTTTGAAATTTGAAAGAAATTAATCTGAAATGATGATGATGATGATGAT 2520

QY 2521 ACTGCATATAGGGCTAATTTCTGGAGTATATAACATTAATTTGATATATATATATC 2580
Db 2521 ACTGCATATAGGGCTAATTTCTGGAGTATATAACATTAATTTGATATATATATATC 2580
QY 2581 TATGCATATATAGTATATAGTTTAAAGACAGACAGACACACCCGATCTCTTTATACG 2640
Db 2581 TATGCATATATAGTATATAGTTTAAAGACAGACAGACACACCCGATCTCTTTATACG 2640
QY 2641 GTTCAATATAGTATATATATATAGTATATATATATATATATATATATATATAT 2700
Db 2641 GTTCAATATAGTATATATATATATAGTATATATATATATATATATATATATAT 2700
QY 2701 GGTAAAGCTTTTCTTCTCTCTCTCCATCAAGACCTTCATTTAGTTTCTTCTTCA 2760
Db 2701 GGTAAAGCTTTTCTTCTCTCTCTCCATCAAGACCTTCATTTAGTTTCTTCTTCA 2760
QY 2761 CTCCCTCAACAATCCCTAGGGAGATTTATCATAGTGGGCTGGTGTATATATATAG 2820
Db 2761 CTCCCTCAACAATCCCTAGGGAGATTTATCATAGTGGGCTGGTGTATATATATAG 2820
QY 2821 TGAATGATACCATCATATGAGCTATTTGGTGAAGAAACAAATGAAAGCTTAGACTA 2880
Db 2821 TGAATGATACCATCATATGAGCTATTTGGTGAAGAAACAAATGAAAGCTTAGACTA 2880
QY 2881 ACAATAGTACTACCCCAAAACCGAGAGATGATTAAGAGCAGTGAAGCTCTT 2940
Db 2881 ACAATAGTACTACCCCAAAACCGAGAGATGATTAAGAGCAGTGAAGCTCTT 2940
QY 2941 GCAAGCAGTCACTAATTAATCTCAGAAACATGAAGCTCCAGTTGATGAATTTTCAGT 3000
Db 2941 GCAAGCAGTCACTAATTAATCTCAGAAACATGAAGCTCCAGTTGATGAATTTTCAGT 3000
QY 3001 AACAGCTTAACCTTAATTTCCCTTTTCCCTCTGACTTTTAAAGAGCTTCTTC 3060
Db 3001 AACAGCTTAACCTTAATTTCCCTTTTCCCTCTGACTTTTAAAGAGCTTCTTC 3060
QY 3061 CTGAGCATCAATTAATGAGTGTACTGTTCTTCTGATTAATGAAGCTTTGAGT 3120
Db 3061 CTGAGCATCAATTAATGAGTGTACTGTTCTTCTGATTAATGAAGCTTTGAGT 3120
QY 3121 TTAATTTGAAAGCCAGTCTCTGTTTATAGAACTATATATATATATATATATAT 3180
Db 3121 TTAATTTGAAAGCCAGTCTCTGTTTATAGAACTATATATATATATATATATAT 3180
QY 3181 TGTAGCATGCAAGACAGACATCTTACACATCTTCTTAATAAATATCTGATTTTC 3240
Db 3181 TGTAGCATGCAAGACAGACATCTTACACATCTTCTTAATAAATATCTGATTTTC 3240
QY 3241 ATCTTGTCTTGTCTTTAGAAAAGTGAAGTGAAGAGAGAAATCTCATGTATCTG 3300
Db 3241 ATCTTGTCTTGTCTTTAGAAAAGTGAAGTGAAGAGAGAAATCTCATGTATCTG 3300
QY 3301 TGTGATTTTCAAGACCTTTATCCATTTTGAAGAAATCAATTTCAATTTGCAATGGT 3360
Db 3301 TGTGATTTTCAAGACCTTTATCCATTTTGAAGAAATCAATTTCAATTTGCAATGGT 3360
QY 3361 GCAATGTGGAAGAGTATATGCTTTTCTGAGTCTTCAAGAGCAGAGAGAGAGA 3420
Db 3361 GCAATGTGGAAGAGTATATGCTTTTCTGAGTCTTCAAGAGCAGAGAGAGAGA 3420
QY 3421 GCAATGTGTCAGAGAAAGATCAACAGAGAGAGAACTGTCAAGCTGTCTGAATAG 3480
Db 3421 GCAATGTGTCAGAGAAAGATCAACAGAGAGAGAACTGTCAAGCTGTCTGAATAG 3480
QY 3481 GTGGTTTGGAGGATTAATTTCTCTCTGTTGGGGTAAAGCAGAAAGCTGTTGTA 3540
Db 3481 GTGGTTTGGAGGATTAATTTCTCTCTGTTGGGGTAAAGCAGAAAGCTGTTGTA 3540
QY 3541 GTAAATGATGACAGACAGTGGGAGCAATTAATCTTTAAATTTCTTTATAGCTTGGAG 3600
Db 3541 GTAAATGATGACAGACAGTGGGAGCAATTAATCTTTAAATTTCTTTATAGCTTGGAG 3600

QY 3601 TCTTGAATAGAAAAGATATCTTTTGGCTTATGTCAAAAGAGATGAAAAGTGA 3660
Db 3601 TCTTGAATAGAAAAGATATCTTTTGGCTTATGTCAAAAGAGATGAAAAGTGA 3660
QY 3661 AAGGCGGAGAAAAGCAGAAAAGAAAGAACATATATATATAGAGACATGTTGACA 3720
Db 3661 AAGGCGGAGAAAAGCAGAAAAGAAAGAACATATATATATAGAGACATGTTGACA 3720
QY 3721 AGGTTTCTTGAATATGCAAAATATGATATATAGAGAAATTTCACTAGGAAATGCTT 3780
Db 3721 AGGTTTCTTGAATATGCAAAATATGATATATAGAGAAATTTCACTAGGAAATGCTT 3780
QY 3781 TTTCACTTAATTTGGGTTTCTCTCTCATTTAAGTTGGGATCCCATCTGATTTGACTT 3840
Db 3781 TTTCACTTAATTTGGGTTTCTCTCTCATTTAAGTTGGGATCCCATCTGATTTGACTT 3840
QY 3841 GAGAGAGAAAAGATGATATGATAGACCTATATCTGTTTCTTAACTAAGCAATG 3900
Db 3841 GAGAGAGAAAAGATGATATGATAGACCTATATCTGTTTCTTAACTAAGCAATG 3900
QY 3901 GAAAAGCTTATTTGATATTTTCCACAAAAGTAAAACTTTCTTTACTGTTGTCA 3960
Db 3901 GAAAAGCTTATTTGATATTTTCCACAAAAGTAAAACTTTCTTTACTGTTGTCA 3960
QY 3961 AAAAGGTGAAATGAAAAGCCTTAATGTTTGGTGAATACATGTTCAAGTCAATTTG 4020
Db 3961 AAAAGGTGAAATGAAAAGCCTTAATGTTTGGTGAATACATGTTCAAGTCAATTTG 4020
QY 4021 AGTAGAGATGTTTAAATCAGAGAGTGCATCATTTGGCTCCCTGAGCACTTGA 4080
Db 4021 AGTAGAGATGTTTAAATCAGAGAGTGCATCATTTGGCTCCCTGAGCACTTGA 4080
QY 4081 GAATTTCTTGGTACACATATAAATCAAGAACATAGTATAGCTTAATAAAGTCA 4140
Db 4081 GAATTTCTTGGTACACATATAAATCAAGAACATAGTATAGCTTAATAAAGTCA 4140
QY 4141 TGCATTAATCTCATCTGTTTAAAGAAATTTGATTAATTTGTTAGGCTCATTAAG 4200
Db 4141 TGCATTAATCTCATCTGTTTAAAGAAATTTGATTAATTTGTTAGGCTCATTAAG 4200
QY 4201 CTGTCCTGGGCGATGCGGCGCTGGGGCTGAGGCTGAGGAGCTCTTAAAGTATC 4260
Db 4201 CTGTCCTGGGCGATGCGGCGCTGGGGCTGAGGCTGAGGAGCTCTTAAAGTATC 4260
QY 4261 TGTATAGATAGTTTGGAGCTGCAAAAACAGGCAAGCATATAGGCTGAGCTGGAT 4320
Db 4261 TGTATAGATAGTTTGGAGCTGCAAAAACAGGCAAGCATATAGGCTGAGCTGGAT 4320
QY 4321 CCCCAGATCCCAAGCTTCACTTCACTCTCTGCTTGTGTTAAGAGGGTGTCAATC 4380
Db 4321 CCCCAGATCCCAAGCTTCACTTCACTCTCTGCTTGTGTTAAGAGGGTGTCAATC 4380
QY 4381 TCTGCCAGCTTTTAAACAGCTTATAGTGTGAGAGTGCACCTGAATTTGATGCTGCTG 4440
Db 4381 TCTGCCAGCTTTTAAACAGCTTATAGTGTGAGAGTGCACCTGAATTTGATGCTGCTG 4440
QY 4441 GTGGCTCTCAGTCCAGAGACCGTCAATTTTAACTCTTTGGAACATCATCAATACTTA 4500
Db 4441 GTGGCTCTCAGTCCAGAGACCGTCAATTTTAACTCTTTGGAACATCATCAATACTTA 4500
QY 4501 AGGATATTAATGAAATGTTTCAAAATGCTTAAATCGGTTTGTCTCTCAATCAAC 4560
Db 4501 AGGATATTAATGAAATGTTTCAAAATGCTTAAATCGGTTTGTCTCTCAATCAAC 4560
QY 4561 TAACTTGCATTTCTAATTTGCTCACTTTGAAGAAACATGAGCAATTAATGCTCAATCTT 4620
Db 4561 TAACTTGCATTTCTAATTTGCTCACTTTGAAGAAACATGAGCAATTAATGCTCAATCTT 4620
QY 4621 TTGATTTCTTATTTTCAAGCTTGAAGAGATGAGATCAAAAGCAATTTGAGAACTGG 4680
Db 4621 TTGATTTCTTATTTTCAAGCTTGAAGAGATGAGATCAAAAGCAATTTGAGAACTGG 4680
QY 4681 ATTTGCTGTTTATGCTCTGAGAAATGCTGCAATTTGACACAGACAAAAGCTGAAAATGA 4740

Db 4661 ATTGCTGTTATGCTCTGAGAAATGCTGATTGACAGAGCAAGCTGAAAAATGA 4740
Qy 4741 ATAATAACCCCTTCCCTGCTAGAAATTAACATTAAGTCCCAAGCATTTT 4797
Db 4741 ATAATAACCCCTTCCCTGCTAGAAATTAACATTAAGTCCCAAGCATTTT 4797

RESULT 2
US-09-354-243B-25

; Sequence 25, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
; APPLICANT: Dumoulier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renaud, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
; TITLE OF INVENTION: (TlFe)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.1
; CURRENT APPLICATION NUMBER: US/09/354,243B
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 25
; LENGTH: 4797
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-354-243B-25

Query Match 100.0%; Score 4797; DB 4; Length 4797;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 4797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACAGCAGAAATCTTCAGAACAGGTTCTCTCCCTCCAGTCACAGATTGCTGAGTTAG 60
Db 1 TGCACAGCAGAAATCTTCAGAACAGGTTCTCTCCCTCCAGTCACAGATTGCTGAGTTAG 60
Qy 61 AATTGCTGCAATGCGCGCCCTGCAAGAAATCTGTAGCTCTTCTCTTATGAGGAGCCCTGG 120
Db 61 AATTGCTGCAATGCGCGCCCTGCAAGAAATCTGTAGCTCTTCTCTTATGAGGAGCCCTGG 120
Qy 121 CCACAGAGTCCCTCTCTCTTCTGAGCCCTCTTGTAGAGGAGAGAGAGCTGAGCCATCA 180
Db 121 CCACAGAGTCCCTCTCTCTTCTGAGCCCTCTTGTAGAGGAGAGAGAGCTGAGCCATCA 180
Qy 181 GCTCCCACTGCAAGGCTTGAACAAGTCCAACTTCAGAGCCCTATATACCAACCCACCT 240
Db 181 GCTCCCACTGCAAGGCTTGAACAAGTCCAACTTCAGAGCCCTATATACCAACCCACCT 240
Qy 241 TCATGTGGCTAAGAGGATATCATCTCAATCTGCTCTTCTGCTGATCTACTTGA 300
Db 241 TCATGTGGCTAAGAGGATATCATCTCAATCTGCTCTTCTGCTGATCTACTTGA 300
Qy 301 ATCCAAATAGTCTTAACTTCTTTCAGAGCATCTTAAGAGCTTTAGAAACCACTGT 360
Db 301 ATCCAAATAGTCTTAACTTCTTTCAGAGCATCTTAAGAGCTTTAGAAACCACTGT 360
Qy 361 TTAATCCCTGAGGATATTAATTTCTGTTTTTTCAGAGACTCTTTGGAAATCTGCTTT 420
Db 361 TTAATCCCTGAGGATATTAATTTCTGTTTTTTCAGAGACTCTTTGGAAATCTGCTTT 420
Qy 421 TTTTCTGTAAGCTTCTCTCTGATTTTGGCCCTTATGATACATATGATGAAATTTT 480
Db 421 TTTTCTGTAAGCTTCTCTCTGATTTTGGCCCTTATGATACATATGATGAAATTTT 480
Qy 481 CCCAAAGAGCGGCATTCAGTAATTCATGTGATGATTTTCTTTATGCTCTG 540
Db 481 CCCAAAGAGCGGCATTCAGTAATTCATGTGATGATTTTCTTTATGCTCTG 540
Qy 541 CATGTCTTAACATCATGACACATCTGAATCTGCTTTAGCTTTATGATGCTCTCT 600

Db 541 CATGTCTTAACATCATGACACATCTGAATCTGCTTTTATGCTTTATGATGCTCTCT 600
Qy 601 GGGAGAGCGGATGGGACACATGCTATGTAATAATTTTTTCTATTTGCTCAATGCC 660
Db 601 GGGAGAGCGGATGGGACACATGCTATGTAATAATTTTTTCTATTTGCTCAATGCC 660
Qy 661 AGACCTTAGTCTTTTCTCTCTTCCAGGCTAGCTTGGCTATACCAACAGACCTTCG 720
Db 661 AGACCTTAGTCTTTTCTCTCTTCCAGGCTAGCTTGGCTATACCAACAGACCTTCG 720
Qy 721 TCTGATGGGAGAAACGTTCCACGAGATGATGTAAGTACATCAAGTTGACAGAG 780
Db 721 TCTGATGGGAGAAACGTTCCACGAGATGATGTAAGTACATCAAGTTGACAGAG 780
Qy 781 CCGTGTGCGGTCACATGAGTACTTGGGAGTGTGATGATGATTTAGCTTATCTCTTA 840
Db 781 CCGTGTGCGGTCACATGAGTACTTGGGAGTGTGATGATGATTTAGCTTATCTCTTA 840
Qy 841 TGACCTTTCTGTTTCCCTTCCACCTGCAATGATGAGCCCTGCTATCTGATGAGAG 900
Db 841 TGACCTTTCTGTTTCCCTTCCACCTGCAATGATGAGCCCTGCTATCTGATGAGAG 900
Qy 901 GTGCTGAATCTCACCTTGAAGAGTGTGCTTCCCTCAATCTGATGATGATGAGCTTAT 960
Db 901 GTGCTGAATCTCACCTTGAAGAGTGTGCTTCCCTCAATCTGATGATGATGAGCTTAT 960
Qy 961 ATGACAGAGTGTGAGCCCTTCTGCGCAGGCTCAGCAACAGAGCTTAAGCATACTAGT 1020
Db 961 ATGACAGAGTGTGAGCCCTTCTGCGCAGGCTCAGCAACAGAGCTTAAGCATACTAGT 1020
Qy 1021 TCAGCTCAGACCTATGCGCACTTACAGGCTTCCCTCTTCCCTTCCACAGAGACCCCTTAC 1080
Db 1021 TCAGCTCAGACCTATGCGCACTTACAGGCTTCCCTCTTCCCTTCCACAGAGACCCCTTAC 1080
Qy 1081 CCCAACTCTCTCTCTTCCCTTACCCCTTACCCCTTACAGAGAGAAAGTCTTGGAGAG 1140
Db 1081 CCCAACTCTCTCTCTTCCCTTACCCCTTACCCCTTACAGAGAGAAAGTCTTGGAGAG 1140
Qy 1141 TGTATCAGAGTCAATTTGGATCATAGATATTTGCTTTGCTTTGACTAGTACATC 1200
Db 1141 TGTATCAGAGTCAATTTGGATCATAGATATTTGCTTTGCTTTGACTAGTACATC 1200
Qy 1201 TTGATTTATAGTGTGATGATGGGATCTGGAATTAAGTGAACAGACCGCATTTG 1260
Db 1201 TTGATTTATAGTGTGATGATGGGATCTGGAATTAAGTGAACAGACCGCATTTG 1260
Qy 1261 TCTTCGAAAAAAGGCACTCAGGTTGCTGAATGAGAAAGGCTTTGGAAAAACATCTA 1320
Db 1261 TCTTCGAAAAAAGGCACTCAGGTTGCTGAATGAGAAAGGCTTTGGAAAAACATCTA 1320
Qy 1321 GCTGTGAAATGATCCATTAGTCTTAAGTGTGAGAGGAGAGGATGCAATGAGAGAA 1380
Db 1321 GCTGTGAAATGATCCATTAGTCTTAAGTGTGAGAGGAGAGGATGCAATGAGAGAA 1380
Qy 1381 ATTGAAGAGAAAGTGGGAAATGGGAGCTTAAAGTCTGCTGCTGCGACATGCTT 1440
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Db 1501 CATTTGAATCATGAAAAAAGTTTGAATGAGTGGGCGCAGTAAAGGCGCTAGACTT 1560
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Db 1561 ACTGAAGAGGCTTAATTTTCAATGATGATGTTTATGATCAATTTCTGTTTAAAGCTG 1620
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DB 4741 ATTAATCAACCCCTTTTCTGCTGTAAGAAATACATTTGATGCCCCCAAGGATTTT 4797

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RESULT 3
 US-09-178-973B-8
 ; Sequence 8, Application US/09178973B
 ; Patent No. 6274710
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumoutier, Laure
 ; APPLICANT: Louhed, Jamila
 ; APPLICANT: Renaud, Jean-Christophe

```

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fe
; TITLE OF INVENTION: (Title)
; FILE REFERENCE: LUD 5543
; CURRENT APPLICATION NUMBER: US/09/178,973B
; CURRENT FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 8
; LENGTH: 7445
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-178-973B-8

Query Match 14.3% Score 686; DB 4; Length 7445;
Best Local Similarity 53.8%; Pred. No. 1.3e-182;
Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;

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DB 2034 CTCCTCTCCTACTATACAACTTTGACACTTTGCGATCTGATGCTGTCTGAGAA 2093
QY 89 ATCTGAGCTCTTCTCTTATGAGGACCTGCGCACACAGCTGCTTCTCTGGCCCT 148
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QY 149 CTGTGACAGGAGAGACAGCTGCGCCCATGACCTCCACTGAGGCTTGACAGTCCAA 208
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Db 4701 TTTCT 4752
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Db 6644 TGCTCTTCTGCTCTTCTTCAAAAGACATATAGATCCCTGAATGAACTTTT 6695

RESULT 4
US-09-419-568F-8
Sequence 8, Application US/09419568F
Patent No. 6331613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Renauld, Jamila
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419, 568F
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354, 243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178, 973
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 8

LENGTH: 7445
 TYPE: DNA
 ORGANISM: Mus musculus
 FEATURE:
 US-09-419-568F-8

Query Match 14.3% Score 686; DB 4; Length 7445;
 Best Local Similarity 53.8%; Pred. No. 1,3e-182;
 Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;

QY 29 CTCCTTCCCGATCACCAGTTGCTCGAGTTAGATTGCTGCAATGAGCCGCCCTGCAGAA 88
 Db CTCCTCTCACTTATTAACCTGTTGACATGTGCGCATCTCTATGCTCTCTGCGAGAA 2093
 QY 89 ATCTGAGCTCTTTCTTTATGGGAGCCTGGCCACAGCTGCTCTCTTTGGCCCT 148
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 QY 149 CTGTGTAAGAGGAGGAGCAGCTGGCCCATCAGCTCCACCTGCAGGCTTGACAGTCAA 208
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 QY 209 CTTCAGCAGCCCTATATACCAACGCACTTCATGCTGAGTAAAGAGTATCATCTC 268
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 QY 269 AATCTGCTCTTCTGCTGATCTACTTGAATCCAAATAGTTCTTAACTTTCTTCA 328
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 QY 329 GAGCATCTCAAGAGCTTGAAGAACCACTGTTTATCCCTGAGGATGATAATTTCTG 388
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 QY 389 TTTTTCAGAGCATCTTTGGGAATCTGGCTTTTCTTTTCTTGAATCTCTCTTCAT 448
 Db ACTCTTAAAGACCTGGCTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2442
 QY 449 TTTGGCTTTATGATACATATGATGATTTTTCCTCAAGAGCGGCACTTCAGTATCAT 508
 Db CTGGCTTCAGAGCATATCTGATTTTATCTACAGAGGCGCATTT--AGAAAGCCA 2500
 QY 509 CTGATGATTTTCTTCTTATGCTCTGCTGCTGATGTTCTTAACTATGACATCATCTG 568
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 QY 809 GGTGTGATGATGTTAGTCTTATCTCTTATGACCCCTTCTGTTTCCCTTCCACTGC 868
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 QY 1821 TGGGCAAAATTAAGAGCTTAAATTCAGAGTGAATTTAGTATCTTCAATGGGTG 1880
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 Db CATCAGGATGAGACCAAGATCTCCAGAAATGTCAAGAAAGCTGAAGAGCAAGTGA 3933

QY	2001	AAAGGTGAGCTAGTAATACCTGCAATGCTAGTATGCAATGAGAGAGCAAAATGTTT	2060
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Db	4051	TTTCTCTGCTTCCAGTCCCTTCTACTTTGTACATTTTATTTGACTCTGTCTACTATCTG	4110
QY	2121	GGCGATTA---CTTGGGTCTGTGTATGTATGATATATCTATATATCTAGATGTCA	2176
Db	4111	GTCCATTACTGCTTACTGCTGACCTGATCTAGGTGGGTCTATGATCTTTCAATCTGTG	4170
QY	2177	TCCAAATCTTGCAAAATGTAGAAATTTCTAGAACTGTGGGATCTTACTGCTCTAGTCAC	2236
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QY	2237	ATTAACCTCAGATTCTGGGAGATGTGCATGTGGAGAGATAGGGCTGTAGTGCAGGCTCTG	2296
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QY	2297	AATCCCAAGCCAGCACTTTTCCCGGTGTATACAGATTAGTTTGTGTACCAATTAATCT	2356
Db	4288	ATTCCCAAGCTGTGAC--TTGCTATGTGGCCATGTGTAACTTGTGGCTGATTAAGTAT	4346
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Db	4347	TTGGGAAA--GCCAGTTTCCACGGAGCTTACATCTGAAAGAACATGCAATTGAAAATA	4404
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QY	2769	ACAAATCCCTTAGGAGCATTTATCATGATGTGGGTGGGTGATCATTTCTATATGTAATGAT	2828
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QY	3006	GCTTAACCTTAATTTCCCTTTTCCCTTGTGACTTTTAAAAAAAGCTTTCTTCTGAG	3065
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QY 2347 CATTAATCTTAGGAAATTTCAAGTTCCTATTGACTCATGTAACTGAAAGACTCTTG 2406
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RESULT 7
 US-09-419-568F-29
 ; Sequence 29, Application US/09419568F
 ; Patent No. 6331613
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumoutier, Laure
 ; APPLICANT: Louned, Jamila

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; APPLICANT: Renault, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
; TITLE OF INVENTION: (Tifs) The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.2
; CURRENT APPLICATION NUMBER: US/09/419.568F
; PRIOR APPLICATION NUMBER: US09/354,243
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO: 29
; LENGTH: 5935
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; US-09-419-568F-29

Query Match          13.6%; Score 650; DB 4; Length 5935;
Best Local Similarity 56.5%; Pred. No. 1.5e-112;
Matches 1863; Conservative 0; Mismatches 1285; Indels 152; Gaps 29;

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QY 1631 GAGATCAATGATGATGATTTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1690
| | | | |
Db 1918 GAGGTTAAGCTCAGGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1956
| | | | |
QY 1691 AAATGCAAACTCAGTAGATTTTCCAAAGATGAGAGAGTCTTCTTCTTCTTCTTCTTCT 1750
| | | | |
Db 1957 TGTGAGAACTTCTCAGTAGATTTTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAG 2016
| | | | |
QY 1751 CTGATTTCTGCTCTCAAGAGAAATTCAAGAGCTCAGAGAAATTCTAGTCTCTTGAATC 1810
| | | | |
Db 2017 CTGATTTCTCAGTCTCTTCAAGAGAAAGAAATGCTCAGAGAAATTCTAGTCTCTTGAATC 2076
| | | | |
QY 1811 TAGGATTTGCTGAGAGAAATTCTAGAGCTTATTTCTCAGGAGTGAATGATGATCTC 1870
| | | | |
Db 2077 AGGTCAAGGAGGAGAAATGATGAGAGCTCTTATTTCTCAGGAGTGAATGATGATCTC 2136
| | | | |

QY 1871 CATGCTGTGAGAGTTTATTAAGTTTCAGACAAATTAGATGATGATGATGATGATGATG 1930
| | | | |
Db 2137 AGATATATCTAGGATTTGGGCTCCACAGGATTAAGATTTCTGTTAGTA-GTCTGCTTTA 2195
| | | | |
QY 1931 TTTATATGATATTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1990
| | | | |
Db 2196 TTTTTCAGACATCTAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2255
| | | | |
QY 1991 ACACATGAAAAAGTATGAG 2050
| | | | |
Db 2256 AGACATGAAAAAGTATGAG 2315
| | | | |
QY 2051 AATGTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2110
| | | | |
Db 2316 GGGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2373
| | | | |
QY 2111 CTACACAGAGGAGAT---ACTTGTGCTGCTGATGATGATGATGATGATGATGATGATGAT 2166
| | | | |
Db 2374 CTACTGTGTGCTCATTTACTCATTTACTGATGATGATGATGATGATGATGATGATGAT 2433
| | | | |
QY 2167 GATGCTGATTTCCAAATCTTGCAGAAATTGAGAAATTCTAGAACTGTTGGGATCTTAGCTT 2226
| | | | |
Db 2434 TCAATCTGTGCTTAAATTT---GTAAGTCAAAATCTGAGCTGAGAGAGAGAGAGAGAG 2490
| | | | |
QY 2227 GTCTAGTCAATACCTCAGATTTCTGGGAGTGTGATGAGAGAGATGAGGCTGAGATGC 2286
| | | | |
Db 2491 AGCAGTCTCAGTGCAGCTTGTGAGAGAGGCTTGTGAGAGAGTCAATCTGAGAGAG 2550
| | | | |
QY 2287 AGGTCTCTGAAATCCCAAGCAGCAGCTTTTCCGCTGTGATGATGATGATGATGATGATG 2346
| | | | |
Db 2551 AGCATCTCTGATTTCCAGCTCTGAC-TTGGTATGCTGAGAGAGAGAGAGAGAGAGAG 2609
| | | | |
QY 2347 CATTAATCTTGAAGAAATTTGATGATCTTATGATGATGATGATGATGATGATGATGAT 2406
| | | | |
Db 2610 GATTAAGATTTGGGAAA---GCCAATTTCCACACCATCAATTTCCGAGAGAGAGAGAG 2466
| | | | |
QY 2407 TTTTAAAAAGAAAAATGCTTATGAGGAAATTTTGAAGTCAATTTTGAAGTCAATTTTGA 2466
| | | | |
Db 2668 TTGAAAACTGAAAA---GCTGGGACAAATTTCTGAGAGAGATTTTGAAGTCAATTTTGA 2723
| | | | |
QY 2467 TGCAATGCTTGAAGTCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2526
| | | | |
Db 2724 ACTGATGCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2783
| | | | |
QY 2527 ATATAGGCTTAATTTCTGAGTAAATTAACCTTAT-----TTGATTTATCTAATA 2578
| | | | |
Db 2784 AAATAGGCAAGTATTTAGATCACTGATTTAAGCTGATCACTTATTTAATAATATAG 2843
| | | | |
QY 2579 TCT---ATCAGATATGATTTATGATTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 2634
| | | | |
Db 2844 TGTCTATTTTACTGCTTATTTAAGATTAACAGAGAGAGAGAGAGAGAGAGAGAGAG 2903
| | | | |
QY 2635 ATACAGGTTCAATAGAGTAAATTAATAGTAAAGATTTTATAGTAAATGAGAGTCT 2694
| | | | |
Db 2904 GGCCTGTTTCAATAGAGTAAATTAATAGTAAATGATTTATAGTAAATGAGAGTCT 2963
| | | | |
QY 2695 TGAATGTAAGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2754
| | | | |
Db 2964 TGAATGTAAGC---CTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3020
| | | | |
QY 2755 CTTTCTCTCTCTCAAGAAATCCCTAGAGAGATTTATCCATGAGTGTGATGATGATGAT 2814
| | | | |
Db 3021 TCTTCAACCTCTGATCAAGCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3080
| | | | |
QY 2815 CTATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2872
| | | | |
Db 3081 TTACAGCAAAACATTTCTGCTGTGCTCTTTTGGGAGAGAGAGAGAGAGAGAGAGAG 3140
| | | | |
QY 2873 TTAGACTAACAA-TAGTACTCACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2931
| | | | |
Db 3141 TCAGGCTGCAAGTGTGAGTCAACCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3200
| | | | |
QY 2932 GACGCTCTT-GCAAGCAGTACACTAATAATCTAGAAACATGAGAGCTCCAGTGTAGG 2990
| | | | |

DB 3201 GAGGCTTACAGAGGCTGCTGCTTACGATATACAGAAAGGCTGCTGATGAG 3260
QY 2991 AATTTTCAGTAACAAGCTTACCTTATATCCCTTTTCCCTCTGACTTTTAAAAA 3050
DB 3261 AATTATCAGTAAGATATCAACCTTATCTCC-----TTCTTCTATAGAGTAACGG 3313
QY 3051 GGGTTTCTTCTGAGCATATTTATGAGTGTGACTGTTTCTTTGATTAATGAGG 3110
DB 3314 TCTCTCTTCTTGTGTGTGAGGCTGATAAACAGCTTTGT--TTCTTTTGAAGTGTATG 3371
QY 3111 CTTTGAATTTAAATGTGAAGCCAGTCTCTTGTATAGAAATATATCAGACAG 3170
DB 3372 CTTTGAAGATTTTCAAGTGTCTGCGAGTCTTGT--TAAGAGTTTGTATCACTGACCC 3429
QY 3171 GAGGCTGATGTAGATGACCAACAGACAGGATGCTTTACATCTTGTCTTAAATAAT 3230
DB 3430 TGGGCTTGATGTAGATGACCAAGGACACACTTGTGATGCTGTGTAAGATGAT 3489
QY 3231 TACTGATTTTCACTTGTGCTTGTCTTTAGAAAAAGTGAAGTGAAGAGAGATCTCA 3290
DB 3490 TATTCATTTACT-----TTGCTTTGAAAGTGAAGTGTGTGAAGAAAGATCA 3541

RESULT 8
US-09-354-243B-29
Sequence 29, Application US/09354243B
Patent No. 6359117
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
TITLE OF INVENTION: (title)
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 29
LENGTH: 5935
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-354-243B-29

Query Match 13.6%; Score 650; DB 4; Length 5935;
Best Local Similarity 56.5%; Pred. No. 1,5e-172;
Matches 1863; Conservative 0; Mismatches 1285; Indels 152; Gaps 29;

QY 29 CTCCTTCCCAGTACACAGTGTCTGAGTGAATGTCTGCAATGCGCCCTGCAAA 88
DB 356 CTCCTCTCAGTATACACTTTTGAACCTTGTGCAATCGTATGCTGTCTCTGAGAA 415
QY 89 ATGTGAGCTCTTTTCTTATGAGGACCTGCGCACAGCTGCTCTCTTGTGGCCCT 148
DB 416 ATCTAAGATTTTCCCTTAATGAGGACTTTGGCCGCACTGCTGTCTTCTCATATGCCCT 475
QY 149 CTGTGATACAGGAGGAGAGCTGCGCATCAGCTCCCATGCAAGGCTTGAACAATCCAA 208
DB 476 GTGGGCCCCAGAGGCAATGCGCTGCCATCAACCCGCTGCAAGTTAGAGTGTCCA 535
QY 209 CTTTCAAGACCCCTATATACCAACCGACCTTCACTGCTGCTAAGAGGATATACATCTC 268
DB 536 CTTTCAAGACCCCTATATACCAACCGACCTTCACTGCTGCTAAGAGGATATACATCTC 595
QY 269 AATCTGCTCTTCTCTGCTGAGATCTACTTGAATCCAAATAGTTCTTAACTTTCTTCA 328
DB 596 TCTCTTCTCTCATACCGGCTTGCATTTCTGGAAGCACTTGCAAACTTTTAAAGGGGC 655
QY 329 GAGCATCTTAAGAGCTTGAAGAACCACTGTTATCCCTGAGGCTGATTAATTTTCTG 388

DB 656 GCTTTATCTCCGACGCTCACTACCTATGTTTTCTGTCT-----CTTAAAG 703
QY 389 TTTTTCAGAGACTCTTTGGGAATCTGACTTTTCTTTTCTTGAACCTTCTCTTCAT 448
DB 704 ACTCTTAAAGACTGATCTTTTCTATTTCTATTTCAAGGCTCAGACCATTTCTCAT 763
QY 449 TTTGGCTTTATGATATCATATGATTAATTTTCCAAAGAGGGCATTCAGTATCAT 508
DB 764 CTGGCCTTCAAGACATATCTGAATTTTATCTACAGAGGGGGTTC--AGAAAGCA 821
QY 509 CTGATATTTTCTTCCCTTATATGCTGCTGATCTGTTCTTAACTCATGACATCTG 568
DB 822 CCGACACTGCAATCTTTCATCTGTTGTGCTCTCTTCAATCATCTCTTGGC 881
QY 569 AATCTGCTTTTATGCTTTATGATGCTGTCTGAGAGACGGGATGGGACATGTAT 628
DB 882 TACTC-----CTGAGACCACTGGGACATATCATCTCTAC 916
QY 629 GTATTAATTTTCTTATTTGCTCAATGCTCAGACCTTATCTTTCTTCTCCAG 688
DB 917 TTACAGGCTTTCTTCCATCTCTCTGTACCCAGGCACTTATGAGTTTTC--TCTCTTCAG 975
QY 689 GCTACCTTGGCTGATTAACAACAAGCTGCTCATTTGGGAGAACTGTCCACGGA 748
DB 976 GCCAGCCTTGACAGATTAACAACAAGCTGCTCATGCGGAGAACTGTCCAGGA 1035
QY 749 GTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 808
DB 1036 GTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1082
QY 809 GGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 868
DB 1083 GGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1138
QY 869 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 928
DB 1139 AGGCTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1198
QY 929 TGTTCCTCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 988
DB 1199 TGTTCCTCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1258
QY 989 GGTCAAGCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1048
DB 1259 AACTAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1318
QY 1049 CTCCTTCCCTCTTCCACAGAGACCCCTTACCCCACTCTCTCTCTCTCTCTCTCTCTCT 1108
DB 1319 CTCCTTCCCTCTTCCACAGAGACCCCTTACCCCACTCTCTCTCTCTCTCTCTCTCTCT 1378
QY 1109 TAAAGTACAGAGAAAGTGTCTTGGCAGCACTGTATACAGAGTCA-----TTTGGG 1161
DB 1379 GGAAGGCTCAGACACACACACATATAGGCCACTTGAATATGTCACAAAGCTTGGC 1438
QY 1162 ATCATGAGATATTTGCTTGTGCTTGTGCTGATGATGATGATGATGATGATGATGATGAT 1221
DB 1439 TTTCAATGATATTAATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1498
QY 1222 GGGTCTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1281
DB 1499 AGAAATCAACTCAATTTCTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1558
QY 1282 AGGTTCGATA--GATGAGAAAGTGTGGGAAACATCTAGCTGTGAAATGATGATCA 1338
DB 1559 AGAGAAACAGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1618
QY 1339 TTGAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1398
DB 1619 CTGAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1678
QY 1399 AATGAGAAAGCTTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1450

1679 AATGACACAGACAAAAGTTGAAGGAAGAGAGATGAGAGGCTCATGTTGGGG 1738
1451 TGTGATGGGAGCCCAAAAATCGAGAGCGTGTGAATGATGCCCTGAAATTGAAAC 1510
1739 TGTGAAAGGTCACTCTTTTCCATGTGATGAGAGATTGAAGAAAATGAGTGTAGTT 1798
1511 TATGAAAAAAGTTGATGAGAGAGTGGCCCAAGAAAAGCCCTAGAGACTTACTGAAGAG 1570
1799 TATGTCTTCAACACCCCACTAGTGGAGACTGGGAGACTGGCACTTTAGGGA-AGG 1857
1571 GCTTAATTTTCAATGAGATGTTTATGATGATGATGATGATGATGATGATGATGATG 1630
1858 CCGGCTTTTCAACAGAGAACTTTATGCTCATCTTGTGCTGCTGCTGCTGCTGCTGCT 1917
1631 GAGATACGATGAGGTTTATCTTACAGAAATTGCAATAACTACTGCGCTTTTCCAC 1690
1918 GAGGTAACTGAGGTTTCTGTTCT-----ACCGTCTTCTAC 1956
1691 AATGCAAACTCTAGTGAATTTCCCAAGATGAGAGAGTCTCTTGTGAGGAAGTA 1750
1957 TGGTGAAGAACTTCAAGTGAATTTCCCAAGAGAGAGAGTCTCTTGTGAGGAAGTA 2016
1751 CTGAGATCTGGGCTCCAGAGGAATTGAAGGCTCAGAAATCTAGGTCATGTTGAATC 1810
2017 CTGAGATCTGGGCTCCAGAGGAATTGAAGGCTCAGAAATCTAGGTCATGTTGAATC 2076
1811 TAGGTCATTTGGGCAAAATTAATAAGCTTTAATTTCCAGTGAATTTGATCTGATCTC 1870
2077 AGGTCAACAGGCGCAAAATTAATAAGCTTTAATTTCCAGTGAATTTGATCTGATCTC 2136
1871 CATGGGTGAGAGTTTCAATAACTTCAAGACAACTAATGATGATGATGATGATGATG 1930
2137 AGATATAGAGGATATGGGCTCCCAAGGATTAATCTGTTAGTA-GTCTGCTTTTA 2195
1931 TTTTATAGATATTTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATG 1990
2196 TTTTGAAGACATCACTGATGAGACCAAGCAATCAAGAAATGTCAGAGGCTGAAAG 2255
1991 ACACAGTGAAGAAAGTGAAGTGAATGATGATGATGATGATGATGATGATGATGATG 2050
2256 AGACAGTGAAGAAAGTGAAGTGAATGATGATGATGATGATGATGATGATGATGATG 2315
2051 AATGTTGTTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2110
2316 GGGATTTCTTCT 2373
2111 CTACCAAGGAGGATTT---ACTTGGTGTCTGTGTATGATGATGATGATGATGATGATG 2166
2374 CTACTGTCTGTCTCACTTACTCACTTACTGACCTGACCTGACCTGACCTGACCTGAC 2433
2167 GATGTCAGTTTCAAAATTTGCAAAATTTGTAAGATTTGTAAGATTTGTAAGATTTG 2226
2434 TCATCTGTCTCAAAATTT---GTAACTCAAAATTTGTAAGATTTGTAAGATTTG 2490
2227 GTCTACTCATTAACCTCAGATTTCTGGGATGCTGAGTGCAGAGTGAAGGCTGAAGTC 2286
2491 AGCCAGTCTCATGAGACTTGTCTGGAGATGCTTGTGACAGAGTCAATGCTGAAGAC 2550
2287 AGGTCTCTGATTTCCCAAGCAGACTTTTCCCGGTGTGTATCAAGATTAAGTTTGTG 2346
2551 AGCATCTCTGATTTCCCAAGCAGACTTGTGACAGAGTCAATGCTGAAGAC 2609
2347 CATTAATTTCTAGGAAATTTGATTTCTTATGATGATGATGATGATGATGATGATG 2406
2610 GATTAAGTATTTGGGAAA--GCCAATTTCCCAAGCAGCTTATATTCGAAAGACATGCA 2667
2407 TTTAAAAACAGAAAAATGCTATGAGCAATTTATTTGAAGTCAATTTTGAATCAATTA 2466
2668 TTGAAAACTAGAAA-----GCTGGGCAAACTTACTAGAGATATTTTGAAGTCAATTA 2723
2467 TGATATGCTTTGAAGTCTGGAAGATTAATCAAGAAATGAGAAAAAGCTGAGATGCTG 2526
2724 ACTGATGCTCTGAAATGTGATCAAAATCAACCCAGAAATTAACAAAGAAAGCTGATTTGC 2783

2527 AATAGGCTAATTTCTGAGTAAATAACCTTAT-----TTTGAATTATCATATA 2578
2784 AATAGGCAAGTATTTGAATCACTGATTTAAAGCTGTCATCTTATTAATAATAG 2843
2579 TCT---ATCAGATATGATTAATGATTTAAAGCAAGCAGACAC-CCCGATCTCTTT 2634
2844 TGTCTATTTAGTGTCTTATTTAGATTTAAACCAAGAGTGAATTAATTTCCATTTAG 2903
2635 ATACAGTTCATTAATGATTAATAATATTAAGTGAAGATTTATTAATGATTAATGAG 2694
2904 GCGCTGTTTCAATAGATTAATAATATGATGATTAATTAATGATGATGATGATGATG 2963
2695 TGAATTTGATGATTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2754
2964 TGAATTTGATGATTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3020
2755 CCTGATCTCTCAACAAATCCCTGAGGAGCTTATGATGATGATGATGATGATGATGATG 2814
3021 TCTTCAACCTGATTAAGCACTGATTAAGCACTGATGATGATGATGATGATGATGATG 3080
2815 CTATAGTATGATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2872
3081 TTACAGCAAAACATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3140
2873 TTAGACTAACA--TAGTACTACCCCAACCGAGATGATTTAGAGCTGATGAT 2931
3141 TCAGGCTAGCAAGTCTGACCTCAACCTTAAGCCAGAGGCTGATGATGATGATGATG 3200
2932 GAGGCTCTT--GCAACAGGTATCAATAATATCTCAAGAAACATGAAGGCTCCAGTTGATG 2990
3201 GAGGCTCTTCAACAGT 3260
2991 AATTTAGTATCAAGATTAACCTTAATTTCCCTTTTCCCTCTGATCTTTTAAATAA 3050
3261 AATTTAGTATCAAGATTAACCTTAATTTCCCTTTTCCCTCTGATCTTTTAAATAA 3313
3051 GCGTCTCTCTGAGCATATTTAATGATGATGATGATGATGATGATGATGATGATGATG 3110
3314 TCTCTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3371
3111 CTTTGATTTTAAATTTGGAAGCCAGTCTCTGTTATGAACTATTAATGATGATGATG 3170
3372 CTTTGAGATTTTCAAGT 3429
3171 GAGGCTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3230
3430 TGGGCTTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3489
3231 TACTGATTTTCACTTGT 3290
3490 TATCTATTACT-----TTGTCTTGAAGGATGATGATGATGATGATGATGATGATGATG 3541

RESULT 9
US-09-419-568F-24
; Sequence 24, Application US/09419568F
; Patent No. 6331613
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
; FILE REFERENCE: LND 5543.2
; CURRENT APPLICATION NUMBER: US/09/419,568F
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US09/354,243
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 24

LENGTH: 690
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 US-09-419-568F-24

Query Match 5.4%; Score 258; DB 4; Length 690;
 Best Local Similarity 100.0%; Pred. No. 1.1e-62;
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACAGAGAAATCTTCAGAACAGGTTCTCTCCCAATCAGCAAGTCTGAGTTAG 60
 DB 1 TGCACAGAGAAATCTTCAGAACAGGTTCTCTCCCAATCAGCAAGTCTGAGTTAG 60
 QY 61 AATTGCTGCAATGGCCGCGCTGCAAGAAATCTGTGAGCTTTCTTATGGGAGCCCTGG 120
 DB 61 AATTGCTGCAATGGCCGCGCTGCAAGAAATCTGTGAGCTTTCTTATGGGAGCCCTGG 120
 QY 121 CCACCAAGCTGCTCTCTCTCTTGGCCCTCTTGTATACAGGAGAGCAAGCTGCCCATCA 180
 DB 121 CCACCAAGCTGCTCTCTCTCTTGGCCCTCTTGTATACAGGAGAGCAAGCTGCCCATCA 180
 QY 181 GCTCCACTGACAGGCTTGAAGTCAAGTCCAGAGAGCCCTATATCAACCAAGGACCT 240
 DB 181 GCTCCACTGACAGGCTTGAAGTCCAGAGAGCCCTATATCAACCAAGGACCT 240
 QY 241 TCATGCTGCTAAGAGG 258
 DB 241 TCATGCTGCTAAGAGG 258

RESULT 10

US-09-354-243B-24
 ; Sequence 24, Application US/09354243B
 ; Patent No. 6359117

GENERAL INFORMATION:
 APPLICANT: Dumoutier, Laure
 APPLICANT: Louhed, Jamila
 APPLICANT: Renaud, Jean-Christophe
 TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
 TITLE OF INVENTION: (TIFFS) The Proteins Encoded, and Uses Thereof
 FILE REFERENCE: LUD 5543.1
 CURRENT APPLICATION NUMBER: US/09/354,243B
 CURRENT FILING DATE: 1999-07-16
 PRIOR APPLICATION NUMBER: US09/178,973
 PRIOR FILING DATE: 1998-10-26
 NUMBER OF SEQ ID NOS: 29
 SEQ ID NO 24
 LENGTH: 690
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 US-09-354-243B-24

Query Match 5.4%; Score 258; DB 4; Length 690;
 Best Local Similarity 100.0%; Pred. No. 1.1e-62;
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACAGAGAAATCTTCAGAACAGGTTCTCTCCCAATCAGCAAGTCTGAGTTAG 60
 DB 1 TGCACAGAGAAATCTTCAGAACAGGTTCTCTCCCAATCAGCAAGTCTGAGTTAG 60
 QY 61 AATTGCTGCAATGGCCGCGCTGCAAGAAATCTGTGAGCTTTCTTATGGGAGCCCTGG 120
 DB 61 AATTGCTGCAATGGCCGCGCTGCAAGAAATCTGTGAGCTTTCTTATGGGAGCCCTGG 120
 QY 121 CCACCAAGCTGCTCTCTCTCTTGGCCCTCTTGTATACAGGAGAGCAAGCTGCCCATCA 180
 DB 121 CCACCAAGCTGCTCTCTCTCTTGGCCCTCTTGTATACAGGAGAGCAAGCTGCCCATCA 180
 QY 181 GCTCCACTGACAGGCTTGAAGTCAAGTCCAGAGAGCCCTATATCAACCAAGGACCT 240
 DB 181 GCTCCACTGACAGGCTTGAAGTCCAGAGAGCCCTATATCAACCAAGGACCT 240

DB 181 GCTCCACTGACAGGCTTGAAGTCAAGTCCAGAGAGCCCTATATCAACCAAGGACCT 240
 QY 241 TCATGCTGCTAAGAGG 258
 DB 241 TCATGCTGCTAAGAGG 258

RESULT 11
 US-09-178-973B-9
 ; Sequence 9, Application US/09178973B
 ; Patent No. 6274710

GENERAL INFORMATION:
 APPLICANT: Dumoutier, Laure
 APPLICANT: Louhed, Jamila
 APPLICANT: Renaud, Jean-Christophe
 TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
 TITLE OF INVENTION: (TIFFS) The Proteins Encoded, and Uses Thereof
 FILE REFERENCE: LUD 5543
 CURRENT APPLICATION NUMBER: US/09/178,973B
 CURRENT FILING DATE: 1998-10-26
 NUMBER OF SEQ ID NOS: 17
 SEQ ID NO 9
 LENGTH: 1111
 TYPE: DNA
 ORGANISM: Mus musculus
 US-09-178-973B-9

Query Match 2.7%; Score 127.6; DB 4; Length 1111;
 Best Local Similarity 72.2%; Pred. No. 8.3e-26;
 Matches 166; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 29 CTCCTTCCCAGTCAACAGTCTGAGTTAGAAATTTCTGCATATGCGCCCTGCAGAA 88
 DB 7 CTCCTCTCAAGTATCAACTTTTGAACATTTGGCATGGATGGCTGCTGCAGAA 66
 QY 89 ATCTGTGAGCTCTTTCTTATATGGGAGCCCTGGCCACCACTGCTCTTCTTGGCCCT 148
 DB 67 ACTATGAGTTTTCCTTATATGGGAGCTTTGGCCGCGCACCTGCTCTTCTATTCCTCT 126
 QY 149 CTGTGACAGGAGAGGAGGAGCTGCGCCATCACTGCCACTGAGAGCTGACAAATCCAA 208
 DB 127 GTGGGCGCAGAGGAGCAATGCGCTGCCATCAACACCCGGTGAAGGTGTCAA 186
 QY 209 CTTCAGAGCCCTATATCAACCAACCGCACTTCATGCTGAGTAAAGAG 258
 DB 187 CTTCAGAGCCGATATGTCACCGCACCTTTATGCTGGCCAAAGAGG 236

RESULT 12
 US-09-419-568F-9
 ; Sequence 9, Application US/09419568F
 ; Patent No. 6331613

GENERAL INFORMATION:
 APPLICANT: Dumoutier, Laure
 APPLICANT: Louhed, Jamila
 APPLICANT: Renaud, Jean-Christophe
 TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
 TITLE OF INVENTION: (TIFFS) The Proteins Encoded, and Uses Thereof
 FILE REFERENCE: LUD 5543.2
 CURRENT APPLICATION NUMBER: US/09/419,568F
 CURRENT FILING DATE: 1999-10-18
 PRIOR APPLICATION NUMBER: US09/354,243
 PRIOR FILING DATE: 1999-07-16
 PRIOR APPLICATION NUMBER: US09/178,973
 PRIOR FILING DATE: 1998-10-26
 NUMBER OF SEQ ID NOS: 29
 SEQ ID NO 9
 LENGTH: 1111
 TYPE: DNA
 ORGANISM: Mus musculus
 US-09-419-568F-9

Query Match 2.7%; Score 127.6; DB 4; Length 1111;
Best Local Similarity 72.2%; Pred. No. 8.3e-26;
Matches 166; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

29 CTCCTCCCAAGTCCAGTGTCTGAGTGAATTGCTGCATATGGCCGCTGCAGAA 88
7 CTCCTCTCAGTTATCACTTTTGACCTGTGGGATGGTGAAGGCTGTCTGCAGAA 66
89 ATCTGTAGCTCTTTCTTATGGGAGACCTTGCCACAGCTGCTCTTCTTTGGCCCT 148
67 ATCTATAGTTTTCCTTATGGGAGCTTTGGCCGACGCTGCTCTTCTATTTGCCCT 126
149 CTGGTACAGGAG 208
127 GTGGGCCAGGAG 186
209 CTCACAG 258
187 CTCACAG 236

RESULT 13

US-09-354-243B-9
Sequence 9, Application US/09354243B
Patent No. 6359117

GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
TITLE OF INVENTION: (Tifs)
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-354-243B-9

Query Match 2.7%; Score 127.6; DB 4; Length 1111;
Best Local Similarity 72.2%; Pred. No. 8.3e-26;
Matches 166; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

29 CTCCTCCCAAGTCCAGTGTCTGAGTGAATTGCTGCATATGGCCGCTGCAGAA 88
7 CTCCTCTCAGTTATCACTTTTGACCTGTGGGATGGTGAAGGCTGTCTGCAGAA 66
89 ATCTGTAGCTCTTTCTTATGGGAGACCTTGCCACAGCTGCTCTTCTTTGGCCCT 148
67 ATCTATAGTTTTCCTTATGGGAGCTTTGGCCGACGCTGCTCTTCTATTTGCCCT 126
149 CTGGTACAGGAG 208
127 GTGGGCCAGGAG 186
209 CTCACAG 258
187 CTCACAG 236

RESULT 14
US-09-178-973B-7
Sequence 7, Application US/09178973B
Patent No. 6274710
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure

APPLICANT: Louhed, Jamila
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
TITLE OF INVENTION: (Tifs)
FILE REFERENCE: LUD 5543
CURRENT APPLICATION NUMBER: US/09/178,973B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 7
LENGTH: 1119
TYPE: DNA
ORGANISM: Mus musculus
US-09-178-973B-7

Query Match 2.6%; Score 126; DB 4; Length 1119;
Best Local Similarity 71.7%; Pred. No. 2.3e-25;
Matches 165; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

29 CTCCTCCCAAGTCCAGTGTCTGAGTGAATTGCTGCATATGGCCGCTGCAGAA 88
9 CTCCTCTCAGTTATCACTTTTGACCTGTGGGATGGTGAAGGCTGTCTGCAGAA 68
89 ATCTGTAGCTCTTTCTTATGGGAGACCTTGCCACAGCTGCTCTTCTTTGGCCCT 148
69 ATCTATAGTTTTCCTTATGGGAGCTTTGGCCGACGCTGCTCTTCTATTTGCCCT 128
149 CTGGTACAGGAG 208
129 GTGGGCCAGGAG 188
209 CTCACAG 258
189 CTCACAG 238

RESULT 15

US-09-419-568F-7
Sequence 7, Application US/09419568F
Patent No. 6331613

GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
TITLE OF INVENTION: (Tifs)
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 7
LENGTH: 1119
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-419-568F-7

Query Match 2.6%; Score 126; DB 4; Length 1119;
Best Local Similarity 71.7%; Pred. No. 2.3e-25;
Matches 165; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

29 CTCCTCCCAAGTCCAGTGTCTGAGTGAATTGCTGCATATGGCCGCTGCAGAA 88
9 CTCCTCTCAGTTATCACTTTTGACCTGTGGGATGGTGAAGGCTGTCTGCAGAA 68
89 ATCTGTAGCTCTTTCTTATGGGAGACCTTGCCACAGCTGCTCTTCTTTGGCCCT 148
69 ATCTATAGTTTTCCTTATGGGAGCTTTGGCCGACGCTGCTCTTCTATTTGCCCT 128